

TABLE 1: GENES IN THE APPLICATION

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXN03097	VV0062	3	557	AMMONIUM TRANSPORT SYSTEM
3	4	RXA02099	GR00630	6198	6470	AMMONIUM TRANSPORT SYSTEM
5	6	RXA00104	GR00014	15895	16650	CYSQ PROTEIN, ammonium transport protein

## Polyketide Synthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
7	8	RXA01420	GR00416	775	17	4"-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.3.1.1)
9	10	RXN02581	VV0098	30482	28623	POLYKETIDE SYNTHASE
11	12	F RXA02581	GR00741	1	1527	POLYKETIDE SYNTHASE
13	14	RXA02582	GR00741	1890	6719	PROBABLE POLYKETIDE SYNTHASE CY338.20
15	16	RXA01138	GR00318	1656	2072	ACTINORHODIN POLYKETIDE DIMERASE (EC 2.3.1.1)
17	18	RXA01980	GR00573	1470	838	POLYKETIDE CYCLASE
19	20	RXN01007	VV0021	2572	866	FRNA
21	22	RXN00784	VV0103	27531	28265	FRNE

## Fatty acid and lipid synthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXA02335	GR00672	550	2322	BIOTIN CARBOXYLASE (EC 6.3.4.14)
25	26	RXA02173	GR00641	7473	8924	ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA (EC 6.4.1.2)
27	28	RXA01764	GR00500	2178	3110	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
29	30	RXN02487	VV0007	6367	4664	LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3)
31	32	F RXA02487	GR00718	4937	4650	LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3)
33	34	F RXA02490	GR00720	817	5	LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3)
35	36	RXA01467	GR00422	920	1210	ACYL CARRIER PROTEIN
37	38	RXA00796	GR00212	202	5	Acyl carrier protein phosphodiesterase
39	40	RXA01897	GR00544	617	1159	Acyl carrier protein phosphodiesterase
41	42	RXN02809	VV0342	380	6	Acyl carrier protein phosphodiesterase
43	44	F RXA02809	GR00790	277	5	Acyl carrier protein phosphodiesterase
45	46	RXN00113	VV0129	103	5724	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41;
47	48	F RXA00113	GR00017	2	3295	FATTY-ACID SYNTHASE (EC 2.3.1.85)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
49	50	RXN03111	VV0084	6040	5	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
51	52	F RXA00158	GR00024	2088	4	FATTY ACID SYNTHASE (EC 2.3.1.85)
53	54	F RXA00572	GR00155	2	3832	FATTY ACID SYNTHASE (EC 2.3.1.85)
55	56	RXA02582	GR00741	1890	6719	PROBABLE POLYKETIDE SYNTHASE CY338.20
57	58	RXA02691	GR00754	15347	14541	FATTY ACYL RESPONSIVE REGULATOR
59	60	RXA00880	GR00242	6213	8057	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
61	62	RXA01060	GR00296	9566	10489	OMEGA-3 FATTY ACID DESATURASE (EC 1.14.99.-)
63	64	RXN01722	VV0036	2938	1214	MEDIUM-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.-)
65	66	F RXA01722	GR00488	5746	4022	MEDIUM-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.-)
67	68	RXA01644	GR00456	9854	8577	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (EC 2.1.1.79)
69	70	RXA02029	GR00618	356	1669	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (EC 2.1.1.79)
71	72	RXA01801	GR00509	3396	2380	ENOYL-COA HYDRATASE (EC 4.2.1.17)
73	74	RXN02512	VV0171	16147	15185	LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (EC 2.3.1.-)
75	76	F RXA02512	GR00721	3303	4259	LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (EC 2.3.1.-)
77	78	RXA00899	GR00245	1599	2864	CARDIOLIPIN SYNTHETASE (EC 2.7.8.-)
79	80	RXN00819	VV0054	18127	19455	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
81	82	F RXA00819	GR00221	18	1007	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
83	84	F RXA01766	GR00500	4081	4371	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
85	86	RXN01762	VV0054	15318	13783	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
87	88	F RXA01762	GR00500	1272	10	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
89	90	RXA00681	GR00179	3405	2662	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
91	92	RXA00802	GR00214	3803	4516	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
93	94	RXA02133	GR00639	3	308	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
95	96	RXN01114	VV0182	9118	10341	3-KETOACYL-COA THIOLASE (EC 2.3.1.16)
97	98	F RXA01114	GR00308	2	793	3-KETOACYL-COA THIOLASE (EC 2.3.1.16)
99	100	RXA01894	GR00542	1622	2476	PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41)
101	102	RXA02599	GR00742	3179	3655	PHOSPHATIDYLGLYCEROPHOSPHATASE B (EC 3.1.3.27)
103	104	RXN02638	VV0098	54531	53656	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
105	106	F RXA02638	GR00749	8	511	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
107	108	RXA00856	GR00232	720	1256	CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
109	110	RXA02511	GR00721	2621	3277	CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
111	112	RXN02836	VV0102	32818	33372	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
113	114	F RXA02836	GR00827	106	411	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
115	116	RXA02578	GR00740	2438	3541	PUTATIVE ACYLTRANSFERASE
117	118	RXA02150	GR00639	18858	19658	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
119	120	RXA00607	GR00160	1869	2249	POLY(3-HYDROXYALKANOATE) POLYMERASE (EC 2.3.1.-)
121	122	RXA02397	GR00698	1688	2683	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-)
123	124	RXN03110	VV0083	16568	17929	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
125	126	F RXA00660	GR00171	1027	5	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
127	128	RXA00801	GR00214	3138	3770	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
129	130	RXA00821	GR00221	1469	2311	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
131	132	RXN02966	VV0143	12056	13462	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
133	134	F RXA01833	GR00517	1666	260	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
135	136	RXA01853	GR00525	5561	5010	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)

137	RXN02424	VV0116	10570	11169	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
139	F RXA02424	GR00706	808	428	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
141	RXN00419	VV0112	1024	266	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
143	F RXA00419	GR00095	3	464	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
145	F RXA00421	GR00096	565	723	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
147	RXN02923	VV0088	3301	2564	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
149	RXN02922	VV0321	11407	10328	ACYL-COA DEHYDROGENASE, SHORT-CHAIN SPECIFIC (EC 1.3.99.2)
151	RXN03065	VV0038	6237	6629	Holo-acyl-carrier protein] SYNTHASE (EC 2.7.8.7)
153	RXN03132	VV0127	39053	39472	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-)
155	RXN03157	VV0188	1607	1170	LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN KDTB (AE000805) LPS biosynthesis RfbU related protein [Methanobacterium thermoautotrophicum]
157	RXN00934	VV0171	15181	14099	ACYL-COA DEHYDROGENASE, SHORT-CHAIN SPECIFIC (EC 1.3.99.2)
159	RXN00792	VV0321	10328	9132	ACYL-COA THIOESTERASE II (EC 3.1.2.-)
161	RXN00931	VV0171	13011	12166	thioesterase II
163	F RXA00931	GR00253	4959	4114	ACYLTRANSFERASE (EC 2.3.1.-)
165	RXN01421	VV0122	16024	15638	BIOTIN--[ACETYL-COA-CARBOXYLASE] SYNTHETASE (EC 6.3.4.15)
167	RXN02342	VV0078	3460	4266	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
169	RXN00563	VV0038	1	2739	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
171	RXN02168	VV0100	2894	81	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
173	RXN01090	VV0155	6483	5686	Lipopolysaccharide N-acetylglucosaminyltransferase
175	RXN02062	VV0222	3159	1990	Lipopolysaccharide N-acetylglucosaminyltransferase
177	RXN02148	VV0300	16561	17703	Lipopolysaccharide N-acetylglucosaminyltransferase
179	RXN02595	VV0098	11098	9935	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
181	RXS00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)
183	RXS00149	VV0167	7995	9842	LIPOATE-PROTEIN LIGASE A (EC 6.-.-.-)
185	RXS02106	VV0123	22649	21594	LIPOATE-PROTEIN LIGASE B (EC 6.-.-.-)
187	RXS01746	VV0185	934	1686	LIPOIC ACID SYNTHETASE
189	RXS01747	VV0185	1826	2869	protein involved in lipid metabolism
191	RXC01748	VV0185	3001	3780	Cytosolic Protein involved in lipid metabolism
193	RXC00354	VV0135	33604	32792	Membrane Spanning Protein involved in lipid metabolism
195	RXC01749	VV0185	3953	5569	

Fatty acid degradation

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
197	198	RXA02268	GR00655	2182	3081	LIPASE (EC 3.1.1.3)
199	200	RXA02269	GR00655	3094	4065	LIPASE (EC 3.1.1.3)
201	202	RXA01614	GR00449	8219	7197	LYSOPHOSPHOLIPASE L2 (EC 3.1.1.5)
203	204	RXA01983	GR00573	3559	3053	LIPASE (EC 3.1.1.3)
205	206	RXN02947	VV0078	1319	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
207	208	F RXA02320	GR00667	593	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
209	210	F RXA02851	GR00851	524	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
211	212	RXN02321	VV0078	3291	1663	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
213	214	F RXA02321	GR00667	1380	937	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
215	216	F RXA02343	GR00675	1403	1816	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
217	218	F RXA02850	GR00850	2	493	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
219	220	RXA02583	GR00741	6743	8290	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
221	222	RXA00870	GR00239	809	2320	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27) 2-Methyl-3-oxopropanoate:NAD+ oxidoreductase (CoA-propanoylating)
223	224	RXA01260	GR00367	2381	1200	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
225	226	RXA01261	GR00367	2607	2437	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
227	228	RXA01136	GR00318	685	1116	ISOVALERYL-COA DEHYDROGENASE (EC 1.3.99.10)
229	230	RXN00559	VW0103	7568	6552	PROTEIN VDLD
231	232	F RXA00559	GR00149	218	6	PROTEIN VDLD
233	234	RXA01580	GR00440	707	6	Glycerophosphoryl diester phosphodiesterase
235	236	RXA02677	GR00754	3119	3877	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46)
237	238	RXS01166	VW0117	18142	16838	EXTRACELLULAR LIPASE PRECURSOR (EC 3.1.1.3)

Terpenoid biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
239	240	RXA00875	GR00241	2423	1857	ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (EC 5.3.3.2)
241	242	RXA01292	GR00373	1204	2388	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
243	244	RXA01293	GR00373	2370	2696	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
245	246	RXA02310	GR00665	1132	2394	GERANYLGERANYL HYDROGENASE
247	248	RXA02718	GR00758	18539	19585	GERANYLGERANYL PYROPHOSPHATE SYNTHASE (EC 2.5.1.1)
249	250	RXA01067	GR00298	1453	2181	undecaprenyl-diphosphate synthase (EC 2.5.1.31)
251	252	RXA01269	GR00367	20334	19894	UNDECAPRENYL-PHOSPHATE GALACTOSEPHOSPHOTRANSFERASE (EC 2.7.8.6)
253	254	RXA01205	GR00346	3	533	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
255	256	RXA01576	GR00438	8053	8811	DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE (EC 2.4.1.117)
257	258	RXN02309	VW0025	28493	29542	OCTAPRENYL-DIPHOSPHATE SYNTHASE (EC 2.5.1.-)
259	260	F RXA02309	GR00665	978	4	OCTAPRENYL-DIPHOSPHATE SYNTHASE (EC 2.5.1.-)
261	262	RXN00477	VW0086	38905	37262	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
263	264	F RXA00477	GR00119	13187	11544	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
265	266	RXA00478	GR00119	14020	13190	PHYTOENE SYNTHASE (EC 2.5.1.-)
267	268	RXA01291	GR00373	345	1277	PHYTOENE SYNTHASE (EC 2.5.1.-)
269	270	RXA00480	GR00119	17444	16329	FARNESYL DIPHOSPHATE SYNTHASE (EC 2.5.1.1) (EC 2.5.1.10)
271	272	RXS01879	VW0105	1505	573	isopentenyl-phosphate kinase (EC 2.7.4.-)
273	274	RXS02023	VW0160	3234	4001	P450 cytochrome, isopentenyltransf, ferridox
275	276	RXS00948	VW0107	4266	5384	12-oxophytodienoate reductase (EC 1.3.1.42)
277	278	RXS02228	VW0068	1876	2778	TRNA DELTA(2)-ISOPENTENYL PYROPHOSPHATE TRANSFERASE (EC 2.5.1.8)
279	280	RXC01971	VW0105	4545	3715	Metal-Dependent Hydrolase involved in metabolism of terpenoids
281	282	RXC02697	VW0017	31257	32783	membrane protein involved in metabolism of terpenoids



ABC-Transporter

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
283	284	RXN01946	VV0228	2	1276	Hypothetical ABC Transporter ATP-Binding Protein
285	286	F RXA01946	GR00559	1849	575	(AL021184) ABC transporter ATP binding protein [Mycobacterium tuberculosis]
287	288	RXN00164	VV0232	1782	94	Hypothetical ABC Transporter ATP-Binding Protein
289	290	F RXA00164	GR00025	1782	94	, P, G, R ATPase subunits of ABC transporters
291	292	RXN00243	VV0057	28915	27899	, P, G, R ATPase subunits of ABC transporters
293	294	F RXA00243	GR00037	930	4	, P, G, R ATPase subunits of ABC transporters
295	296	RXA00259	GR00039	8469	6268	, P, G, R ATPase subunits of ABC transporters
297	298	RXN00410	VV0086	51988	51323	, P, G, R ATPase subunits of ABC transporters
299	300	F RXA00410	GR00092	829	164	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
301	302	RXN00456	VV0076	6780	8156	, P, G, R ATPase subunits of ABC transporters
303	304	F RXA00456	GR00114	316	5	, P, G, R ATPase subunits of ABC transporters
305	306	F RXA00459	GR00115	1231	245	, P, G, R ATPase subunits of ABC transporters
307	308	RXN01604	VV0137	8117	7470	, P, G, R ATPase subunits of ABC transporters
309	310	F RXA01604	GR00448	2	607	, P, G, R ATPase subunits of ABC transporters
311	312	RXN02547	VV0057	27726	25588	, P, G, R ATPase subunits of ABC transporters
313	314	F RXA02547	GR00726	22055	19932	, P, G, R ATPase subunits of ABC transporters
315	316	RXN02571	VV0101	12331	13359	, P, G, R ATPase subunits of ABC transporters
317	318	F RXA02571	GR00736	1469	2497	MALTOSE/MALTODEXTRIN TRANSPORT ATP-BINDING PROTEIN MALK
319	320	RXN02074	VV0318	12775	11153	TRANSPORT ATP-BINDING PROTEIN CYDD
321	322	F RXA02074	GR00628	5798	4176	, P, G, R ATPase subunits of ABC transporters
323	324	RXA02095	GR00629	14071	15474	, P, G, R ATPase subunits of ABC transporters
325	326	RXA02225	GR00652	3156	2275	, P, G, R ATPase subunits of ABC transporters
327	328	RXA02253	GR00654	20480	21406	, P, G, R ATPase subunits of ABC transporters
329	330	RXN01881	VV0105	529	95	, P, G, R ATPase subunits of ABC transporters
331	332	F RXA01881	GR00537	3092	3532	Hypothetical ABC Transporter ATP-Binding Protein
333	334	RXA00526	GR00136	1353	664	ATPase components of ABC transporters with duplicated ATPase domains
335	336	RXN00733	VV0132	1647	2531	Hypothetical ABC Transporter ATP-Binding Protein
337	338	F RXA00733	GR00197	411	4	Hypothetical ABC Transporter ATP-Binding Protein
339	340	RXA00735	GR00198	849	181	Hypothetical ABC Transporter ATP-Binding Protein
341	342	RXA00878	GR00242	3733	1871	Hypothetical ABC Transporter ATP-Binding Protein
343	344	RXN01191	VV0169	10478	12067	Hypothetical ABC Transporter ATP-Binding Protein
345	346	F RXA01191	GR00341	1571	165	Hypothetical ABC Transporter ATP-Binding Protein
347	348	RXN01212	VV0169	3284	4207	Hypothetical ABC Transporter ATP-Binding Protein
349	350	F RXA01212	GR00350	1	813	Hypothetical ABC Transporter ATP-Binding Protein
351	352	RXA02749	GR00764	4153	5028	Hypothetical ABC Transporter ATP-Binding Protein
353	354	RXA02224	GR00652	2271	475	Hypothetical ABC Transporter ATP-Binding Protein
355	356	RXN01602	VV0229	1109	2638	Hypothetical ABC Transporter ATP-Binding Protein
357	358	RXN02515	VV0087	962	1717	Hypothetical ABC Transporter ATP-Binding Protein
359	360	RXN00525	VV0079	26304	27566	Hypothetical ABC Transporter Permease Protein
361	362	RXN02096	VV0126	20444	22135	Hypothetical ABC Transporter Permease Protein
363	364	RXN00412	VV0086	53923	52844	Hypothetical Amino Acid ABC Transporter ATP-Binding Protein
365	366	RXN00411	VV0086	52844	52170	Hypothetical Amino Acid ABC Transporter Permease Protein
367	368	RXN02614	VV0313	5964	5236	TAURINE TRANSPORT ATP-BINDING PROTEIN TAUB
369	370	RXN02613	VV0313	5223	4267	TAURINE-BINDING PERIPLASMIC PROTEIN PRECURSOR

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
371	372	RXN00368	VW0226	2300	726	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
373	374	F RXA00368	GR00076	1	579	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
375	376	F RXA00370	GR00077	6	803	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
377	378	RXN01285	VW0215	1780	1055	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
379	380	RXN00523	VW0194	1363	338	FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEFG
381	382	RXN01142	VW0077	5805	6302	NITRATE TRANSPORT ATP-BINDING PROTEIN NRTD
383	384	RXN01141	VW0077	4644	5468	NITRATE TRANSPORT PROTEIN NRTA
385	386	RXN01002	VW0106	8858	8055	PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN PHNC
387	388	RXN01000	VW0106	7252	6407	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
389	390	RXN01732	VW0106	9944	8895	PHOSPHONATES-BINDING PERIPLASMIC PROTEIN PRECURSOR
391	392	RXN03080	VW0045	1670	2449	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
393	394	RXN03081	VW0045	2476	2934	FERRIC ENTEROBACTIN-BINDING PERIPLASMIC PROTEIN PRECURSOR
395	396	RXN03082	VW0045	3131	3451	FERRIC ENTEROBACTIN-BINDING PERIPLASMIC PROTEIN PRECURSOR

## Other transporters

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
397	398	RXA02261	GR00654	30936	32291	AMMONIUM TRANSPORT SYSTEM
399	400	RXA02020	GR00613	1015	5	AROMATIC AMINO ACID TRANSPORT PROTEIN AROP
401	402	RXA00281	GR00043	4721	5404	BACITRACIN TRANSPORT ATP-BINDING PROTEIN BCRA
403	404	RXN00570	VW0147	855	4	BENZOATE MEMBRANE TRANSPORT PROTEIN
405	406	F RXA00570	GR00153	1	498	BENZOATE MEMBRANE TRANSPORT PROTEIN
407	408	RXN00571	VW0173	1298	42	BENZOATE MEMBRANE TRANSPORT PROTEIN
409	410	F RXA00571	GR00154	2	1186	BENZOATE MEMBRANE TRANSPORT PROTEIN
411	412	RXA00962	GR00268	2	667	BENZOATE MEMBRANE TRANSPORT PROTEIN
413	414	RXA02811	GR00792	177	560	BENZOATE MEMBRANE TRANSPORT PROTEIN
415	416	RXA02115	GR00635	2	1198	BENZOATE MEMBRANE TRANSPORT PROTEIN
417	418	RXN00590	VW0178	5043	6230	BENZOATE MEMBRANE TRANSPORT PROTEIN
419	420	F RXA00590	GR00157	178	564	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
421	422	F RXA01538	GR00427	5040	5429	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
423	424	RXA01727	GR00489	1471	194	BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN
425	426	RXA00623	GR00163	6525	7862	C4-DICARBOXYLATE TRANSPORT PROTEIN
427	428	RXA01584	GR00441	55	597	CHROMATE TRANSPORT PROTEIN
429	430	RXA00852	GR00231	3137	2448	COBALT TRANSPORT ATP-BINDING PROTEIN CBIO
431	432	RXA00690	GR00181	1213	68	COBALT TRANSPORT PROTEIN CBIQ
433	434	RXA00827	GR00223	1319	567	COBALT TRANSPORT PROTEIN CBIQ
435	436	RXA00851	GR00231	2448	1840	COBALT TRANSPORT PROTEIN CBIQ
437	438	RXS03220				D-XYLOSE-PROTON SYMPORT
439	440	F RXA02762	GR00768	346	630	D-XYLOSE PROTON-SYMPORTER
441	442	RXN00092	VW0129	27509	26844	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
443	444	F RXA00092	GR00014	1	204	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
445	446	RXN03060	VW0030	6227	5376	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
447	448	F RXA02618	GR00745	1914	2351	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
449	450	F RXA02900	GR10040	2979	2128	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
451	452	RXS03212				GLYCINE BETAIN TRANSPORTER BETP
453	454	F RXA01591	GR00446	3	947	GLYCINE BETAIN TRANSPORTER BETP
455	456	RXN00201	VV0096	197	6	HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
457	458	F RXA00201	GR00032	191	6	HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
459	460	RXA01221	GR00354	2108	2833	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN BRAG
461	462	RXA01222	GR00354	2844	3542	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN LIVF
463	464	RXA01219	GR00354	151	1032	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVH
465	466	RXA01220	GR00354	1032	2108	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVM
467	468	RXA00091	GR00013	7762	8514	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
469	470	RXA00228	GR00032	29232	28642	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
471	472	RXA00346	GR00064	1054	1743	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
473	474	RXA00524	GR00135	779	1111	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
475	476	RXA01823	GR00516	591	1367	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
477	478	RXA02767	GR00770	1032	1814	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
479	480	RXA02792	GR00777	8581	7829	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
481	482	RXN02929	VV0090	36837	37874	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
483	484	F RXA01235	GR00358	1165	194	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
485	486	RXN02794	VV0134	10625	9552	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
487	488	F RXA01419	GR00415	888	1151	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
489	490	F RXA02794	GR00777	10172	9552	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
491	492	RXN03079	VV0045	644	1660	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
493	494	F RXA02865	GR10007	3832	2816	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
495	496	RXA00181	GR00028	3954	2383	PROLINE TRANSPORT SYSTEM
497	498	RXA00591	GR00158	229	1581	PROLINE/BETAINE TRANSPORTER
499	500	RXA01629	GR00453	3476	1965	PROLINE/BETAINE TRANSPORTER
501	502	RXA02030	GR00618	3072	1687	PROLINE/BETAINE TRANSPORTER
503	504	RXA00186	GR00028	12242	12988	SHORT-CHAIN FATTY ACIDS TRANSPORTER
505	506	RXA00187	GR00028	13097	13447	SHORT-CHAIN FATTY ACIDS TRANSPORTER
507	508	RXA01667	GR00464	703	1908	SODIUM/GLUTAMATE SYMPORT CARRIER PROTEIN
509	510	RXA02171	GR00641	6571	4919	SODIUM/PROLINE SYMPORTER
511	512	RXA00902	GR00245	4643	5875	SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN
513	514	RXA00941	GR00257	1999	683	sodium-dependent phosphate transport protein
515	516	RXN00449	VV0112	30992	32572	Sodium-Dicarboxylate Symport Protein
517	518	F RXA00449	GR00109	2040	1036	Sodium-Dicarboxylate Symport Protein
519	520	F RXA01755	GR00498	352	5	Sodium-Dicarboxylate Symport Protein
521	522	RXA00269	GR00041	1826	1038	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POT
523	524	RXA00369	GR00076	583	1299	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POT
525	526	RXA02073	GR00628	4176	2647	TRANSPORT ATP-BINDING PROTEIN CYDC
527	528	RXA01399	GR00409	1	1119	TRANSPORT ATP-BINDING PROTEIN CYDD
529	530	RXA01339	GR00389	8408	7164	TYROSINE-SPECIFIC TRANSPORT PROTEIN
531	532	RXA02527	GR00725	5519	6847	2-OXOGLUTARATE/MALATE TRANSLATOR PRECURSOR
533	534	RXN00298	VV0176	40228	42072	HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN
535	536	F RXA00298	GR00048	4459	6303	Ectoine/Proline/Glycine betaine carrier ectP

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
537	538	RXA00596	GR00159	335	787	potassium efflux system protein phaE C4-DICARBOXYLATE-BINDING PERIPLASMIC PROTEIN PRECURSOR, transport protein
539	540	RXA02364	GR00686	841	215	
541	542	RXN01411	VV0050	26015	26779	SHIKIMATE TRANSPORTER
543	544	RXN00960	VV0075	1139	105	PROTON/SODIUM-GLUTAMATE SYMPORT PROTEIN
545	546	RXN02447	VV0107	14297	13203	GALACTOSE-PROTON SYMPORT
547	548	RXN02395	VV0176	16747	14858	GLYCINE BETAINE TRANSPORTER BETP
549	550	RXN02348	VV0078	6027	7910	KUP SYSTEM POTASSIUM UPTAKE PROTEIN
551	552	RXN00297	VV0176	38630	39541	Hypothetical Malonate Transporter
553	554	RXN03103	VV0070	845	1087	GLUTAMATE-BINDING PROTEIN PRECURSOR
555	556	RXN02993	VV0071	736	65	GLUTAMINE-BINDING PROTEIN
557	558	RXN00349	VV0135	35187	36653	Hypothetical Trehalose Transport Protein
559	560	RXN03095	VV0057	4056	4424	CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG
561	562	RXN03160	VV0189	5150	5617	CHROMATE TRANSPORT PROTEIN
563	564	RXN02955	VV0176	8666	9187	DICARBOXYLATE TRANSPORTER
565	566	RXN03109	VV0082	659	6	HEMIN TRANSPORT SYSTEM PERMEASE PROTEIN HMUU
567	568	RXN02979	VV0149	2150	2383	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
569	570	RXN02987	VV0234	527	294	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
571	572	RXN03084	VV0048	900	1817	IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
573	574	RXN03183	VV0372	1	417	TREHALOSE/MALTOSE BINDING PROTEIN
575	576	RXN01139	VV0077	2776	1823	CATION EFFLUX SYSTEM PROTEIN CZCD
577	578	RXN00378	VV0223	8027	5418	Cation transport ATPases
579	580	RXN01338	VV0032	2	1903	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1.-)
581	582	RXN00980	VV0149	2635	4428	CATION-TRANSPORTING P-TYPE ATPASE B (EC 3.6.1.-)
583	584	RXN00099	VV0129	18876	17704	CYANATE TRANSPORT PROTEIN CYNX
585	586	RXN02662	VV0315	1461	1724	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
587	588	RXN02442	VV0217	5970	6818	zinc transport system membrane protein
589	590	RXN02443	VV0217	6818	7771	zinc-binding periplasmic protein precursor
591	592	RXN00842	VV0138	8686	7487	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
593	594	F RXA00842	GR00228	3208	2009	Permeases
595	596	RXN00832	VV0180	3133	4182	CALCIUM/PROTON ANTIPORTER
597	598	RXN00466	VV0086	63271	64266	Ferrichrome transport proteins
599	600	RXN01936	VV0127	40116	41387	MACROLIDE-EFFLUX PROTEIN
601	602	RXN01995	VV0182	2139	3476	PUTATIVE 3-(3-HYDROXYPHENYL) PROPIONATE TRANSPORT PROTEIN
603	604	RXN00661	VV0142	9718	9029	PNUC PROTEIN

Permeases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
605	606	RXN02566	VV0154	11823	13031	NUCLEOSIDE PERMEASE NUPG
607	608	F RXA02561	GR00732	664	5	NUCLEOSIDE PERMEASE NUPG
609	610	F RXA02566	GR00733	782	345	NUCLEOSIDE PERMEASE NUPG
611	612	RXA00051	GR00008	5770	7173	PROLINE-SPECIFIC PERMEASE PROY
613	614	RXA01172	GR00334	2687	4141	SULFATE PERMEASE
615	616	RXA02128	GR00637	2906	4600	SULFATE PERMEASE



<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
617	618	RXA02634	GR00748	6045	7655	SULFATE PERMEASE
619	620	RXN02233	VV0068	6856	8142	URACIL PERMEASE
621	622	F RXA02233	GR00653	6856	8067	URACIL PERMEASE
623	624	RXN02372	VV0213	9311	11197	XANTHINE PERMEASE
625	626	F RXA02372	GR00688	6	560	XANTHINE PERMEASE
627	628	F RXA02377	GR00689	3336	4526	XANTHINE PERMEASE
629	630	RXA02676	GR00754	2697	1309	GLUCONATE PERMEASE
631	632	RXN00432	VV0112	14751	13267	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
633	634	F RXA00432	GR00100	1	891	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
635	636	F RXA00436	GR00101	45	569	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
637	638	RXA00847	GR00230	1829	381	OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR (permease)
639	640	RXN01382	VV0119	8670	9761	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR
641	642	F RXA01382	GR00405	1067	6	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR (permease)
643	644	RXA02659	GR00753	2	313	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR (permease)
645	646	RXN02933	VV0176	30042	29233	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
647	648	RXN02991	VV0072	618	4	GLUTAMINE TRANSPORT SYSTEM PERMEASE PROTEIN GLNP
649	650	RXN02992	VV0072	842	621	GLUTAMINE TRANSPORT SYSTEM PERMEASE PROTEIN GLNP
651	652	RXN02996	VV0069	1980	2648	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVH
653	654	RXN03126	VV0112	9894	9001	TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG
655	656	RXN00443	VV0112	21572	20769	MOLYBDATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
657	658	RXN00444	VV0112	20785	19949	MOLYBDENUM TRANSPORT SYSTEM PERMEASE PROTEIN MODB
659	660	RXN00193	VV0371	1	594	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM PERMEASE PROTEIN AMYD
661	662	RXN01298	VV0116	2071	1142	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM PERMEASE PROTEIN AMYD

Channel Proteins

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
663	664	RXA01737	GR00493	2913	3971	POTASSIUM CHANNEL PROTEIN
665	666	RXN02348	VV0078	6027	7910	KUP SYSTEM POTASSIUM UPTAKE PROTEIN
667	668	RXA02426	GR00707	2165	633	PROBABLE NA(+)/H(+) ANTIPORTER
669	670	RXN03164	VV0277	1586	2455	POTASSIUM CHANNEL BETA SUBUNIT
671	672	RXN00024	VV0127	64219	63275	POTASSIUM CHANNEL BETA SUBUNIT

Lipoprotein and Lipopolysaccharide synthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
673	674	RXN01164	VV0117	15894	14260	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) / APOLIPOPROTEIN N-ACYLTRANSFERASE (EC 2.3.1.-)
675	676	RXN01168	VV0117	14224	13415	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) / APOLIPOPROTEIN N-ACYLTRANSFERASE (EC 2.3.1.-)

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkf	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dcfAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete <sup>1</sup> )	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5"-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of &phi;304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

<sup>1</sup> A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.



TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							



Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum				B11473				
Corynebacterium	acetoglutamicum				B11475				
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum				B3671				
Corynebacterium	ammoniagenes	6872							2399
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

[illegible]

Corynebacterium	glutamicum	19051								
Corynebacterium	glutamicum	19052								
Corynebacterium	glutamicum	19053								
Corynebacterium	glutamicum	19054								
Corynebacterium	glutamicum	19055								
Corynebacterium	glutamicum	19056								
Corynebacterium	glutamicum	19057								
Corynebacterium	glutamicum	19058								
Corynebacterium	glutamicum	19059								
Corynebacterium	glutamicum	19060								
Corynebacterium	glutamicum	19185								
Corynebacterium	glutamicum	13286								
Corynebacterium	glutamicum	21515								
Corynebacterium	glutamicum	21527								
Corynebacterium	glutamicum	21544								
Corynebacterium	glutamicum	21492								
Corynebacterium	glutamicum			B8183						
Corynebacterium	glutamicum			B8182						
Corynebacterium	glutamicum			B12416						
Corynebacterium	glutamicum			B12417						
Corynebacterium	glutamicum			B12418						
Corynebacterium	glutamicum			B11476						
Corynebacterium	glutamicum	21608								
Corynebacterium	lilium		P973							
Corynebacterium	nitrilophilus	21419							11594	
Corynebacterium	spec.		P4445							
Corynebacterium	spec.		P4446							
Corynebacterium	spec.	31088								
Corynebacterium	spec.	31089								
Corynebacterium	spec.	31090								
Corynebacterium	spec.	31090								



Corynebacterium	spec.	31090								
Corynebacterium	spec.	15954								20145
Corynebacterium	spec.	21857								
Corynebacterium	spec.	21862								
Corynebacterium	spec.	21863								

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4<sup>th</sup> edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

**TABLE 4: ALIGNMENT RESULTS**

<u>ID #</u>	<u>length</u> (NT)	<u>Genbank Hit</u>	<u>Length</u>	<u>Accession</u>	<u>Name of Genbank Hit</u>	<u>Source of Genbank Hit</u>	<u>% homology</u> (GAP)	<u>Date of</u> <u>Deposit</u>
rx00051	1527	GB_HTG3:AC009685	210031	AC009685	Homo sapiens chromosome 15 clone 91_E_13 map 15, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	34,247	29-Sep-99
		GB_HTG3:AC009685	210031	AC009685	Homo sapiens chromosome 15 clone 91_E_13 map 15, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	34,247	29-Sep-99
		GB_HTG7:AC009511	271896	AC009511	Homo sapiens clone RP11-860B13, *** SEQUENCING IN PROGRESS ***, 59 unordered pieces.	Homo sapiens	35,033	09-DEC-1999
rx00091	876	GB_BA1:D50453	146191	D50453	Bacillus subtilis DNA for 25-36 degree region containing the amyE-srfA region, complete cds.	Bacillus subtilis	54,452	10-Feb-99
		GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid l51.	Streptomyces coelicolor A3(2)	36,806	16-Aug-99
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,642	17-Apr-96
rx00092	789	GB_BA1:SCH35	45396	AL078610	Streptomyces coelicolor cosmid H35.	Streptomyces coelicolor	49,934	4-Jun-99
		GB_HTG3:AC011498_0312343	AC011498		Homo sapiens chromosome 19 clone CIT978SKB_50L17, *** SEQUENCING IN PROGRESS ***, 190 unordered pieces.	Homo sapiens	37,117	13-Dec-99
		GB_HTG3:AC011498_0312343	AC011498		Homo sapiens chromosome 19 clone CIT978SKB_50L17, *** SEQUENCING IN PROGRESS ***, 190 unordered pieces.	Homo sapiens	37,117	13-Dec-99
rx00104	879	GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	36,732	10-Feb-99
		GB_PL2:T24M8	68251	AF077409	Arabidopsis thaliana BAC T24M8.	Arabidopsis thaliana	37,150	3-Aug-98
		GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	42,874	10-Feb-99
rx00113	5745	GB_BA1:MAFASGEN	10520	X87822	B.ammoniaenes FAS gene.	Corynebacterium ammoniagenes	68,381	03-OCT-1996
		GB_BA1:BAFASAA	10549	X64795	B.ammoniaenes FAS gene.	Corynebacterium ammoniagenes	57,259	14-OCT-1997
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,870	17-Jun-98
rx00164	1812	GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,714	03-DEC-1999
		GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,714	03-DEC-1999
		GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,334	03-DEC-1999
rx00181	1695	GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	100,000	8-Sep-97
		GB_BA2:U32814	10393	U32814	Haemophilus influenzae Rd section 129 of 163 of the complete genome.	Haemophilus influenzae Rd	36,347	29-MAY-1998
		GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	37,454	8-Sep-97
rx00186	870	GB_PR3:AC004843	136655	AC004843	Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.	Homo sapiens	37,315	5-Nov-98

**TABLE 4: ALIGNMENT RESULTS**

GB_HTG2:HS745I14	133309	AL033532	Homo sapiens chromosome 1 clone RP4-745I14 map q23.1-24.3, *** SEQUENCING	Homo sapiens	38,129	03-DEC-1999
GB_HTG2:HS745I14	133309	AL033532	IN PROGRESS ***, in unordered pieces.			
GB_GSS10:AQ184082	506	AQ184082	Homo sapiens chromosome 1 clone RP4-745I14 map q23.1-24.3, *** SEQUENCING	Homo sapiens	38,129	03-DEC-1999
GB_GSS1:CNS008ZZ	1101	AL052951	IN PROGRESS ***, in unordered pieces.			
GB_GSS10:AQ184082	506	AQ184082	HS_3216_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216 Col=15 Row=M, genomic survey sequence.	Homo sapiens	37,297	1-Nov-98
GB_GSS1:CNS008ZZ	1101	AL052951	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR18L01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	34,120	3-Jun-99
GB_GSS10:AQ184082	506	AQ184082	HS_3216_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216 Col=15 Row=M, genomic survey sequence.	Homo sapiens	39,655	1-Nov-98
GB_PR3:HSJ824F16	139330	AL050325	Human DNA sequence from clone 824F16 on chromosome 20, complete sequence.	Homo sapiens	34,520	23-Nov-99
GB_BA1:RCSECA	2724	X89411	R.capsulatus DNA for secA gene.	Rhodobacter capsulatus	38,163	6-Jan-96
GB_EST34:AV122904	242	AV122904	AV122904 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone	Mus musculus	38,889	1-Jul-99
GB_EST15:AA486042	515	AA486042	2610529H07, mRNA sequence.	Homo sapiens	37,500	06-MAR-1998
GB_EST15:AA486042	515	AA486042	ab40c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:843278 5', mRNA sequence.	Homo sapiens	38,816	06-MAR-1998
GB_PR2:CNS01DS5	101584	AL121655	BAC sequence from the SPG4 candidate region at 2p21-2p22, complete sequence.	Homo sapiens	37,001	29-Sep-99
GB_HTG3:AC011408	79332	AC011408	Homo sapiens clone CIT978SKB_65D22, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Homo sapiens	38,040	06-OCT-1999
GB_HTG3:AC011408	79332	AC011408	Homo sapiens clone CIT978SKB_65D22, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Homo sapiens	38,040	06-OCT-1999
GB_HTG1:CEY62E10	254217	AL031580	Caenorhabditis elegans chromosome IV clone Y62E10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,776	6-Sep-99
GB_HTG1:CEY62E10	254217	AL031580	Caenorhabditis elegans chromosome IV clone Y62E10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,776	6-Sep-99
GB_PL2:YSCCHROMI	41988	L22015	Saccharomyces cerevisiae chromosome I centromere and right arm sequence.	Saccharomyces cerevisiae	39,260	05-MAR-1998
GB_HTG4:AC009974	219565	AC009974	Homo sapiens chromosome unknown clone NH0459119, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	37,358	29-OCT-1999
GB_HTG4:AC009974	219565	AC009974	Homo sapiens chromosome unknown clone NH0459119, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	37,358	29-OCT-1999
GB_BA1:AB017508	32050	AB017508	Bacillus halodurans C-125 genomic DNA, 32 kb fragment, complete cds.	Bacillus halodurans	44,622	14-Apr-99
GB_BA1:SCE8	24700	AL035654	Streptomyces coelicolor cosmid E8.	Streptomyces coelicolor	36,328	11-MAR-1999
GB_BA1:SCU51332	3216	U51332	Streptomyces coelicolor histidine kinase homolog (absA1) and response regulator homolog (absA2) genes, complete cds.	Streptomyces coelicolor	39,089	14-Sep-96
GB_HTG4:AC011122	187123	AC011122	Homo sapiens chromosome 8 clone 23_D_19 map 8, *** SEQUENCING IN PROGRESS ***, 27 ordered pieces.	Homo sapiens	38,658	14-OCT-1999
GB_BA1:CGECTP	2719	AJ001436	Corynebacterium glutamicum ectP gene.	Corynebacterium glutamicum	100,000	20-Nov-98

**TABLE 4: ALIGNMENT RESULTS**

	GB_BA1:CGECTP	2719	AJ001436	Corynebacterium glutamicum ectP gene.	Corynebacterium glutamicum	100,000	20-Nov-98
	GB_EST24:AI234006	432	AI234006	EST230694 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUCU01 3' end, mRNA sequence.	Rattus sp.	46,552	31-Jan-99
rx000346 813	GB_BA1:SC2E9	20850	AL021530	Streptomyces coelicolor cosmid 2E9.	Streptomyces coelicolor	43,267	28-Jan-98
	GB_BA1:SC9B1	24800	AL049727	Streptomyces coelicolor cosmid 9B1.	Streptomyces coelicolor	44,613	27-Apr-99
	GB_BA1:ECU70214	123171	U70214	Escherichia coli chromosome minutes 4-6.	Escherichia coli	39,490	21-Sep-96
rx000368 1698	GB_BA2:AF065159	35209	AF065159	Bradyrhizobium japonicum putative arylsulfatase (arsA), putative soluble lytic transglycosylase precursor (sltA), dihydroadipiculate synthase (dapA), MscL (mscL), SmpB (smpB), BcpB (bcpB), RnpO (rnpO), RelA/SpoT homolog (relA), PdxJ (pdxJ), and acyl carrier protein synthase AcpS (acpS) genes, complete cds; prokaryotic type I signal peptidase SipF (sipF) gene, sipF-sipS allele, complete cds; RNase III (rnc) gene, complete cds; GTP-binding protein Era (era) gene, partial cds; and unknown genes.	Bradyrhizobium japonicum	40,409	27-OCT-1999
	GB_BA1:AEOCHIT1	6861	D63139	Aeromonas sp. gene for chitinase, complete and partial cds.	Aeromonas sp. 10S-24	38,577	13-Feb-99
	GB_EST4:D62996	314	D62996	HUM347G01B Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-347G01 5', mRNA sequence.	Homo sapiens	41,613	29-Aug-95
rx000369 817	GB_BA1:YP102KB	119443	AL031866	Yersinia pestis 102 kbases unstable region: from 1 to 119443.	Yersinia pestis	35,396	4-Jan-99
	GB_GSS8:AQ012142	501	AQ012142	8750H1A037010398 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 8750H1A037010398, genomic survey sequence.	Rhodobacter sphaeroides	54,800	4-Jun-98
	GB_HTG2:AC005081	180096	AC005081	Homo sapiens clone RG270D13, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	45,786	12-Jun-98
rx000410 789	GB_BA1:ATPLOCC	8870	Z30328	A.tumefaciens Ti plasmid pTiAch5 genes for OccR, OccQ, OccM, OccP, OccT, OoxB, Agrobacterium tumefaciens	Agrobacterium tumefaciens	46,490	10-OCT-1994
	GB_BA2:U67591	9829	U67591	OoxA and ornithine cyclodeaminase.	Methanococcus jannaschii	45,677	28-Jan-98
	GB_BA1:TIPOCCQMPJ4350	M80607	M80607	Plasmid pTiA6 (from Agrobacterium tumefaciens) periplasmic-type octopine permease (occR, occQ, occM, occP, and occJ) and lysR-type regulatory protein (occR) genes, complete cds.	Plasmid pTiA6	46,490	24-Apr-96
rx000419 882	GB_BA2:MSU46844	16951	U46844	Mycobacterium smegmatis catalase-peroxidase (katG), putative arabinosyl transferase (embC, embA, embB), genes complete cds and putative propionyl-coA carboxylase beta chain (pccB) genes, partial cds.	Mycobacterium smegmatis	57,029	12-MAY-1997
	GB_EST28:AI513245	471	AI513245	GH13311.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH13311 3prime, mRNA sequence.	Drosophila melanogaster	37,696	16-MAR-1999
	GB_HTG4:AC010066	187240	AC010066	Drosophila melanogaster chromosome 3L72A4 clone RPCI98-25O1, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	39,607	16-OCT-1999
rx000432 1608	GB_BA1:BSUB0015	218410	Z99118	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.	Bacillus subtilis	49,810	26-Nov-97
	GB_PL1:CAC35A5	42565	AL033396	C.albicans cosmid Ca35A5.	Candida albicans	35,041	5-Nov-98
	GB_EST13:AA336266	378	AA336266	EST40981 Endometrial tumor Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	39,733	21-Apr-97
rx000449 1704	GB_HTG2:AC008199	124050	AC008199	Drosophila melanogaster chromosome 3 clone BACR01K08 (D756) RPCI-98 01.K.8 map 94D-94D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	38,392	2-Aug-99



**TABLE 4: ALIGNMENT RESULTS**

	GB_HTG2:AC008199	124050	AC008199	Drosophila melanogaster chromosome 3 clone BACR01K08 (D756) RPCI-98 01.K.8 map 94D-94D strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 83 unordered pieces.	38,392	2-Aug-99
rxa00456	GB_RO:RATLNKP2	177	M22337	Rat link protein gene, exon 2.		
	GB_GSS1:FR0030597	476	AL026966	Fugu rubripes GSS sequence, clone 091C22aF9, genomic survey sequence.	40,678	27-Apr-93
	GB_GSS5:AQ786587	556	AQ786587	HS_3086_B1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3086 Col=9 Row=P, genomic survey sequence.	47,407	25-Jun-98
	GB_GSS14:AQ526586	434	AQ526586	HS_5198_B1_B03_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=774 Col=5 Row=D, genomic survey sequence.	38,406	3-Aug-99
rxa00477	GB_EST17:AA610489	407	AA610489	np93e05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133888 similar to gb:M11353 HISTONE H3.3 (HUMAN);, mRNA sequence.	36,951	11-MAY-1999
	GB_PR1:HS33G4	1015	X05857	Human H3.3 gene exon 4.	41,791	09-DEC-1997
	GB_EST30:AI637667	579	AI637667	tt10g11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240420 3', mRNA sequence.	38,182	24-Jan-96
	GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS *** , 12 unordered pieces.	35,417	27-Apr-99
rxa00478	GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS *** , 12 unordered pieces.	38,769	3-Aug-99
	GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS *** , 12 unordered pieces.	38,769	3-Aug-99
	GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS *** , 12 unordered pieces.	36,797	3-Aug-99
	GB_HTG1:HSJ575L21	94715	AL096841	Homo sapiens chromosome 1 clone RP4-575L21, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	38,138	23-Nov-99
rxa00480	GB_HTG1:HSJ575L21	94715	AL096841	Homo sapiens chromosome 1 clone RP4-575L21, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	38,138	23-Nov-99
	GB_RO:AC005960	158414	AC005960	Mus musculus chromosome 17 BAC citb20h22 from the MHC region, complete sequence.	38,712	01-DEC-1998
	GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	40,284	16-Aug-99
	GB_BA2:AF082879	3434	AF082879	Yersinia enterocolitica ABC transporter enterochelin/enterobactin gene cluster, complete sequence.	55,634	20-OCT-1999
rxa00526	GB_BA1:BSP132617	5192	AJ132617	Burkholderia sp. P-transporter operon and flanking genes.	40,793	13-Jul-99
	GB_BA1:BSUB0008	208230	Z99111	Bacillus subtilis complete genome (section 8 of 21); from 1394791 to 1603020.	54,534	26-Nov-97
	GB_BA2:AF012285	46864	AF012285	Bacillus subtilis mobA-nprE gene region.	54,534	1-Jul-98
	GB_BA1:D90725	13796	D90725	Escherichia coli genomic DNA. (19.7 - 20.0 min).	51,481	7-Feb-99
rxa00559	GB_BA2:CAU77910	3385	U77910	Corynebacterium ammoniagenes sequence upstream of the 5-phosphoribosyl-1-pyrophosphate amidotransferase (purF) gene.	39,007	1-Jan-98
	GB_EST4:H34952	382	H34952	EST108261 Rat PC-12 cells, untreated Rattus sp. cDNA clone RPCK07 similar to NADH-ubiquinone oxidoreductase complex l 23 kDa precursor (iron-sulfur protein), mRNA sequence.	39,267	2-Apr-98
	GB_BA2:AE000963	22014	AE000963	Archaeoglobus fulgidus section 144 of 172 of the complete genome.	38,338	15-DEC-1997
	GB_GSS12:AQ422451	563	AQ422451	RPCI-11-185C3.TV RPCI-11 Homo sapiens genomic clone RPCI-11-185C3, genomic survey sequence.	38,767	23-MAR-1999



**TABLE 4: ALIGNMENT RESULTS**

rx00571	1280	GB_EST28:AI504741	568	AI504741	v16c01.x1 Stralagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:972384 3' similar to gb:Z14044 M.musculus mRNA for valosin-containing protein (MOUSE);, mRNA sequence.	Mus musculus	37,900	11-MAR-1999
		GB_EST18:AA712043	68	AA712043	vu29f10.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1182091 5' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);, mRNA sequence.	Mus musculus	42,647	24-DEC-1997
		GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	38,468	17-Jun-98
		GB_PR3:AC005788	36224	AC005788	Homo sapiens chromosome 19, cosmid R26652, complete sequence.	Homo sapiens	36,911	06-OCT-1998
		GB_PR3:AC005338	34541	AC005338	Homo sapiens chromosome 19, cosmid R31646, complete sequence.	Homo sapiens	36,911	30-Jul-98
rx00590	1288	GB_HTG6:AC010932	203273	AC010932	Homo sapiens chromosome 15 clone RP11-296E22 map 15, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	37,242	30-Nov-99
		GB_HTG6:AC010932	203273	AC010932	Homo sapiens chromosome 15 clone RP11-296E22 map 15, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	36,485	30-Nov-99
		GB_BA1:MSG26CS	37040	L78816	Mycobacterium leprae cosmid B26 DNA sequence.	Mycobacterium leprae	39,272	15-Jun-96
rx00591	1476	GB_IN1:CEK09E9	30098	Z79602	Caenorhabditis elegans cosmid K09E9, complete sequence.	Caenorhabditis elegans	34,092	2-Sep-99
		GB_PR4:AF135802	4965	AF135802	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA, complete cds.	Homo sapiens	36,310	9-Apr-99
		GB_PR4:AF104256	4365	AF104256	Homo sapiens transcriptional co-activator CRSP150 (CRSP150) mRNA, complete cds.	Homo sapiens	36,617	4-Feb-99
rx00596	576	GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.	Homo sapiens	34,321	02-MAY-1998
		GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.	Homo sapiens	35,739	02-MAY-1998
		GB_PR1:HUMCBP2	2047	D83174	Human mRNA for collagen binding protein 2, complete cds.	Homo sapiens	40,404	6-Feb-99
rx00607	504	GB_BA1:MTV010	3400	AL021186	Mycobacterium tuberculosis H37Rv complete genome; segment 119/162.	Mycobacterium tuberculosis	40,862	23-Jun-99
		GB_BA1:MTV010	3400	AL021186	Mycobacterium tuberculosis H37Rv complete genome; segment 119/162.	Mycobacterium tuberculosis	38,833	23-Jun-99
rx00623	1461	GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	60,552	17-Jun-98
		GB_BA1:RSPNGR234	34010	Z68203	Rhizobium sp. plasmid NGR234a DNA.	Rhizobium sp.	51,992	8-Aug-96
		GB_BA2:AE000101	10057	AE000101	Rhizobium sp. NGR234 plasmid pNGR234a, section 38 of 46 of the complete plasmid sequence.	Rhizobium sp. NGR234	51,992	12-DEC-1997
rx00681								
rx00690	1269	GB_HTG5:AC008338	136685	AC008338	Drosophila melanogaster chromosome X clone BACR30J04 (D908) RPCI-98 30.J.4 map 19C-19E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces.	Drosophila melanogaster	35,341	15-Nov-99
		GB_HTG4:AC009766	170502	AC009766	Homo sapiens chromosome 11 clone 404_A_03 map 11, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	37,984	19-OCT-1999
		GB_HTG4:AC009766	170502	AC009766	Homo sapiens chromosome 11 clone 404_A_03 map 11, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	37,984	19-OCT-1999

**TABLE 4: ALIGNMENT RESULTS**

rx00733	1008	GB_EST30:AU054038	245	AU054038	AU054038	Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLK472, mRNA sequence.	Dictyostelium discoideum	43,265	28-Apr-99
		GB_EST30:AU054038	245	AU054038	AU054038	Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLK472, mRNA sequence.	Dictyostelium discoideum	43,265	28-Apr-99
rx00735	692	GB_BA1:MTCY50	36030	Z77137		Mycobacterium tuberculosis H37Rv complete genome; segment 55/162.	Mycobacterium tuberculosis	36,819	17-Jun-98
		GB_BA1:D90904	150894	D90904		Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448.	Synechocystis sp.	52,585	7-Feb-99
		GB_BA1:D90904	150894	D90904		Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448.	Synechocystis sp.	39,699	7-Feb-99
rx00796	298	GB_GSS14:AQ579838	651	AQ579838		T135342b shotgun sub-library of BAC clone 31P06 Medicago truncatula genomic clone 31-P-06-C-054, genomic survey sequence.	Medicago truncatula	37,153	27-Sep-99
		GB_PR4:AC007625	174701	AC007625		Genomic sequence of Homo sapiens clone 2314F2 from chromosome 18, complete sequence.	Homo sapiens	38,014	30-Jun-99
		GB_EST14:AA427576	580	AA427576		zw54b04.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773839 3' similar to gb:M86852 PEROXISOME ASSEMBLY FACTOR-1 (HUMAN);, mRNA sequence.	Homo sapiens	42,731	16-OCT-1997
rx00801	756	GB_BA1:MTV022	13025	AL021925		Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	59,350	17-Jun-98
		GB_RO:AC002109	160048	AC002109		Genomic sequence from Mouse 9, complete sequence.	Mus musculus	39,398	9-Sep-97
		GB_BA1:MTV022	13025	AL021925		Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	36,842	17-Jun-98
rx00802	837	GB_GSS14:AQ563349	642	AQ563349		HS_5335_B2_A09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=911 Col=18 Row=B, genomic survey sequence.	Homo sapiens	37,649	29-MAY-1999
		GB_BA1:DIHCLPBA	2441	M32229		B.nodosus clpB gene encoding a regulatory subunit of ATP-dependent protease.	Dichelobacter nodosus	41,140	26-Apr-93
		GB_GSS3:B61538	698	B61538		T17M17TR TAMU Arabidopsis thaliana genomic clone T17M17, genomic survey sequence.	Arabidopsis thaliana	36,946	21-Nov-97
rx00819	1452	GB_HTG3:AC008691_1110000		AC008691		Homo sapiens chromosome 5 clone CIT978SKB_63A22, *** SEQUENCING IN PROGRESS ***, 253 unordered pieces.	Homo sapiens	38,270	3-Aug-99
		GB_HTG3:AC008691_1110000		AC008691		Homo sapiens chromosome 5 clone CIT978SKB_63A22, *** SEQUENCING IN PROGRESS ***, 253 unordered pieces.	Homo sapiens	38,270	3-Aug-99
		GB_HTG3:AC009127	186591	AC009127		Homo sapiens chromosome 16 clone RPCI-11_498D10, *** SEQUENCING IN PROGRESS ***, 49 unordered pieces.	Homo sapiens	38,947	3-Aug-99
rx00821	966	GB_HTG1:HS32B1	271488	AL023693		Homo sapiens chromosome 6 clone RP1-32B1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,565	23-Nov-99
		GB_HTG1:HS32B1	271488	AL023693		Homo sapiens chromosome 6 clone RP1-32B1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,565	23-Nov-99
rx00827	876	GB_PR3:AC004919	75547	AC004919		Homo sapiens PAC clone DJ0895B23 from UL, complete sequence.	Homo sapiens	34,346	19-Sep-98
		GB_EST6:W06539	300	W06539		T2367 MVAT4 bloodstream form of serodeme WRA Ta1.1 Trypanosoma brucei rhodesiense cDNA 5', mRNA sequence.	Trypanosoma brucei rhodesiense	40,000	12-Aug-96
		GB_PR4:AC008179	181745	AC008179		Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	35,903	28-Sep-99
		GB_EST18:AA710415	533	AA710415		v153f08.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1166823 5', mRNA sequence.	Mus musculus	41,562	24-DEC-1997
rx00842	1323	GB_PR2:AC002379	118595	AC002379		Human BAC clone GS165104 from 7q21, complete sequence.	Homo sapiens	36,321	23-Jul-97
		GB_PR2:AC002379	118595	AC002379		Human BAC clone GS165104 from 7q21, complete sequence.	Homo sapiens	37,284	23-Jul-97

**TABLE 4: ALIGNMENT RESULTS**

rx00847	1572	GB_IN1:CEF02D8	31624	Z78411	Caenorhabditis elegans cosmid F02D8, complete sequence.	Caenorhabditis elegans	38,163	23-Nov-98
		GB_OV:XELRDS38A	1209	L79915	Xenopus laevis rds/peripherin (rds38) mRNA, complete cds.	Xenopus laevis	36,044	30-Jul-97
		GB_HTG4:AC007920	234529	AC007920	Homo sapiens chromosome 3q27 clone RPC111-208N14, *** SEQUENCING IN PROGRESS ***; 51 unordered pieces.	Homo sapiens	33,742	21-OCT-1999
rx00851	732	GB_HTG4:AC007920	234529	AC007920	Homo sapiens chromosome 3q27 clone RPC111-208N14, *** SEQUENCING IN PROGRESS ***; 51 unordered pieces.	Homo sapiens	33,742	21-OCT-1999
		GB_HTG2:AC004064	185000	AC004064	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 10 unordered pieces.	Homo sapiens	39,833	9-Jul-98
		GB_HTG2:AC004064	185000	AC004064	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 10 unordered pieces.	Homo sapiens	39,833	9-Jul-98
		GB_PR3:HSJ824F16	139330	AL050325	Human DNA sequence from clone 824F16 on chromosome 20, complete sequence.	Homo sapiens	39,833	23-Nov-99
rx00852	813	GB_HTG3:AC010120	121582	AC010120	Drosophila melanogaster chromosome 3 clone BACR22N13 (D1061) RPCI-98	Drosophila melanogaster	36,855	24-Sep-99
		GB_HTG3:AC010120	121582	AC010120	22.N.13 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 83 unordered pieces.	Drosophila melanogaster	36,855	24-Sep-99
		GB_HTG3:AC010120	121582	AC010120	22.N.13 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 83 unordered pieces.	Drosophila melanogaster	36,855	24-Sep-99
rx00856		GB_HTG2:AC006898	299308	AC006898	Caenorhabditis elegans clone Y73B6x, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Caenorhabditis elegans	36,768	24-Feb-99
		GB_BA1:STMMSDA	3986	L48550	Streptomyces coelicolor methylmalonic acid semialdehyde dehydrogenase (msdA) gene, complete cds.	Streptomyces coelicolor	63,743	09-MAY-1996
rx00875	690	GB_PAT:192043	713	192043	Sequence 10 from patent US 5726299.	Unknown.	38,850	01-DEC-1998
		GB_PAT:178754	713	178754	Sequence 10 from patent US 5693781.	Unknown.	38,850	3-Apr-98
		GB_BA2:AF119715	549	AF119715	Escherichia coli isopentyl diphosphate isomerase (idi) gene, complete cds.	Escherichia coli	54,827	22-Apr-99
rx00878	1986	GB_BA2:AE000372	12144	AE000372	Escherichia coli K-12 MG1655 section 262 of 400 of the complete genome.	Escherichia coli	51,416	12-Nov-98
		GB_BA1:ECU28375	55175	U28375	Escherichia coli K-12 genome; approximately 64 to 65 minutes.	Escherichia coli	51,416	08-DEC-1995
		GB_HTG2:AC007472	114003	AC007472	Drosophila melanogaster chromosome 2 clone BACR30D19 (D587) RPCI-98	Drosophila melanogaster	36,592	2-Aug-99
rx00880	1968	GB_HTG2:AC007472	114003	AC007472	30.D.19 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 79 unordered pieces.	Drosophila melanogaster	36,592	2-Aug-99
		GB_HTG2:AC006798	207370	AC006798	Drosophila melanogaster chromosome 2 clone BACR30D19 (D587) RPCI-98	Drosophila melanogaster	36,592	2-Aug-99
		GB_EST4:H22888	468	H22888	30.D.19 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 79 unordered pieces.	Drosophila melanogaster	36,592	2-Aug-99
rx00899	1389	GB_GSS13:AQ426858	516	AQ426858	Caenorhabditis elegans clone Y51F8, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Caenorhabditis elegans	36,699	25-Feb-99
		GB_EST4:H22888	468	H22888	Caenorhabditis elegans clone Y51F8, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Caenorhabditis elegans	36,699	25-Feb-99
		GB_GSS13:AQ426858	516	AQ426858	ym54e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52158 5', mRNA sequence.	Homo sapiens	37,179	6-Jul-95
rx00899	1389	GB_PR1:AB002335	6289	AB002335	CITBI-E1-2578F1.TF CITBI-E1 Homo sapiens genomic clone 2578F1, genomic survey sequence.	Homo sapiens	38,447	24-MAR-1999
		GB_BA1:NGU58849	2401	U58849	Human mRNA for KIA0337 gene, complete cds.	Homo sapiens	35,799	13-Feb-99
		GB_BA1:NGU58849	2401	U58849	Neisseria gonorrhoeae pilS6 silent pilus locus.	Neisseria gonorrhoeae	40,623	20-Jun-96

**TABLE 4: ALIGNMENT RESULTS**

rx00902	1333	GB_BA1:PLPDHOS	3119	L06822	Plasmid pSa (from <i>Escherichia coli</i> ) dihydropteroate synthase gene, 3' end.	Plasmid pSa	38,966	20-MAR-1996
		GB_BA1:PDGINTORF	6747	L06418	Integron In7 (from Plasmid pDGO100 from <i>Escherichia coli</i> ) integrase (int), aminoglycoside adenyltransferase (aad), quaternary ammonium compound-resistance protein, dihydrofolate reductase (dhfrX), and dihydropteroate synthase (sulf) genes.	Plasmid pDGO100	38,966	20-MAR-1996
		GB_GSS15:AQ606873	581	AQ606873	HS_5404_B2_H05_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=10 Row=P, genomic survey sequence.	Homo sapiens	37,900	10-Jun-99
		GB_GSS9:AQ163442	658	AQ163442	nbxb0007A07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0007A07f, genomic survey sequence.	Oryza sativa	41,885	12-Sep-98
		GB_PL1:PSST70	4974	X69213	P.sativum Psst70 gene for heat-shock protein.	Pisum sativum	36,866	3-Jul-96
		GB_GSS1:FR0025208	612	AL018047	F.rubripes GSS sequence, clone 145D10aA8, genomic survey sequence.	Fugu rubripes	37,815	10-DEC-1997
		GB_GSS1:FR0021844	252	AL014715	F.rubripes GSS sequence, clone 069K22aG5, genomic survey sequence.	Fugu rubripes	37,698	10-DEC-1997
		GB_GSS12:AQ403344	593	AQ403344	HS_2257_B1_B03_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=5 Row=D, genomic survey sequence.	Homo sapiens	31,552	13-MAR-1999
		GB_BA1:MTCY180	44201	Z97193	Mycobacterium tuberculosis H37Rv complete genome; segment 85/162.	Mycobacterium tuberculosis	37,902	17-Jun-98
		GB_BA1:MTCY180	44201	Z97193	Mycobacterium tuberculosis H37Rv complete genome; segment 85/162.	Mycobacterium tuberculosis	39,140	17-Jun-98
		GB_BA2:MSGKATG	1745	L14268	Mycobacterium tuberculosis ethyl methane sulphonate resistance protein (katG) gene, 3'end.	Mycobacterium tuberculosis	42,517	26-Aug-99
		GB_HTG6:AC010998	144338	AC010998	Homo sapiens clone RP11-95116, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Homo sapiens	39,497	08-DEC-1999
		GB_GSS1:GGA340111	990	AJ232089	Gallus gallus anonymous sequence from Cosmid mapping to chromosome 2 (Cosmid 34 - Contig 15), genomic survey sequence.	Gallus gallus	37,970	25-Aug-98
		GB_HTG6:AC010998	144338	AC010998	Homo sapiens clone RP11-95116, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Homo sapiens	38,226	08-DEC-1999
		GB_BA1:ECTTN7	2280	AJ001816	<i>Escherichia coli</i> left end of transposon Tn7 including type 2 integron.	<i>Escherichia coli</i>	38,822	4-Nov-97
		GB_IN2:AF176377	8220	AF176377	<i>Caenorhabditis briggsae</i> CES-1 (ces-1) gene, complete cds; and CPN-1 (cpn-1) gene, partial cds.	<i>Caenorhabditis briggsae</i>	39,921	09-DEC-1999
		GB_GSS10:AQ196728	429	AQ196728	CIT-HSP-2381F4. TR CIT-HSP Homo sapiens genomic clone 2381F4, genomic survey sequence.	Homo sapiens	39,019	16-Sep-98
		GB_BA1:U00016	42931	U00016	<i>Mycobacterium leprae</i> cosmid B1937.	<i>Mycobacterium leprae</i>	58,303	01-MAR-1994
		GB_BA1:SYCGROESL	3256	D12677	<i>Synechocystis</i> sp. groES and groEL genes.	<i>Synechocystis</i> sp.	34,593	3-Feb-99
		GB_BA1:D90905	139467	D90905	<i>Synechocystis</i> sp. PCC6803 complete genome, 7/27, 781449-920915.	<i>Synechocystis</i> sp.	34,593	7-Feb-99
		GB_BA1:PSEFAOAB	3480	D10390	<i>P. fragi</i> faoA and faoB genes, complete cds.	<i>Pseudomonas fragi</i>	51,919	2-Feb-99
		GB_BA1:AB014757	6057	AB014757	<i>Pseudomonas</i> sp. 61-3 genes for PhbR, acetoacetyl-CoA reductase, beta-ketothiolase and PHB synthase, complete cds.	<i>Pseudomonas</i> sp. 61-3	50,573	26-DEC-1998
		GB_BA1:SC8D9	38681	AL035569	<i>Streptomyces coelicolor</i> cosmid 8D9.	<i>Streptomyces coelicolor</i>	42,200	26-Feb-99
		GB_EST11:AA244557	379	AA244557	mx07a01.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:679464 5', mRNA sequence.	Mus musculus	39,050	10-MAR-1997
		GB_EST14:AA407673	306	AA407673	EST01834 Mouse 7.5 dpc embryo ectoplacental cone cDNA library Mus musculus cDNA clone C0014F02 3', mRNA sequence.	Mus musculus	38,562	26-Aug-98
		GB_EST26:A1390328	604	A1390328	mx07a01.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:679464 5', mRNA sequence.	Mus musculus	33,136	2-Feb-99



**TABLE 4: ALIGNMENT RESULTS**

rx01138	540	GB_OV:XLXINT1 GB_PR4:AC006054	1278 143738	X13138 AC006054	Xenopus laevis int-1 mRNA for int-1 protein. Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Xenopus laevis Homo sapiens	40,038 37,996	31-MAR-1995 1-Apr-99
rx01172	1578	GB_PR4:AC006054 GB_BA1:SCE39 GB_BA1:MSU50335	143738 23550 5193	AC006054 AL049573 U50335	Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence. Streptomyces coelicolor cosmid E39. Mycobacterium smegmatis phage resistance (mpr) gene, complete cds.	Homo sapiens Streptomyces coelicolor Mycobacterium smegmatis	36,053 62,357 37,853	1-Apr-99 31-MAR-1999 1-Feb-97
rx01191	1713	GB_BA1:BACTHRTRNA15467 GB_PR2:HS1191B2	60828 60828	D84213 AL022237	Bacillus subtilis genome, trnI-feuABC region. Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.	Bacillus subtilis Homo sapiens	53,807 38,366	6-Feb-99 23-Nov-99
rx01205	554	GB_PR2:HS1191B2	60828	AL022237	Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.	Homo sapiens	39,595	23-Nov-99
rx01212	1047	GB_BA1:MTCY373 GB_PL1:ATY12776 GB_PL2:ATT6K21 GB_BA2:SCD25	35516 38483 99643 41622	Z73419 Y12776 AL021889 AL118514	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162. Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus. Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSA project). Streptomyces coelicolor cosmid D25.	Mycobacterium tuberculosis Arabidopsis thaliana Arabidopsis thaliana Streptomyces coelicolor A3(2)	57,762 32,971 35,273 39,654	17-Jun-98 7-Sep-98 16-Aug-99 21-Sep-99
rx01219	1005	GB_BA1:SLGLYUB GB_BA1:SCH10 GB_PAT:A68024 GB_PAT:A68025 GB_PAT:A68027	2576 39524 520 193 193	X65556 AL049754 A68024 A68025 A68027	S.lividans tRNA-GlyU beta gene. Streptomyces coelicolor cosmid H10. Sequence 19 from Patent WO9743409. Sequence 20 from Patent WO9743409. Sequence 22 from Patent WO9743409.	Streptomyces lividans Streptomyces coelicolor unidentified unidentified unidentified	54,493 44,638 42,553 43,229 38,342	20-DEC-1993 04-MAY-1999 05-MAY-1999 05-MAY-1999 05-MAY-1999
rx01220	1200	GB_PR3:HS512B11 GB_EST6:N99239 GB_EST16:AA554268	64356 424 400	AL031058 N99239 AA554268	Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence. zb76h11.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:309573 3', mRNA sequence. nk36c09.s1 NCL_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1015600 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);, mRNA sequence.	Homo sapiens Homo sapiens Homo sapiens	35,478 39,623 36,111	23-Nov-99 20-Aug-96 8-Sep-97
rx01221	849	GB_PR4:AF179633 GB_VI:EHVU20824 GB_BA2:AE000407 GB_PAT:AR068625	96371 184427 10601 28804	AF179633 U20824 AE000407 AR068625	Homo sapiens chromosome 16 map 16q23.3-q24.1 sequence. Equine herpesvirus 2, complete genome. Escherichia coli K-12 MG1655 section 297 of 400 of the complete genome. Sequence 1 from patent US 5854034.	Homo sapiens Equine herpesvirus 2 Escherichia coli Unknown.	40,199 37,001 39,471 40,574	5-Sep-99 2-Feb-96 12-Nov-98 29-Sep-99



**TABLE 4: ALIGNMENT RESULTS**

GB_BA2:SSU51197	28804	U51197	SpHingomonas S88 sphingam polysaccharide synthesis (spsG), (spsS), (spsR), glycosyl transferase (spsQ), (spsI), glycosyl transferase (spsK), glycosyl transferase (spsL), (spsJ), (spsF), (spsD), (spsC), (spsE), Urf 32, Urf 26, ATP-binding cassette transporter (atrD), ATP-binding cassette transporter (atrB), glucosyl-isoprenylphosphate transferase (spsB), glucose-1-phosphate thymidyltransferase (rhsA), dTDP-6-deoxy-D-glucose -3,5-epimerase (rhsC) dTDP-D-glucose-4,6-dehydratase (rhsB), dTDP-6-deoxy-L-mannose-dehydrogenase (rhsD), Urf 31, and Urf 34 genes, complete cds.	40,574	16-MAY-1996
GB_IN1:BBU44918	2791	U44918	Babesia bovis ATP-binding protein (babC) mRNA, complete cds.	39,228	9-Aug-97
GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	99,923	1-Feb-99
GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	59,056	17-Jun-98
GB_PR3:AC005618	176714	AC005618	Homo sapiens chromosome 5, BAC clone 249h5 (LBNL H149), complete sequence.	36,270	5-Sep-98
GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	100,000	1-Feb-99
GB_HTG4:AC010045	164829	AC010045	Drosophila melanogaster chromosome 3L75A1 clone RPCI98-17C17, *** SEQUENCING IN PROGRESS ***, 50 unordered pieces.	50,512	16-OCT-1999
GB_HTG4:AC010045	164829	AC010045	Drosophila melanogaster chromosome 3L75A1 clone RPCI98-17C17, *** SEQUENCING IN PROGRESS ***, 50 unordered pieces.	50,512	16-OCT-1999
GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	56,071	01-DEC-1999
GB_BA1:AB002668	24907	AB002668	Actinobacillus actinomycetemcomitans DNA for glycosyltransferase, lytic transglycosylase, dTDP-4-rhamnose reductase, complete cds.	46,679	21-Feb-98
GB_BA1:AB010415	23112	AB010415	Actinobacillus actinomycetemcomitans gene cluster for 6-deoxy-L-talan synthesis, complete cds.	46,679	13-Feb-99
GB_STS:AU027820	238	AU027820	Rattus norvegicus, OTSUKA clone, OT78.02/918b07, microsatellite sequence, sequence tagged site.	34,874	02-MAR-1999
GB_STS:AU027820	238	AU027820	Rattus norvegicus, OTSUKA clone, OT78.02/918b07, microsatellite sequence, sequence tagged site.	34,874	02-MAR-1999
GB_HTG3:AC006445	174547	AC006445	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	34,812	15-Sep-99
GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.	37,802	26-Nov-97
GB_HTG3:AC010580	121119	AC010580	Drosophila melanogaster chromosome 3 clone BACR48J06 (D1102) RPCI-98 48.J.6 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces.	35,637	01-OCT-1999
GB_HTG3:AC010580	121119	AC010580	Drosophila melanogaster chromosome 3 clone BACR48J06 (D1102) RPCI-98 48.J.6 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces.	35,637	01-OCT-1999
GB_GSS8:AQ001809	705	AQ001809	CIT-HSP-2290D17.TF CIT-HSP Homo sapiens genomic clone 2290D17, genomic survey sequence.	42,021	26-Jun-98
GB_GSS8:AQ001809	705	AQ001809	CIT-HSP-2290D17.TF CIT-HSP Homo sapiens genomic clone 2290D17, genomic survey sequence.	40,323	26-Jun-98

**TABLE 4: ALIGNMENT RESULTS**

rx01339	1111	GB_PL1:MGU60290	4614	U60290	Magnaporthe grisea nitrogen regulatory protein (NUT1) gene, complete cds.	Magnaporthe grisea	38,707	3-Jul-96
		GB_HTG3:AC011371	189187	AC011371	Homo sapiens chromosome 5 clone CIT978SKB_107C20, *** SEQUENCING IN PROGRESS ***; 31 unordered pieces.	Homo sapiens	39,741	06-OCT-1999
		GB_HTG3:AC011371	189187	AC011371	Homo sapiens chromosome 5 clone CIT978SKB_107C20, *** SEQUENCING IN PROGRESS ***; 31 unordered pieces.	Homo sapiens	39,741	06-OCT-1999
rx01382	1192	GB_HTG4:AC009892	138122	AC009892	Homo sapiens chromosome 19 clone CIT978SKB_83J4, *** SEQUENCING IN PROGRESS ***; 6 ordered pieces.	Homo sapiens	40,154	31-OCT-1999
		GB_HTG4:AC009892	138122	AC009892	Homo sapiens chromosome 19 clone CIT978SKB_83J4, *** SEQUENCING IN PROGRESS ***; 6 ordered pieces.	Homo sapiens	40,154	31-OCT-1999
		GB_PR3:AC002416	128915	AC002416	Human Chromosome X, complete sequence.	Homo sapiens	37,521	29-Jan-98
rx01399	1142	GB_EST9:AA096601	524	AA096601	mo03b09.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:552473 5' similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN); gb:L04280 Mus musculus ribosomal protein (MOUSE); mRNA sequence.	Mus musculus	40,525	15-Feb-97
		GB_EST37:AI982114	626	AI982114	pat.pk0074.e9.f chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0074.e9.f 5' similar to H-ATPase B subunit, mRNA sequence.	Gallus gallus	37,785	15-Sep-99
		GB_OV:GGU20766	1645	U20766	Gallus gallus vacuolar H+-ATPase B subunit gene, complete cds.	Gallus gallus	38,244	07-DEC-1995
rx01420	1065	GB_HTG2:AC005690	193424	AC005690	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	37,464	11-Apr-99
		GB_HTG2:AC005690	193424	AC005690	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	37,464	11-Apr-99
		GB_HTG2:AC006637	22092	AC006637	Caenorhabditis elegans clone F41B4, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	Caenorhabditis elegans	37,488	23-Feb-99
rx01467	414	GB_HTG1:CEY102G3_2110000	AL020985	AL020985	Caenorhabditis elegans chromosome V clone Y102G3, *** SEQUENCING IN	Caenorhabditis elegans	35,437	3-Dec-98
		GB_HTG1:CEY102G3_2110000	AL020985	AL020985	Caenorhabditis elegans chromosome V clone Y102G3, *** SEQUENCING IN	Caenorhabditis elegans	35,437	3-Dec-98
		GB_HTG1:CEY113G7_4110000	AL031113	AL031113	Caenorhabditis elegans chromosome V clone Y113G7, *** SEQUENCING IN	Caenorhabditis elegans	35,437	12-Jan-99
rx01576	882	GB_BA2:AF030975	2511	AF030975	Aeromonas salmonicida chaperonin GroES and chaperonin GroEL genes, complete cds.	Aeromonas salmonicida	41,516	2-Apr-98
		GB_BA2:AF030975	2511	AF030975	Aeromonas salmonicida chaperonin GroES and chaperonin GroEL genes, complete cds.	Aeromonas salmonicida	38,171	2-Apr-98
		GB_EST22:AI068560	965	AI068560	mgae0003aC11f Magnaporthe grisea Appressorium Stage cDNA Library Pyricularia	Pyricularia grisea	40,073	09-DEC-1999
rx01580	840	GB_GSS14:AQ554460	681	AQ554460	grisea cDNA clone mgae0003aC11f 5', mRNA sequence.	Homo sapiens	36,522	28-MAY-1999
		GB_IN2:AC005449	85518	AC005449	RPCI-11-419F2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-419F2, genomic survey sequence.	Homo sapiens	36,609	23-DEC-1998
		GB_IN2:AC005449	85518	AC005449	Drosophila melanogaster, chromosome 2R, region 44C4-44C5, P1 clone DS06765, complete sequence.	Drosophila melanogaster	33,612	23-DEC-1998
rx01584					Drosophila melanogaster, chromosome 2R, region 44C4-44C5, P1 clone DS06765, complete sequence.	Drosophila melanogaster		
rx01604	771	GB_HTG3:AC011352	160167	AC011352	Homo sapiens chromosome 5 clone CIT-HSPC_327F10, *** SEQUENCING IN PROGRESS ***; 15 unordered pieces.	Homo sapiens	33,688	06-OCT-1999

**TABLE 4: ALIGNMENT RESULTS**

GB_HTG3:AC011352	160167	AC011352	Homo sapiens chromosome 5 clone CIT-HSPC_327F10, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
GB_HTG3:AC011402	168868	AC011402	Homo sapiens chromosome 5 clone CIT978SKB_38B5, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	42,284	11-Aug-98
GB_EST17:AA608825	439	AA608825	af03g07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030620 3' similar to TR:G976083 G976083 HISTONE H2A RELATED. ; mRNA sequence.	Homo sapiens	40,092	02-MAR-1998
GB_PR4:AC005377	102311	AC005377	Homo sapiens PAC clone DJ1136G02 from 7q32-q34, complete sequence.	Homo sapiens	37,811	28-Apr-99
GB_BA1:CGPROPGEN 2936	2936	Y12537	C.glutamicum proP gene.	Corynebacterium glutamicum	100,000	17-Nov-98
GB_BA1:CGPROPGEN 2936	2936	Y12537	C.glutamicum proP gene.	Corynebacterium glutamicum	100,000	17-Nov-98
GB_PR4:AF191071	88481	AF191071	Homo sapiens chromosome 8 clone BAC 388D06, complete sequence.	Homo sapiens	35,612	11-OCT-1999
GB_BA1:MSGB577COS37770	37770	L01263	M. leprae genomic dna sequence, cosmid b577.	Mycobacterium leprae	55,604	14-Jun-96
GB_BA1:MLCB2407	35615	AL023596	Mycobacterium leprae cosmid B2407.	Mycobacterium leprae	36,416	27-Aug-99
GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	55,844	24-Jun-99
GB_BA1:CGU43536	3464	U43536	Corynebacterium glutamicum heat shock, ATP-binding protein (clpB) gene, complete cds.	Corynebacterium glutamicum	100,000	13-MAR-1997
GB_HTG4:AC009841	164434	AC009841	Drosophila melanogaster chromosome 3L/77E1 clone RPC198-13F11, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	33,205	16-OCT-1999
GB_HTG4:AC009841	164434	AC009841	Drosophila melanogaster chromosome 3L/77E1 clone RPC198-13F11, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	33,205	16-OCT-1999
GB_GSS1:FR0022586	522	AL015452	F.rubripes GSS sequence, clone 077P23aB10, genomic survey sequence.	Fugu rubripes	40,192	10-DEC-1997
GB_GSS1:FR0022584	485	AL015450	F.rubripes GSS sequence, clone 077P23aB11, genomic survey sequence.	Fugu rubripes	35,876	10-DEC-1997
GB_IN1:CET26H2	37569	Z82055	Caenorhabditis elegans cosmid T26H2, complete sequence.	Caenorhabditis elegans	34,759	19-Nov-99
GB_BA2:CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake carrier (brnQ) genes, complete cds, and hypothetical protein YhbW (yhbW) gene, partial cds.	Corynebacterium glutamicum	99,929	4-Jun-98
GB_HTG6:AC011037	167849	AC011037	Homo sapiens clone RP11-7F18, WORKING DRAFT SEQUENCE, 19 unordered pieces.	Homo sapiens	36,903	30-Nov-99
GB_HTG6:AC011037	167849	AC011037	Homo sapiens clone RP11-7F18, WORKING DRAFT SEQUENCE, 19 unordered pieces.	Homo sapiens	35,642	30-Nov-99
GB_BA1:SCGD3	33779	AL096822	Streptomyces coelicolor cosmid GD3.	Streptomyces coelicolor	38,054	8-Jul-99
GB_HTG1:CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	35,147	05-OCT-1999
GB_HTG1:CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	35,147	05-OCT-1999
GB_BA1:MTCI28	36300	Z97050	Mycobacterium tuberculosis H37Rv complete genome; segment 10/162.	Mycobacterium tuberculosis	49,574	23-Jun-98
GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	44,049	24-MAR-1999
GB_BA1:SCE29	26477	AL035707	Streptomyces coelicolor cosmid E29.	Streptomyces coelicolor	40,246	12-MAR-1999

**TABLE 4: ALIGNMENT RESULTS**

rx01764	1056	GB_PL2:SPAC343	42947	AL109739	S.pombe chromosome I cosmid c343.	Schizosaccharomyces pombe	37,084	6-Sep-99
		GB_PL2:SPAC343	42947	AL109739	S.pombe chromosome I cosmid c343.	Schizosaccharomyces pombe	34,890	6-Sep-99
rx01801	1140	GB_EST38:AW066306	334	AW066306	687009D03.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.	Zea mays	46,108	12-OCT-1999
		GB_GSS13:AQ484750	375	AQ484750	RPCI-11-248N4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-248N4, genomic survey sequence.	Homo sapiens	32,000	24-Apr-99
		GB_GSS13:AQ489971	252	AQ489971	RPCI-11-247N23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-247N23, genomic survey sequence.	Homo sapiens	36,111	24-Apr-99
rx01823	900	GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	35,779	16-Aug-99
		GB_BA1:ECU82598	136742	U82598	Escherichia coli genomic sequence of minutes 9 to 12.	Escherichia coli	39,211	15-Jan-97
		GB_BA1:BSUB0018	209510	Z99121	Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.	Bacillus subtilis	36,999	26-Nov-97
rx01853	675	GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	37,612	17-Jun-98
		GB_HTG3:AC010189	265962	AC010189	Homo sapiens clone RPCI11-296K13, *** SEQUENCING IN PROGRESS ***, 80 unordered pieces.	Homo sapiens	39,006	16-Sep-99
		GB_HTG3:AC010189	265962	AC010189	Homo sapiens clone RPCI11-296K13, *** SEQUENCING IN PROGRESS ***, 80 unordered pieces.	Homo sapiens	39,006	16-Sep-99
rx01881	558	GB_HTG4:AC011117	148447	AC011117	Homo sapiens chromosome 4 clone 173_C_09 map 4, *** SEQUENCING IN PROGRESS ***, 10 ordered pieces.	Homo sapiens	39,130	14-OCT-1999
		GB_HTG4:AC011117	148447	AC011117	Homo sapiens chromosome 4 clone 173_C_09 map 4, *** SEQUENCING IN PROGRESS ***, 10 ordered pieces.	Homo sapiens	39,130	14-OCT-1999
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	37,893	18-Jun-98
rx01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELF46H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-96
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces.	Drosophila melanogaster	31,579	18-Aug-99
rx01897	666	GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	34,703	1-Apr-99
		GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	34,703	1-Apr-99
		GB_HTG1:CEY53F4_2	110000	Z92860	Caenorhabditis elegans chromosome II clone Y53F4, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	33,333	15-Oct-99
rx01946	1298	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	65,560	17-Jun-98
		GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	50,648	24-MAY-1999
		GB_BA1:SCARD1GN	2321	X84374	S.capreolus ard1 gene.	Streptomyces capreolus	44,973	23-Aug-95



**TABLE 4: ALIGNMENT RESULTS**

rx01980	756	GB_PL2:AC008262	99698	AC008262	Genomic sequence for Arabidopsis thaliana BAC F4N2 from chromosome I, complete sequence.	Arabidopsis thaliana	35,310	21-Aug-99
		GB_PL1:AB013388	73428	AB013388	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence.	Arabidopsis thaliana	35,505	20-Nov-99
		GB_PL1:AB013388	73428	AB013388	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence.	Arabidopsis thaliana	39,973	20-Nov-99
rx01983	630	GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Drosophila melanogaster	36,672	27-OCT-1999
		GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Drosophila melanogaster	36,672	27-OCT-1999
		GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Drosophila melanogaster	32,367	27-OCT-1999
rx02020	1111	GB_BA1:CGDNAAROP 2612	X85965	X85965	C.glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	100,000	30-Nov-97
		GB_PAT:A58887	1612	A58887	Sequence 1 from Patent WO9701637.	unidentified	100,000	06-MAR-1998
		GB_BA1:STYCARABA 4378	M95047	M95047	Salmonella typhimurium transport protein, complete cds, and transfer RNA-Arg.	Salmonella typhimurium	50,547	13-MAR-1996
rx02029	1437	GB_HTG2:AC003023	104768	AC003023	Homo sapiens chromosome 11 clone pDJ363p2, *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Homo sapiens	35,820	21-OCT-1997
		GB_HTG2:AC003023	104768	AC003023	Homo sapiens chromosome 11 clone pDJ363p2, *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Homo sapiens	35,820	21-OCT-1997
		GB_HTG2:HS118B18	104729	AL034344	Homo sapiens chromosome 6 clone RP1-118B18 map p24.1-25.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	34,355	03-DEC-1999
rx02030	1509	GB_PR4:AC007695	63247	AC007695	Homo sapiens 12q24 BAC RPC111-124N23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	38,681	1-Sep-99
		GB_PR4:AC006464	99908	AC006464	Homo sapiens BAC clone NH0436C12 from 2, complete sequence.	Homo sapiens	35,445	22-OCT-1999
		GB_PR4:AC006464	99908	AC006464	Homo sapiens BAC clone NH0436C12 from 2, complete sequence.	Homo sapiens	35,968	22-OCT-1999
rx02073	1653	GB_BA1:CGGDHA	2037	X72855	C.glutamicum GDHA gene.	Corynebacterium glutamicum	39,655	24-MAY-1993
		GB_BA1:CGGDH	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	44,444	30-Jul-99
		GB_BA2:SC2H4	25970	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	38,452	19-OCT-1999
rx02074								
rx02095	1527	GB_EST18:AA703380	471	AA703380	zj12b06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450035 3' similar to contains LTR5.i3 LTR5 repetitive element ;, mRNA sequence.	Homo sapiens	36,518	24-DEC-1997
		GB_HTG6:AC009769	122911	AC009769	Homo sapiens chromosome 8 clone RP11-202112 map 8, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,473	07-DEC-1999



**TABLE 4: ALIGNMENT RESULTS**

rx02099	373	GB_EST7:W70175	436	W70175	zd52c02.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344258 5' similar to contains LTR5.b2 LTR5 repetitive element;; mRNA sequence.	Homo sapiens	34,174	16-OCT-1996
		GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial fisY and srp genes.	Corynebacterium glutamicum	100,000	14-MAY-1999
		GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***, 35 unordered pieces.	Homo sapiens	33,423	07-OCT-1999
		GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***, 35 unordered pieces.	Homo sapiens	33,423	07-OCT-1999
rx02115	1197	GB_HTG5:AC010126	175986	AC010126	Homo sapiens clone GS502B02, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	36,717	13-Nov-99
		GB_HTG5:AC010126	175986	AC010126	Homo sapiens clone GS502B02, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	36,092	13-Nov-99
		GB_PR1:HUMHM145	2214	D10925	Human mRNA for HM145.	Homo sapiens	39,171	3-Feb-99
rx02128	1818	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	38,682	17-Jun-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	35,746	17-Jun-98
		GB_GSS10:AQ161109	738	AQ161109	nbxb0006D03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0006D03r, genomic survey sequence.	Oryza sativa	38,482	12-Sep-98
rx02133	329	GB_BA2:MPAE000058	28530	AE000058	Mycoplasma pneumoniae section 58 of 63 of the complete genome.	Mycoplasma pneumoniae	32,317	18-Nov-96
		GB_HTG4:AC008308	151373	AC008308	Drosophila melanogaster chromosome 3 clone BACR10M16 (D743) RPCI-98 10.M.16 map 93C-93D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 186 unordered pieces.	Drosophila melanogaster	34,579	20-OCT-1999
		GB_HTG4:AC008308	151373	AC008308	Drosophila melanogaster chromosome 3 clone BACR10M16 (D743) RPCI-98 10.M.16 map 93C-93D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 186 unordered pieces.	Drosophila melanogaster	34,579	20-OCT-1999
rx02150	924	GB_EST37:AW012260	358	AW012260	um06e09.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2182312 5' similar to SW:AMPL_BOVIN P00727 CYTOSOL AMINOPEPTIDASE.; mRNA sequence.	Mus musculus	39,385	10-Sep-99
		GB_GSS3:B87734	389	B87734	RPCI11-30D24.TP RPCI-11 Homo sapiens genomic clone RPCI-11-30D24, genomic survey sequence.	Homo sapiens	37,629	9-Apr-99
		GB_PR4:AC005042	192218	AC005042	Homo sapiens clone NH0552E01, complete sequence.	Homo sapiens	36,901	14-Jan-99
rx02171	1776	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	53,714	12-MAY-1998
		GB_EST24:A1170522	367	A1170522	EST216450 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUCO75 3' end, mRNA sequence.	Rattus sp.	44,186	20-Jan-99
		GB_PL1:PHVDLECA	1441	K03288	P.vulgaris phytohemagglutinin gene encoding erythroagglutinating phytohemagglutinin (PHA-E), complete cds.	Phaseolus vulgaris	39,103	27-Apr-93
rx02173	1575	GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	44,118	17-Feb-95
		GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	36,189	17-Feb-95

**TABLE 4: ALIGNMENT RESULTS**

rx02224	1920	GB_BA2:AE000104	10146	AE000104	Rhizobium sp. NGR234 plasmid pNGR234a, section 41 of 46 of the complete plasmid sequence.	Rhizobium sp. NGR234	38,487	12-DEC-1997
		GB_BA2:CXU21300	8990	U21300	Corynebacterium striatum hypothetical protein YbhB gene, partial cds; ABC transporter TetB (tetB), ABC transporter TetA (tetA), transposase, 23S rRNA methyltransferase, and transposase genes, complete cds; and unknown genes.	Corynebacterium striatum	37,264	9-Apr-99
		GB_HTG3:AC009185	87184	AC009185	Homo sapiens chromosome 5 clone CIT-HSPC_248O19, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	36,459	07-OCT-1999
		GB_HTG3:AC009185	87184	AC009185	Homo sapiens chromosome 5 clone CIT-HSPC_248O19, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	36,459	07-OCT-1999
rx02225	905	GB_BA2:MPAE000058	28530	AE000058	Mycoplasma pneumoniae section 58 of 63 of the complete genome.	Mycoplasma pneumoniae	35,498	18-Nov-96
		GB_EST26:AI337275	618	AI337275	tb96h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062245 3' similar to TR:Q15392 Q15392 ORF, COMPLETE CDS. ; mRNA sequence.	Homo sapiens	35,589	18-MAR-1999
		GB_EST26:AI337275	618	AI337275	tb96h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062245 3' similar to TR:Q15392 Q15392 ORF, COMPLETE CDS. ; mRNA sequence.	Homo sapiens	42,786	18-MAR-1999
rx02233	1410	GB_BA1:ERWPNLB	1291	M65057	Erwinia carotovora pectin lyase (prl) gene, complete cds.	Erwinia carotovora	37,780	26-Apr-93
		GB_EST30:AV021947	313	AV021947	AV021947 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190024M23, mRNA sequence.	Mus musculus	39,423	28-Aug-99
		GB_EST33:AV087117	251	AV087117	AV087117 Mus musculus tongue C57BL/6J adult Mus musculus cDNA clone 2310028C15, mRNA sequence.	Mus musculus	47,410	25-Jun-99
rx02253	1050	GB_EST11:AA250210	532	AA250210	mx79g10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692610 5' similar to TR:E236517 E236517 F44G4.1 ; mRNA sequence.	Mus musculus	36,136	12-MAR-1997
		GB_EST11:AA250210	532	AA250210	mx79g10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692610 5' similar to TR:E236517 E236517 F44G4.1 ; mRNA sequence.	Mus musculus	36,202	12-MAR-1997
rx02261	1479	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGENE	2028	X93513	C. glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1996
		GB_BA1:CORPEPC	4885	M25819	C. glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
rx02268	1023	GB_PL2:AF087130	3478	AF087130	Neurospora crassa siderophore regulation protein (sre) gene, complete cds.	Neurospora crassa	39,268	22-OCT-1998
		GB_EST30:AI663709	408	AI663709	ud47a06.y1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:1449010 5' similar to TR:O75585 O75585 MITOGEN- AND STRESS-ACTIVATED PROTEIN KINASE-2 ; mRNA sequence.	Mus musculus	41,523	10-MAY-1999
		GB_RO:AF074714	3120	AF074714	Mus musculus mitogen- and stress-activated protein kinase-2 (mMSK2) mRNA, complete cds.	Mus musculus	38,347	24-OCT-1998
rx02269	1095	GB_GSS4:AQ742825	847	AQ742825	HS_5482_B2_A04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1058 Col=8 Row=B, genomic survey sequence.	Homo sapiens	37,703	16-Jul-99
		GB_HTG3:AC009293	162944	AC009293	Homo sapiens chromosome 18 clone 53_L_06 map 18, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	37,006	13-Aug-99
		GB_HTG3:AC009293	162944	AC009293	Homo sapiens chromosome 18 clone 53_L_06 map 18, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	37,006	13-Aug-99

**TABLE 4: ALIGNMENT RESULTS**

rx02309	1173	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	52,344	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	52,344	03-DEC-1996
		GB_HTG2:AC007163	186618	AC007163	Homo sapiens clone NH0091M05, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	Homo sapiens	37,263	23-Apr-99
rx02310	1386	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,861	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	36,861	03-DEC-1996
		GB_PR3:HS279N11	169998	Z98255	Human DNA sequence from PAC 279N11 on chromosome Xq11.2-13.3.	Homo sapiens	34,516	23-Nov-99
rx02321	1752	GB_BA1:AB018531	4961	AB018531	Corynebacterium glutamicum dtsR1 and dtsR2 genes, complete cds.	Corynebacterium glutamicum	99,030	19-OCT-1998
		GB_PAT:E17019	4961	E17019	Brevibacterium lactofermentum dtsR and dtsR2 genes.	Corynebacterium glutamicum	98,973	28-Jul-99
		GB_BA1:AB018530	2855	AB018530	Corynebacterium glutamicum dtsR gene, complete cds.	Corynebacterium glutamicum	99,030	19-OCT-1998
rx02335	1896	GB_BA1:CGU35023	3195	U35023	Corynebacterium glutamicum thiosulfate sulfurtransferase (thiR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds.	Corynebacterium glutamicum	99,947	16-Jan-97
		GB_BA1:U00012	33312	U00012	Mycobacterium leprae cosmid B1308.	Mycobacterium leprae	40,247	30-Jan-96
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	67,568	10-Feb-99
rx02364	750	GB_BA1:AP000006	319000	AP000006	Pyrococcus horikoshii OT3 genomic DNA, 1165001-1485000 nt. position (6/7).	Pyrococcus horikoshii	36,130	8-Feb-99
		GB_BA1:AP000006	319000	AP000006	Pyrococcus horikoshii OT3 genomic DNA, 1165001-1485000 nt. position (6/7).	Pyrococcus horikoshii	34,543	8-Feb-99
rx02372	2010	GB_HTG3:AC011461	100974	AC011461	Homo sapiens chromosome 19 clone CIT-HSPC_429L19, *** SEQUENCING IN PROGRESS ***; 4 ordered pieces.	Homo sapiens	36,138	07-OCT-1999
		GB_HTG3:AC011461	100974	AC011461	Homo sapiens chromosome 19 clone CIT-HSPC_429L19, *** SEQUENCING IN PROGRESS ***; 4 ordered pieces.	Homo sapiens	36,138	07-OCT-1999
		GB_EST21:AA992021	279	AA992021	α36c01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618848 3', mRNA sequence.	Homo sapiens	41,219	3-Jun-98
rx02397	1119	GB_HTG4:AC009273	76175	AC009273	Arabidopsis thaliana chromosome 1 clone T1N6, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Arabidopsis thaliana	38,566	12-OCT-1999
		GB_HTG4:AC009273	76175	AC009273	Arabidopsis thaliana chromosome 1 clone T1N6, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Arabidopsis thaliana	38,566	12-OCT-1999
		GB_BA1:D90826	19493	D90826	E.coli genomic DNA, Kohara clone #335(40.9-41.3 min.).	Escherichia coli	39,600	21-MAR-1997
rx02424	723	GB_EST13:AA334108	275	AA334108	EST38262 Embryo, 9 week Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,603	21-Apr-97
		GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	36,111	14-Aug-98
		GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	33,427	14-Aug-98
rx02426	1656	GB_PAT:A06664	1350	A06664	B.stearothermophilus lct gene.	Bacillus stearothermophilus	39,936	29-Jul-93
		GB_PAT:A04115	1361	A04115	B.stearothermophilus recombinant lct gene.	synthetic construct	40,042	17-Feb-97
		GB_BA1:BACLDHL	1361	M14788	B.stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds.	Bacillus stearothermophilus	40,338	26-Apr-93

**TABLE 4: ALIGNMENT RESULTS**

rx02487	1827	GB_BA2:AF007101	32870	AF007101	Streptomyces hygroscopicus putative pteridine-dependent dioxygenase, PKS modules 1,2,3 and 4, and putative regulatory protein genes, complete cds and putative hydroxylase gene, partial cds.	Streptomyces hygroscopicus	43,298	13-Jan-98
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	44,352	17-Jun-98
		GB_BA2:AF119621	15986	AF119621	Pseudomonas abietaniphila BKME-9 Dtl (ditl), dioxygenase DtlA oxygenase component small subunit (ditA2), dioxygenase DtlA oxygenase component large subunit (ditA1), DtlH (ditH), DtlG (ditG), DtlF (ditF), DtlR (ditR), DtlE (ditE), DtlD (ditD), aromatic diterpenoid extradiol ring-cleavage dioxygenase (ditC), DtlB (ditB), and dioxygenase DtlA ferredoxin component (ditA3) genes, complete cds; and unknown genes.	Pseudomonas abietaniphila	43,611	28-Apr-99
rx02511	780	GB_PR4:AC002470	235395	AC002470	Homo sapiens Chromosome 22q11.2 BAC Clone b135h6 In BCRL2-GGT Region, complete sequence.	Homo sapiens	37,971	30-Nov-99
		GB_PR4:AC002472	147100	AC002472	Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCRL2-GGT Region, complete sequence.	Homo sapiens	38,239	13-Sep-99
		GB_EST34:AI806938	118	AI806938	wf24b07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356501 3' similar to SW:PLZF_HUMAN Q05516 ZINC FINGER PROTEIN PLZF ;, mRNA sequence.	Homo sapiens	38,983	7-Jul-99
rx02512	1086	GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	37,407	17-Jun-98
		GB_BA1:MLCL581	36225	Z96801	Mycobacterium leprae cosmid L581.	Mycobacterium leprae	43,193	24-Jun-97
		GB_OV:GGU43396	2738	U43396	Gallus gallus tropomyosin receptor kinase A (ctrkA) mRNA, complete cds.	Gallus gallus	38,789	18-Jan-96
rx02527	1452	GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rrmB-dnaB genomic region.	Bacillus subtilis	37,395	4-Feb-98
		GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rrmB-dnaB genomic region.	Bacillus subtilis	36,218	4-Feb-98
		GB_HTG2:AC005861	112369	AC005861	Arabidopsis thaliana clone F23B24, *** SEQUENCING IN PROGRESS ***; 6 unordered pieces.	Arabidopsis thaliana	38,407	29-Apr-99
rx02547	2262	GB_PL1:AB006530	7344	AB006530	Citrullus lanatus Sat gene for serine acetyltransferase, complete cds and 5'-flanking region.	Citrullus lanatus	35,449	20-Aug-97
		GB_PL1:CNASA	5729	D85624	Citrullus vulgaris serine acetyltransferase (Sat) DNA, complete cds.	Citrullus lanatus	35,449	6-Feb-99
		GB_PL1:AB006530	7344	AB006530	Citrullus lanatus Sat gene for serine acetyltransferase, complete cds and 5'-flanking region.	Citrullus lanatus	34,646	20-Aug-97
rx02566	1332	GB_EST32:AI727189	619	AI727189	BNLGH7498 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AB020715) KIAA0908 protein [Homo sapiens], mRNA sequence.	Gossypium hirsutum	35,099	11-Jun-99
		GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	38,562	8-Sep-97
		GB_PL2:SPAC13G6	33481	Z54308	S.pombe chromosome I cosmid c13G6.	Schizosaccharomyces pombe	35,774	18-OCT-1999
rx02571	1152	GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,872	9-Apr-97
		GB_EST35:AI857385	488	AI857385	w155e03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2428828 3', mRNA sequence.	Homo sapiens	39,139	26-Aug-99
		GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	38,552	9-Apr-97



**TABLE 4: ALIGNMENT RESULTS**

rx02578	1227	GB_PL1:AB016871	79109	AB016871	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence.	Arabidopsis thaliana	34,213	20-Nov-99
		GB_PL1:AB025602	55790	AB025602	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F14A1, complete sequence.	Arabidopsis thaliana	36,461	20-Nov-99
		GB_IN1:CELF36H9	35985	AF016668	Caenorhabditis elegans cosmid F36H9.	Caenorhabditis elegans	35,977	8-Aug-97
rx02581	1983	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	38,517	17-Jun-98
		GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	39,173	17-Jun-98
rx02582	4953	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	38,548	24-Jun-99
		GB_BA1:MTCY338	29372	Z74697	Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.	Mycobacterium tuberculosis	46,263	17-Jun-98
		GB_BA1:SEERYABS	20444	X62569	S.erythraea eryA gene for 6-deoxyerythronolide B synthase II & III.	Saccharopolyspora erythraea	45,053	28-Feb-92
rx02583	1671	GB_BA2:AF113605	1593	AF113605	Streptomyces coelicolor propionyl-CoA carboxylase complex B subunit (pccB) gene, complete cds.	Streptomyces coelicolor	58,397	08-DEC-1999
		GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	52,916	15-Jan-99
		GB_BA1:AB018531	4961	AB018531	Corynebacterium glutamicum dtsR1 and dtsR2 genes, complete cds.	Corynebacterium glutamicum	58,809	19-OCT-1998
rx02599	600	GB_BA1:AEMMIL	2585	X99639	Ralstonia eutropha mmlH, mmlI & mmlJ genes.	Ralstonia eutropha	35,264	22-Jan-98
		GB_EST15:AA508926	422	AA508926	MBAFCW1C08T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia malayi cDNA clone AFCW1C08 5', mRNA sequence.	Brugia malayi	43,377	8-Jul-97
		GB_BA1:AEMMIL	2585	X99639	Ralstonia eutropha mmlH, mmlI & mmlJ genes.	Ralstonia eutropha	41,148	22-Jan-98
rx02634	1734	GB_BA1:SYNPOO	1964	X17439	Synechocystis ndhC, psbG genes for NDH-C, PSII-G and ORF157.	Synechocystis PCC6803	38,145	10-Feb-99
		GB_GSS9:AQ101527	184	AQ101527	HS_2265_A1_E11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2265 Col=21 Row=I, genomic survey sequence.	Homo sapiens	38,798	27-Aug-98
		GB_IN1:MNE133341	399	AJ133341	Melarhaphe neritoides partial caM gene, exons 1-2.	Melarhaphe neritoides	39,098	2-Jun-99
rx02638	999	GB_BA2:AE001756	10938	AE001756	Thermotoga maritima section 68 of 136 of the complete genome.	Thermotoga maritima	40,104	2-Jun-99
		GB_GSS12:AQ423878	689	AQ423878	CITBI-E1-2575E20.TF CITBI-E1 Homo sapiens genomic clone 2575E20, genomic survey sequence.	Homo sapiens	36,451	23-MAR-1999
		GB_HTG2:AC006765	274498	AC006765	Caenorhabditis elegans clone Y43H11, *** SEQUENCING IN PROGRESS***, 7 unordered pieces.	Caenorhabditis elegans	39,072	23-Feb-99
rx02659	335	GB_EST36:AI900317	436	AI900317	sc04a02.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:Gm-c1012-1155 5' similar to SW:PRS6_SOLTU P54778 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG. ; mRNA sequence.	Glycine max	41,566	06-DEC-1999
		GB_GSS12:AQ342831	683	AQ342831	RPC111-122K17.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-122K17, genomic survey sequence.	Homo sapiens	34,762	07-MAY-1999
		GB_EST36:AI900856	779	AI900856	sb95c11.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1012-429 5' similar to SW:PRS6_SOLTU P54778 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG. ; mRNA sequence.	Glycine max	39,063	06-DEC-1999
rx02676	1512	GB_IN2:CELB0213	39134	AF039050	Caenorhabditis elegans cosmid B0213.	Caenorhabditis elegans	35,814	2-Jun-99



**TABLE 4: ALIGNMENT RESULTS**

882	rx02677	GB_GSS1:CNS00PZB	364	AL085157	Arabidopsis thaliana genome survey sequence SP6 end of BAC F10D11 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	38,462	28-Jun-99
		GB_RO:RNITPR2R	10708	X61677	Rat ITPR2 gene for type 2 inositol triphosphate receptor.	Rattus norvegicus	37,543	21-OCT-1991
		GB_RO:D89728	5002	D89728	Mus musculus mRNA for LOK, complete cds.	Mus musculus	38,829	7-Feb-99
		GB_GSS8:AQ062004	362	AQ062004	CIT-HSP-2346O14.TR CIT-HSP Homo sapiens genomic clone 2346O14, genomic survey sequence.	Homo sapiens	36,565	31-Jul-98
		GB_GSS14:AQ555818	462	AQ555818	HS_5230_B1_G06_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=806 Col=11 Row=N, genomic survey sequence.	Homo sapiens	36,534	29-MAY-1999
		GB_IN1:DME9736	7411	AJ009736	Drosophila melanogaster Idefix retroelement: gag, pol and env genes, partial.	Drosophila melanogaster	36,522	19-Jan-99
		GB_PR4:AC004801	193561	AC004801	Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	39,341	2-Feb-99
		GB_PR4:AC004801	193561	AC004801	Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	37,037	2-Feb-99
		GB_EST34:AV132028	258	AV132028	AV132028 Mus musculus C57BL/6J 11-day embryo Mus musculus cDNA clone 2700087F01, mRNA sequence.	Mus musculus	43,529	1-Jul-99
		GB_GSS10:AQ240654	452	AQ240654	CIT-HSP-2385D24.TFB.1 CIT-HSP Homo sapiens genomic clone 2385D24, genomic survey sequence.	Homo sapiens	40,044	30-Sep-98
		GB_GSS11:AQ309500	576	AQ309500	CIT-HSP-2384D24.TFD CIT-HSP Homo sapiens genomic clone 2384D24, genomic survey sequence.	Homo sapiens	38,869	22-DEC-1998
		GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	Zymomonas mobilis	39,024	4-Nov-98
		GB_BA1:SYCSLRB	146271	D64000	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999.	Synechocystis sp.	34,573	13-Feb-99
		GB_BA2:AE001306	13316	AE001306	Chlamydia trachomatis section 33 of 87 of the complete genome.	Chlamydia trachomatis	38,940	2-Sep-98
		GB_BA2:AF126953	1638	AF126953	Corynebacterium glutamicum cystathionine gamma-synthase (metB) gene, complete cds.	Corynebacterium glutamicum	100,000	10-Sep-99
		GB_BA1:SC15	6661	AL079332	Streptomyces coelicolor cosmid I5.	Streptomyces coelicolor	37,486	16-Jun-99
		GB_PR3:HS90L6	190837	Z97353	Human DNA sequence from clone 90L6 on chromosome 22q11.21-11.23. Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	Homo sapiens	34,149	23-Nov-99
		GB_BA2:AF099015	5000	AF099015	Streptomyces coelicolor strain A3(2) integrase (int), Fe-containing superoxide dismutase II (sodF2), Fe uptake system permease (ftrE), and Fe uptake system integral membrane protein (ftrD) genes, complete cds.	Streptomyces coelicolor	36,721	1-Jun-99
		GB_BA1:ECOUIW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,787	17-Apr-96
		GB_HTG3:AC011361	186148	AC011361	Homo sapiens chromosome 5 clone CIT-HSPC_482N19, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces.	Homo sapiens	43,577	06-OCT-1999
		GB_PR4:AC005998	96556	AC005998	Homo sapiens clone DJ0622E21, complete sequence.	Homo sapiens	37,298	29-Jul-99
		GB_PR4:AC006008	57554	AC006008	Homo sapiens clone DJ0820A21, complete sequence.	Homo sapiens	36,638	17-Jun-99
		GB_PR3:HSDJ73H14	95556	AL080272	Human DNA sequence from clone 73H14 on chromosome Xq26.3-28, complete sequence.	Homo sapiens	39,726	23-Nov-99

**TABLE 4: ALIGNMENT RESULTS**

rx02809	375	GB_RO:MUSPCTLT	3172	M22527	Mouse cytotoxic T lymphocyte-specific serine protease CCP1 gene, complete cds.	Mus musculus	47,518	19-Jan-96
		GB_RO:MUSGRC	894	M18459	Mouse granzyme C serine esterase mRNA, complete cds.	Mus musculus	44,939	12-Jun-93
		GB_RO:RNU57062	880	U57062	Rattus norvegicus natural killer cell protease 4 (RNKP-4) mRNA, complete cds.	Rattus norvegicus	41,554	31-Jul-96
rx02811	484	GB_GSS6:AQ832862	476	AQ832862	HS_5261_A2_E10_SP6E RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=837 Col=20 Row=i, genomic survey sequence.	Homo sapiens	35,610	27-Aug-99
		GB_GSS5:AQ784593	515	AQ784593	HS_3248_A2_F02_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3248 Col=4 Row=K, genomic survey sequence.	Homo sapiens	38,956	3-Aug-99
		GB_GSS13:AQ473140	397	AQ473140	CITBI-E1-2589G6.TF CITBI-E1 Homo sapiens genomic clone 2589G6, genomic survey sequence.	Homo sapiens	34,761	23-Apr-99
rx02836	678	GB_EST18:AA696785	316	AA696785	GM08392.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM08392 5prime, mRNA sequence.	Drosophila melanogaster	40,604	28-Nov-98
		GB_EST18:AA696785	316	AA696785	GM08392.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM08392 5prime, mRNA sequence.	Drosophila melanogaster	38,281	28-Nov-98
rxs03212	1452	GB_BA1:CGBETPGEN	2339	X93514	C.glutamicum batP gene.	Corynebacterium glutamicum	99,931	8-Sep-97
		GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor A3(2)	57,557	24-MAY-1999
		GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rrnB-dnaB genomic region.	Bacillus subtilis	40,000	4-Feb-98
rxs03220	725	GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.	Chlorella kessleri	45,328	17-Feb-97
		GB_EST38:AW048153	383	AW048153	UI-M-BH1-alq-h-05-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alq-h-05-0-UI 3', mRNA sequence.	Mus musculus	41,758	18-Sep-99
		GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.	Chlorella kessleri	38,106	17-Feb-97

## APPENDIX A: DNA SEQUENCES

>RXA00051-upstream

CAGTAAAAGTGCACCGACACTAAGAATCCTTATCCTTCAGAGTAAGGTGATCTGCGTCAA  
AAAATGTCCGCTATTCACCCGAAACGAGGTCAGCATCTCG

>RXA00051

ATGAATGCCTCCCCTGCCCCAACCCGATCTTTTAAAGGATTGCGGGCTCGACACATTCAC  
TTCATCGCGCTGGGTTCGCGATCGGCACCGGCTTGTTCTACGGTTCCGCTGGCGCAATC  
CAAGCAGCTGGTCCATCTGTACTCTTGGTCTACCTTCTCGGTGGCGCCGTCGTGTACTTC  
ATGCTGCGCGCACTCGGCGAGATGGCTGTGCATCACCCAGTCCGTGGTTCCTTCGCGGTC  
TACACCCGCGCACACCTTGGCGGATGGGCAGGCTACATCACCGGCTGGATGTTGCGGTTT  
GAGATGCTCATCGTCTGCCTGGCTGACCTCACAGCCATCGGCATCTATATGAACTTCTGG  
TTCCCCGGCACCCCAACAATGGACTTGGGTGGTAGCCACCCTTCTTATTGTCGGTGGCGCA  
AACCTCGCATCAGTGCCTTGGTTCGGTGAGCTCGAGTTCATCTTCACCATCATTAAGGTC  
ACCGCAGTTGTGCGCATGATCGTTCGGCGGCGCAGCCATCCTCGCATTCGGTCTCGGCGCC  
AACGCTGAAGTTGCCGGCGTATCCAACCTCTGGGAGCACGGCGGATTCTTCCCCAACGGT  
GTTGAAGGCATGATCGCAGCCTTCATCCTTGTCTCTTCGCATTCGGTGGCACCAGAAATC  
ATCGGTGTTGCAGGCTCTGAAGCTGAAGATCCTGAGAAGTCCATCCCCAAGGCTGTTAAT  
ACTGTCCCAGTACGCATCCTCCTCTTCTATGTGGGTGCCATCCTGGTGATCCTTGCCCTT  
AATCCTTGGCCTTCCATCACCGGCGAAGAATCCCCATTTCGTCCAGATCTTCGACACCCTC  
GGCGTCAACTGGGCTGCTGGTCTCCTCAACGCCGTGGTTCATCACCGCTGCACTGTCTGCC  
ATCAACGCTGACCTCTTCGGCGCTGGCCGCGTTCTCACTGGTCTTGCGAAGGAAAACCTC  
GCACCAAAGGCCATGGGCAAGATCGCCAAGAACGGCGTTCCAGTCATGACCACCACCATC  
ATGATCATCGTCTTGATCGTGGGAGTAATCCTCAACGCAGTGCTTCCCGAGCGCGTCTTC  
GAGATCGTCGCTTCCCTAGCAACCTTCGCCACAGTTTACGTCTGGCTGATGATCCTGCTC  
GCACAGGTGGGATCCCGCCGAAACATGCCTGCCGACGAGGTCAAGTCCCTGAAGTTCCCT  
GTCCCCTTCTACCCCTTCGGACAATACTTCGCGATCCTATTTATCGCCTTCACCTTCGGC  
ATCATGGTCTGGTACGACAATACTACACCTGCCACTCGCCGTCCGGCGTTGGATTCCTTGTC  
CTGATGACAATCCTTTACTACGCCACAGGCCGACCAAAGGCGATCGCTCCGATCGATTAT  
GAAGAGCTAGATCCGCGACGCGAT

>RXA00051-downstream

TAATCTAGACTCGCACGAAAAAG

>RXA00091-upstream

TCATGAACCACGTGTTCCGCGCACAAGGCGTCGTGTCCATCATTATTGAGATGGTCGGCG  
GTACCGTCTTCCTCATCGTCATCCTCAGAAAGGGCAGACT

>RXA00091

GTGATTACGTAACTAATGTCCGCAAGGAATACTCCAGCGACGTTGCCATCGGCCCCGTC  
AACCTTGAGATCCCAGCCGGCGGCATCACCGCGTTGGTCGGCCCCAACGGTGCAGGCAAG  
TCAACACTGCTCACCATGATCGGTGCACTCCTCGGCATCGATGAAGGCAACATCACCGTA  
GCCTCCTACGATGTACCTCAACCGCATCCAAAGATCTGGCCAAGATCATCTCCATCCTG  
CGCCAGGAAAACCACTTTGTTACCAAGCTGACCGTGCGCCAGCTCGTAGGTTTCGGACGC  
TTCCCATATAGCAAGGGCCGGCTGACGGAAGAAGACGAGGGAATCATCTCCCGCTACATC  
GACTTCTTCAATCTCACCGAACTCGAAGACCGCTACCTCGACCAGCTTTCGGCGGGCCAG  
CGCCAGCGCGCCTATGTGCGCATGGTGCTGTGCCAAGAGACGGACTACGTGCTTCTCGAC  
GAACCCCTCAACAATCTTGATATCGCACACTCGGTGGAAATGATGAAACACCTCGAGAAT  
GCTGCAGCCCAATTTGGCCGCACCATCATCGTGGTTCCTTCACGACATCAACTTCGCCGCG  
CGCTACGCCGATTACATCGTGGCCGTAAAGCACGGAATGATCGAAAAAGAGGGAACACCT  
GAACAGATCATGAAAAACGAGATCCTTTCAGAAATCTTCAATACAGAGATCGAAGTTATT  
GAAGGACCACACGGCAAGATTGCTTGCTACCAC

>RXA00091-downstream

TAAATGAAGAGAAATAAGCCGAC

>RXA00092

ATCGCGAGAGCCCTCATCGGCCCCCGAAAAATCTTGCTTGCCGACGAACCCACCGGCGCC

CTCGACACCTCCACCGGCGACGCAGTCCTCCGCGTCCTCCGCCAAAGAATCGATTCCGGT  
GCCGCAGGCCTCCTTGTACCCACGAACCCCGCTTCGCCGCGTGGGCAGACCGAACAATC  
ATGCTTAGGGATGGTGAAATCCAG

>RXA00092-downstream  
TGACCACACTTCTAGCAGCAACC

>RXA00104-upstream  
TGCAAAGACATCCCGGAACCACTCCGCTACTTGAGGTCGGAATCGGGAAAGAATGCTTTT  
AGCCATGCCTTAATGTAACCAAACATCTAGAATTGAGAAC

>RXA00104  
ATGACTGCTCAGATTGATGATTGATCCTCACCCATCGTCTCGCCCAAGGCACCGGAGAA  
ATCCTCAAAGGTGTCCGCAATGTTGGGGTGTAAAGAGGTGGAATCTCGGTGATGCCGGC  
GACGAACTCGCACAAAGTTGGATTGCTCGAGTGTTGGAGCAGCACCGCCCCAACGATGGA  
TTCTGTCTGAAGAAGCCGCCGACAACCCAGACCGCCTATCCAAGGACCGCGTGTGGATC  
ATCGATCCCCCTCGACGGCACCAAGAATTGCGCACCGGCCCGCCAGGACTGGGCAGTACAC  
ATCGCACTGGTAGAAAACGGTGTTCACCCACGCCGCTGTTGGCCTCCCCGACCTTGGC  
GTGGTGTTCCTACTCCGCTGATGCCCGCGCCGTGACTGGCCCTTACTCCAAGGTCATCGCC  
ATCTCCCAACAACCGCCCCACCAAGGTTGCTCTATCTTGCGCAGAGCAGCTCGGCTTTGAA  
ACCAAGGCCCTTGGATCCGCAGGCGCTAAAGCAATGCACGTTCTCCTCGGTGACTACGAC  
GCCTACATCCACGCCGGCGGCCAATACGAGTGGGATTCGCGAGCACCAGTCGGCGTCTGC  
AAGGCAGCAGGCTTGCACTGCTCCAGGCTCGACGGTTCGAGCTGACCTACAACAACAAA  
GACACCTACATGCCAGACATCTTGATCTGTGCCCTGAACTTGCAATGAACTTCTCGAG  
ATGTGCGCGAAGTTCTACGAGGAGAATGGAACCTTAC

>RXA00104-downstream  
TAACGCTGTTATGATGACGGCAT

>RXA00113  
GCTTCAGGTGGCGGAGTTGTTGATTCCGCAGCACTTGATGCCTACGCATCCACCGTCACT  
GGTGAAGAAGGCGTCCTGGCAAACGTTGCTCGCGGCATTCTGTCTCAGCTTGGTCTCGAC  
ACCAAGGACGAGGTTGAAGGCGCAGAGATCGACACCGAACTCTACGACGCTGTCGAAGCA  
GAACTGGGCACCGGCTGGCTGAAGCTTGTACCCCAAGTGTCTCCGCTGATCGTGCGATC  
TTGTTTCGACGACCGTTGGGCATCTGCACGTGAAGATCTGGCACGCCTTGCCAACGGCGAG  
GATATTGCCGTCGAGCGCTTTGCTGGAACGGGGGAGACCGTCGTCAAGCAAGCTGCATGG  
TGGGCTGAGCACGTTGAAGACACCGCTCTCGCTGCAACCCCTGAAGCAGGTTTCCGAGGTG  
GCTGCGAAGCCAGCCAACGAGCCACACATCGACGATGTTGCGCTGGTTACCGGTGCGGCT  
CCTGAGTCGATCGCCGGTGCAGTTGCGGCTCGCCTGCTGTCCCAGGGCGCGACCGTCATT  
CTCACCGCATCGAACGTCTCCAGGCGCGTAAGGAATACGCACGCAAGCTCTACGCTGCG  
AACGCAACCCCTAACGCAAAGCTGTGGATTGTTCTGCGAACATGTCTCCTACCGCGAT  
GTTGATGCAGTCATCGATTGGATCGGCAACGAGCAGCGCGTCACCGTCGGCAGCACCGTC  
ACCGTGACCAAGCCAGCTCTGACCCCAACCCCTTGCGTACCCATTTCGCAGCTCCATCCGTA  
TCCGGTACCTTGGCGGATGCAGGCCCACAGGCTGAAAACCAGGCACGCCTGCTCCTCTGG  
TCCGTGGAGCGCACCATCGCAGGACTTGCAATCTTGCATCCCGCGGTGTCGATGGACGC  
GTCCACGTTGTACTCCCAGGTTCCCCGAACCGCGGAATGTTCCGGTGGCGACGGCGCTTAC  
GGCGAAGTCAAGGCTGCTTTTCGACGCCATCCTTGCCAAGTGGGGCTCCGAGACCGGCTGG  
CCACAGTTTGTCTCCCTCGCACAGGCACGCATCGGCTGGGTGCGCAGGCACCGGCCTCATG  
GGTCGCAACGACGTGCTCATCCCTGCCGCTGAAAAGCTGGGCATCCACGTCTACACCCCT  
GAAGAGATCTCTTCCGAAGTGTGGGTCTTGCAATCCCGCAGAAATCCCGCGAAAAGGCTCTG  
GAAGCACCGATCGATTACGACCTGACCGGTGGACTTTCCGGTGGCGTATCCATCGCAGCA  
CTGGCAGCATCCCTCGAGTCCGACGCAGTAGAGACCACCTCTGCAGCAGAAGACACCATC  
AAGGCGCTTCCATCACCTAAGCACCCAGAGCAGCCAGTGGGCACGCCAGTTGGAGAGGTC  
AAGACCGATCTCGAAGACATGGTTGTGATGGTTGGCGTGGCGAAGTCTCCTCATGGGGC  
TCCGGACGTACCCGCTTCGAAGCTGAGTACGGCATCCAGCGCGACGGCTCCGTTGACCTC  
ACCGCAGCAGGCGTCTTGAAGCTTGCAATGGATGATGGGTCTGATCTCCTGGAGCGAAGAT  
CCAAAGCCAGCCTGGTACGACGCTGACGGCACCGAAGTGCTGAAGAAGAGATCTACGAG  
CGCTTCCGCGACGAAGTCATCGCACGATGCGGTGTTGCTGAGCTTGTGACGACGCATTC  
CTCGTCGACGGCGGCTCCCTCGACGCAGCTGAAGTCTTCTCGACCGCGACATCTCCTTC  
TCCGTAACCTCTGCTGAAGAAGCACAGGCCTACGTCGATGCAGATGCTTCCGTGACCGTT  
GAAGAAGCAGACGGCGAATGGATCGTGACCAAGAAGAAGGGCTCCACCTCCTTCGTGCCA



CGCAAGGCAACCCTGACCCGCTCCGTAGCAGGCCAGCTGCCAACCGACTTCGACCCTGCC  
AAGTGGGGTATCCCAGCCTCCATGATCGATGCACTCGACAACATCGCAGCGTGGAACCTG  
GTCAGTGCAGTCGACGCCTTCCTGTCTCCGGCTTCAGCCCAGCAGAACTCCTGCAGTCC  
ATCCACCCAGCTGACGTGTCTCCACCCAGGGCACCAGGTATCGGTGGCATGCAGTCCCTA  
CGCAAGCTGTTTCGTCAACCGCTTCCTCGGCCAGGATCGTCCATCCGACATCCTCCAGGAG  
ACCCTGCCAAACGTTGTGGCTGCACACACCATGCAGTCCTACGTCCGTGGCTACGGCCAG  
ATGATCCACCCAGTGGCAGCATGTGCAACCGCAGCTGTCTCCGTGGAAGAAGGCGTGGAC  
AAGATCCGCCTCAACAAGGCAGATTTTCGTTGTCCGGTGGTATCGATGACATCCAGGTT  
GAATCCCTGACCGGCTTCGGTGACATGAACGCCACCGCAGACACCCAGGCAATGCTGGAC  
AAGGGCATCGACCCACGCTTCATCTCCCGCGCAAACGATCGACGTCCGCGAGGCTTCCTC  
GAAGCAGCAGGTGGCGGTACCGTCTCCTGGCACGTGCATCCGTTGCTGCTGAACTGGGA  
CTGCCAGTTCTCGCAGTTGTTGCACACGCACAGTCTACGCCGATGGTGCTCACACCTCC  
ATCCAGCACCAGGACTTGGCGCACTGGGTGCAGCACGTGGTGGCAAGAAGTCCGTAAT  
GCTCGCGAACTGAACAAATTGGGTCTGACCCAGATGACGTTCCGCGTGGTCTCGAAGCAC  
GACACCTCCACCAACGCCAACGATCCAAACGAGTCCGAGCTGCACAACCTGCTGTGGAAG  
ACCATTTGGACGCGAAGCCGACAACCCGATGTTTCGTCTCCGAGTCCCTTACCGGA  
CACTCAAAGGGCGGTGCAGCACTCTTCCAGATCGGTGGACTTGTCTCCATCCTGGAAACC  
GGCAAGCTGCCACAGAACGCATCCCTTGACTGCGTTGACCCAGAGATGGAAGCAAAGGGC  
GAGAACTTCGTCTGGCTGCGCAAGCCACTGGATCTCGGCGCAGGCTCCATTAAGGCCGGC  
GTAATTAACCTCACTGGGCTTCGGCCACGTGGCTGCAGTCGTCTGCTGGCAACCAGCGGC  
ATCTTCGAGCAGGCAATGCGCAACGCAGGCCTCGACGTGGAAGCATGGCGTGCACGCGCA  
ACCCAGCGCCTGCGCACCGGTGCAAACCGCCTAGAAGCTGGCATGGTTGGCCGAGCACC  
TTGTTTCGAGCAGGTGACGGACGTGCGCTGCCAGAGCATGGCGCTCACCAGCAGAGATC  
AACTTGCTTATCGACGCTGACGCTCGCCTCGGTGCTGACGGCATCTACCAGGGC

>RXA00113-downstream  
TAAACGTTAGATAGCTAAGAAAG

>RXA00158-upstream  
CGTGCCATTTTCTTTACAAAAGAGTATTAACCGAACTTCAGGTCAGGATCCACGCCCTG  
CGTTCATCCCGGCTAAGTTATACAAGGAGCGAGTTCTCAC

>RXA00158  
GTGACCGAATTGAGCAGGAACCTTCGGGGCCAGCCGACTGATTAACCGCTTTGGCCAGGAG  
CCTTTTGCCTTCGCTTTTCGCCGGCCAAGGATATGACTGGTTGAAGACCTTTCGTGCCGCG  
GTTGCCCGCAGGTGCAGGCACCAATGTTAGTGACATCGTCGAGCGCGCAAATGCGCTGCTT  
GCACTAGTTGCAGATGATCTCATTGGCACCCCTTCCATTTGGTTTCGATCCAGTGGCTTGG  
GCTAACAACCTCCGAAGATCCAGCTTTCGATACTGCACAATCTGCAGTGAGCGTGCCGGGT  
ATCTTTGTCTCCAGATCGCAACCCCTGGATTCCCTTGAGGCGCAGCGCCTTGATGTGGAT  
CAGGCTGTGTCCAGCATTGGTTCATTCCAGGGCGTATTGGGCGTGACCTGCTCAATGAT  
GCGACTCGTGCTGATGAACTCGTTGCCATTGCGCAGTTGATCGGTGCAGCGATCACCCGC  
ACCGCACGCATGACGGGCCTGATCGCGCAGGGCGACAACATGCCGATGCTGTGATCGCC  
GGAATTTCCCGCGAACAGCTTCAGCAAGCTATCGACGCGGCCTGCGCCGAAGTCCCTGCG  
GAGATCCGCCCGGTTATCGGTCTGCGCAACTCACGCGATTCTTATGTTTTGGTTGGCCGC  
CCAGACGACAACGCTCGCGTTGTTAAGGTCATTGAGGCAATGGCTGCCAAGGATAAGAAG  
GCCATTGAAGATAAGCTGCGCGGCGGTTCCGCGTTTCAGCCCCCGTATTACTCCGCTGAAG  
GTGCAGGCTGCTTTCCATCACCCAGCTATGAACATGGCTGTGGAGCAGACCGTGGCGTGG  
GCAACCACTGCTGGTTTGGATGTGGAACCTCACCCGCGAGATCGCCGCTGATGTTTTGGTT  
AACCTGTGATTTGGGTAGCACGCGTCAACGAAGCGTATGAGGCTGGCGCTCGCTGGTTC  
CTCGACGTTGGACCAGATGGTGGCATCGTTAAGCTGACTGCCAACATCCTTGAGGGCCGC  
GGCGCGGATTCTTCTATGTTGGTGACGCCGAGGCCAGGCCAAGATATTTGATGCTGGC  
ATGGCACCTGAACTTCCAGTGGATTACCAGGAGTTCGCACCACGCGTTGAGCACGTTGAT  
GGAACCCACGCTGGTTACCAAGTTCACTGAGCTGACCGGCCGACCCCAATGATGCTG  
GCTGGCATGACCCCAACCAACGTTGACCCTGCCATTGTTGCAGCCGCTGCAAACGGTGA  
CACTGGGCTGAGCTCGCTGGTGGCGGACAGGTTACCCAGAGCTGCTGGAAACCCACATC  
GCACAGCTCACCGACATGCTTGAGCCAGGTATCAACGCCAGTTCAACTCCATGTTCTTG  
GATCCATACCTGTGGAAGATGCAGATTGGTGGCAAGCGCCTTGTTCCCTAAGGCCCGCGCT  
AATGGTGCATCCATCGACGGCATCGTCATCACCGCCGGCATTCCTGAAAAGGATGAAGCT  
GTTGCATTGGTCAAGGAACCTGATGCGTGATGGTTTCCCTTGATCGCATTCAGCCAGGT  
GCCATCAAGCAGGTTAACTCTGTGTTGGCTATCGCTAAGGAAGTTCCAGAACTCCCATC  
ATCATTCAGATTGAGGGTGGCGTTGCAGGTGGACACCACTCTTGGGAAGACCTCGATGAG



CTGCTGATCGCCACCTACGGCAAGGTCCGCGCACTGGATAACGTGGTGCTGTGTGTCGGC  
GGTGGCATTGGCTCACCTGAGCGCGCTGCTGATTACGTCACCGGTTCTTGGTCCACTTCC  
TACGGCCTGCCAGCTATGCCTGTTGATGGCATCTTGGTGGGTACCGCTGCGATGGCAACC  
AAGGAAGCAACCACCTCCCAGGCCGTCAAGGAACTTCTTGTTCACCCAGGGCTCTGAT  
GAATGGGTTCTGCTGGTGGCGCAAAGAACGGAATGGCATATGGCCGTTCCCAGCTTGGC  
GCAGACATCCACGAGATCGACAACCTCTTTGCTAAGGCTGGACGCCTTCTTGATGAGGTT  
GCAGGCCATGAAACGGATTTGCAAGCGCGCCCGGATGAGATCATT

>RXA00164-upstream

CTGCTTTGCGGGAGGTTATGAAATGAGTGGGGAGACGTCGAAAAGCATGCGCTTTCCGTT  
GGCCAGCCTGCCGCAAGTGCGGCGCGAGGTGGCCCGGCAG

>RXA00164

GTGGGTCGTATTCCGCGGGCGAAGTGGTGGTTTTTAGGCGCGCTGGTGTGCTGAGTGCG  
GGCGCTTATGCGTCGGTGCTGGTGCCGCAGGTGCTGGGGCGGATTGTGGATCTGGTGTCC  
GATGGCGCGCAGATGCGTGATTTTGTGAGCTCAGTGTGATTCTCATTGCGGTGGCAATT  
GCCGGCGCGGTGCTCAGTGCGTGCGGGTTCTATGTGGTGTCGCGGATTTCTGAGAAGATT  
ATCGCCAATTTGAGGGAAGATATGGTGGGCACCGCGCTTGGGTGCCCCACGCACCAGGTG  
GAAGATGCGGGCTCTGGCGATTTGGTGAGCCGCTCCACCGATGATGTCTCCGAGCTATCC  
GCAGCGGTGACAGAGACCGTCCCGATTTTAAGTTCCTCACTGTTTACCATTGCCGCGACG  
ATCATTGCGCTGTTTTCTTTGGACTGGCAATTTGTGCTCATTCTGTCGTGGTGGCGCCG  
GTGTACTACTTCGCGTCCAAGCACTATTTGAGCAAGGCGCCGGATCGGTATGCGGCAGAA  
CGCGCGGCGATGGCGGAGCGTGCGCGAAAGGTACTTGAGGCTATTCGCGGGCGTGCAACT  
GTGCGGGCGTATTCCATGGAAGATGCCATGCATAATCAGATTGATCAGGCGTCGTGGTCT  
GTGGTGGTCAAGGGTATTCGTGCGCGCACCATGTTGATTTTGAACATGTGGATGCTG  
TTTGCGGAATTCCTCATGCTCGCGGTGCGGTTGGTGATCGGCTACAAGCTGGTCATTGAT  
AATGCGCTGACGATCGGCGCGGTTACCGGTGCCGTGCTGATGATTATTCGTCTGCGTGGC  
CCGATGAATATGTTTCATGCGCGTGCTCGACACCATTCATCCGGCTATGCGTCGCTGGCG  
CGCATCGTGGGAGTTGTTGCGGATCCGCCGATTCCTGTGCCCCGACAGCGGTGTGAAAGCA  
CCTCAGGGCAAAGTGGAATTGCGCAACGTCAGCTTTAGCTATGGCGATTCCTGGGCGGTG  
AAAGACATCGACATCACGATCAATTCGGCGAAACTGTCGCGCTCGTGGGCGCATCTGGC  
GCAGGTAAGACGACGGTCGCCCGCTTGTGGCGGGCTTGGCGGTGCCAGATCAAGGGCAA  
GTGCTTGTGACGACTTCCCCGTCTCTCACCTCTCTGACCGCGAGCGTATCGCCCCGCTTG  
GCCATGGTCAGCCAGGAGGTTTCATGTTTTCTCCGGCACGCTGCGCCAGGATCTCACCTTG  
GCTAAACCAGATGCCTCCGATGAGGAATTAGCGCATGCTCTTGGGCAAGTTAATGCCCTT  
GACTGGTTGGAGAGTCTTCCAGAAGGACTGGACACGGTCGTTGGTGCGCGAGGAATCCAG  
CTAGAACCAGTGGTGGCTCAGCAGTTGGCGTTGGCCCCGGGTGTTGTTGCTCAATCCGGCG  
ATCGTCATCATGGATGAAGCCACGGCAGAAAGCAGGATCGGCGGGTGCCAGCGCACTGGAA  
GAGGCTGCAGATGCAGTGAGCAAGAACCGTTCCGCATTGGTGGTGGCGCACCGGTTGGAT  
CAGGCATCGCGGGCTGATCAGATTCTGGTGATGGATAAGGGGGAGGTTGTGGAATCCGGT  
ACTCACCAGGAGTTATTGGATCACGGGGGTATTTATCAGCGTCTGTGGACTGCGTGGAGT  
GTCGGAAGA

>RXA00164-downstream

TAGTTGACTGTTCAATGCGTTGA

>RXA00181-upstream

GTATATTACAGACACCCACGTCGATTAGTGTTGTAGTTCACAGTGCTTATTTTTTATTTGT  
ATCTTTGCACGTTTGTCCCCTACCCAAAAGGAGAAACCTC

>RXA00181

ATGAGCGATAACACCTGGTTCATCATAGCCATCGTTATCTATATGTTGGTGATGGTGCTC  
ATCGGCTATTGGAGTTACCGCAAGACAGAAAAATACGACGACTACATGCTCGCCGGCCGC  
GGGCTCAACCCTTTTGTGCGCAATGTCCGCAGGTGCCTCAGATATGTCAGGTTGGCTG  
CTCATGGGTCTGCCCGGCGCGCTGTTTGTACCGGCATGTCCGAGTTGTGGATCGCAGTC  
GGACTCACCATTGGTGCATGGGCGAACTGGATGTGGGTGGCACCTCGTCTTCGTTCTTAT  
TCCGAAATCTCGGCCAACTCAATCACCTGCCTTCATTCTTTGAGAACCGACTTCGCGAT  
AAATCTCGCGCGCTTCGCATCATTGCAGCACTAATTATCATTGTGTTCTTCACCTTCTAC  
ATTTCTTCAGGCATGGTTGCTGGTGGAGTGATTGGGAGTCCACGTTTGGTGGAGATTAT  
CTACTCGGTATGGCCATTGTGCGCAGGTGTGACAGTGCTGTATACCTTCATTGGAGGATTC  
CTTGCTGTGTCTTATACAGACGCAGTTCAGGGGACTATCATGTTCTTCTCGTTGATCATC

GTGCCAGTCATGGCATATTTTCGCACTGGCGAACCCCATGGATATTTGGAGCTTTGCAAAC  
TCTAATGATTACGGCCCCGCACACCGATGGAATTGGCAATCCCACCTACTTCTCCATGATC  
AGTGGCATTCTGTCAGCAGCAATCATTGGTAACTTAGGTTGGGGTCTTGGATACTTCGGC  
CAGCCACACATTGTGGTTCGTTTCATGGCACTTCGCACACCAGCTGAAGCAAAGCAAGGT  
CGTCGCATCGGTATTTCTTGGATGATAATCTGCCTGATTGGTGCAACCTTTACCGCAATT  
ATCTCCACAGTTTTCTTTGCACAAAACCCCGACGCCAACATCACTGACACAAGGGCTTAT  
GAGTCCATCTTCCTAGATCTTGCCCGGATGCTGTTCCACCCATTGATCGCTGGACTTATT  
CTGACTGCTGTTCTCGCGGCCATCATGTCTACCATGTCGTCACAGCTGCTGGTCACCGCA  
TCTTCCCTGATTGAGGACCTGCTGAAGGTAGTTAAAAAGGACTCGCTGAGCGAACGCACC  
CTGATCATGCTGTCTCGTGCCACAGTCATCATTCTGGCGATCATTGCAGCAGCCATGGCT  
ATTAACCCGTCTGATTCCATCCTCGGATTGGTGGGATTTGCGTGGGCAGGATTCGGCTCT  
GCATTTGGTCCGATCATACTTGCTAGCCTTTATTGGAAGCGTCTCAACGCCGCCGGCGCT  
ATCTCCGGCATGATTACTGGTGCTATTGTCTCCATCGCGTGGGGTATGTCCCCACTAAGC  
GATACGTTGTATGAAATCATCCCAGGTTTCGCCCTGGCAACCATCGTGATGGTCGTTGTT  
TCCCTCCTGACAAAGGAACCCTCCGAAGAAATCCTCAACGAGTTTGAAACGCCAAGGAT  
CTTGCTGCCGCTGTGGAATCAAACGAGGATGTTGATTTGCTGACGCAGCTCAGAAGCTT  
TCGAAAGAAAGT

>RXA00181-downstream  
TAAGCCTTAGAGGGAACCAAACG

>RXA00186-upstream  
AGAAGCCCAGCATTTTGTGTTAGCTCACCTCTAAAGCTCCTGATCTGGATACGAGGACTCC  
TGCGGAAAACCGTGTGGCTAGTGAAGCTACCCGGCATCTC

>RXA00186  
ATGGGGGAGAAGACTTCTGTGCGGTATGTTTACGATGTTCTGATCAAGGGCGTGCCAGTG  
CGGATATACAATCCGCACCCCAACGACGGGCGCTTCCTGTCTTTATCTACTTCCATGGT  
GGCGGATGGGTTTTGGGGGACCTTGAATCAGTGGATTCCACCGTGCGCGATATTGCCGTT  
GCTTCAGGCGCCCTGTGTATCAGTGTGGATTATCGCCGTGCACCGGAACATCCTTTTCTC  
GCTGCATTGGATGATTGCCAAGTGGTCACGGAAGCTGTCCTCAATGGTGAACCTGCCAGT  
GCTAACAGCATCTAGTGGCAGTCGGCGGGGACAGCGCCGGTGGCAATATTGCGGCGGTC  
ATCGCTCAACAGCTGCGCGATCAGATCACCCACCAAGTTCTTGTGTATCCGGTGATGGAC  
GTAATCTTGCTGGTGATTTGTTCTATCATTACCACTGGTTTTGCGCTGCTCATGCATCCA  
AAGAGCAAGGACAAGACGGAGACGATTTCTGATGAATTCCTCGCAGAGATCCAAGCGGGA  
AGTGAAAAGATCTCCATTCTGCGTTCGACCCCTGCTGAAAAAGCCAATGCGAGCCGTTGG  
ATCATGTACTTCGTTGGCGGAATTGGCCTGCTCTACAGCGTGTTCAGCCTGTGGACAGGT  
GGCGTAACCGGACTGACGTTGAACTCCTTCAACTTCCTGTTCTGCTCACTCGGCATGGTG  
CTCACCGCTAATTACGGGCCAGAGTAT

>RXA00186-downstream  
TAAGCAAAGCTTATTCGCGAAGG

>RXA00187-upstream  
GCTTATTCGCGAAGGCATCCAAGGAACGTGGGGATTCAATTCTTCAATTCCCGTTCTACGC  
AGGCATTTTCGGGTTGATTTCTTACCGGTCTGGGTGTT

>RXA00187  
GTGATCTCCGGATTTTTTACCTCGATTTCCACGGCAACCACGTGGCCTGTCATCGCGTTC  
CTCTACTCTGGACTGCTCAACATCGCGGTGCCTTCAGGTGGCTCGAAATTCATCATCGAA  
GCCCCGTACATCATCCCAACCCAGTGGATCTTGGCGCTGACATGGGCCTTGTCCTGCAG  
GCTTATCAAATGAGTGATGGCGCGACCAACCTGCTCATTCCGTTCTTCGCGCTGCCATAT  
TTGGCCAATTTCAAGATCAAATTCAGCCAAGTGGTGGGCTATACAGTTCCGCCTGTCCTC  
GTTGTTATCGCCGTGATCTGCATTTACCTGTTCTGCGAGCATCAATCATT

>RXA00187-downstream  
TAAAAAGATGCTTCTCG

>RXA00201-upstream  
ACGTCGCGGACTTCAAGTAGTCGGCGATGAAAAAGTCCGTTTACTAAACCCCGATCTGTG

TTACGCCATCGCGCGGCTCGGGCACACCGATACTGGGCA

>RXA00201

GTGGCAGATTGCGGATTACCCATCCCAGAACACGTAGAGATCATCGATTTGGCACTCGTG  
TTTGGGATCCCCACCTTTGAACAAGTACTGAATGCTCTCAAGCCGGAAGTAGTTGTGGAA  
GGCGCGGTGATTGCCGAAGGGGCACCCCAACGTATCCGCGAAATGGTGGATACGGATGTG  
GAAGTT

>RXA00228-upstream

CCGCATGGCATCCGCCGAAAGAATTCCCCTCCGGAGGAATGGCACGCCTCATGGGAGAAC  
GCATCGGCACAAAACCTGAC

>RXA00228

ATGCGCGACCTCCGCTCCATGATCGGCGTCAGCTCCTCCGCATTAGGCAACCGAATCCCC  
TCCGAAGAAAAAGTCTCTGACCTAGTCATCTCCGCAGGCTACGCAATCCTCGGCCGCTGG  
CGGAAGACTACGACGAAATGGACTTCGGACAAGCCACCGAAATCCTCGAACAAGTCGGA  
GCCATGCACCTAGCCGACCGCACCTGGGGAACCTCTCCGAAGGCGAACGCAAACGAGTC  
CTGGTCGCACGCGCACTCATGACCAACCCGGAACCTCATCCTTGACGAACCAACCGCA  
GGAATGGACCTCGGCGGACGCGAAGACCTCGTCGGCTACCTCGGAGAACTCGCCATGGAC  
CCAGACGCACCTGCCATCGTCATGATCACCCACCACGTCGAAGAAATCCCCGCCGGATTC  
ACCCACGCAATGCTCCTCGACGAAGGTGAAATCGTAGCCCAAGGCCTGATCAACACCGTC  
ATGACAAACGAGAACCTATCCAAAGCATTCCACCAGCCAATCCAAGTAGACCGCATCGGG  
GAACGCTACTTTGCCCGCCGTGTGAGAACC GCCAGGAGTCATAGGGCTCAG

>RXA00228-downstream

TAGGTTTTTTGGAGTTGTGGGCC

>RXA00243-upstream

CACTGCGCCAGATTTTTGATGCCGACACTGTGGCAGGTGTGCGCGCTGAGTACGAAAAAT  
TTAACAAGCAGCCCATGATGGAAATGAAGAGGAACAGAA

>RXA00243

GTGACCAGCGAACAAGCTTTAGATCCTATCCACCCAGGTCAGTTCCGTCTTTCTCGGATT  
CAGTTGATCAACTGGGGAACCTTCCACGGAACGGTGGACATTCTGTGACCAGGGAAGGA  
ATCTTAGTTACCGGTGGTTCGGGATCAGGAAAATCCACGCTGATTGATGCGATCACGGCG  
GTATTGCTTCCGCAAGGAAAGCTGAGGTTTAACTCTGCCGCACAGGCTAATACTCCGCGG  
AATAAGGGACGCAGTTTGGTTACCTATATCCGTGGCGCTTGGCGTGCGCAGGAGGATCCG  
CTGCAGGATCAGATTGTCTCCACGTACCTACGTCCCCGCGCAACCTATTTCGCTGGTTGGA  
TTGACTTATTCCAACGGTGAAGGCGTCGAGCACACCTTGGTGGCTATTTTCTATCTGAAA  
TCGGGACACAATTTAACCTCCGATATTTCTTCATATTATGGTGTGTTTCCCGTTGATCAA  
GACATCAATGCGCTGCTGGATTTCTGAAAGAGGGCATCGATAAACGCCAGATCAGAGCT  
GCTTTCAAGGAAGCCATCTTTAGCGAGCAGCATTCTGTATTCTCCGGCAGGTTTAGAAGC  
CGTTTGGGGATCTCCAGTGAGGAAGCTTTGCTGTTGTTGCACCGCGCGCAGTCGGCGAAA  
GATCTTCAAAGCTTGGATGATCTATTTCCGGGATTACATGCTGGTGAACCGGATACGTTT  
AGCATTGCCAAAACCTGCCGTGGAACAATTTCAAAGACCTTGAAGGTGCTTATGAGCAGGTC  
GAAGATATTAAACGGCAGATCCACACCCTGGATCCTTTGGTGCAGCTGAAGAATCGGCGA  
GAGAAAGCGCAACAGTCCAAAGATCATGCCAATGCACTGAAGAAGGCGCTGCCGACTGTC  
GGGAATCGCATTAAGAAGGAAGAGCAA

>RXA00259-upstream

GGCCTTATTAAACATACGGCGGTTCTAGCACACAGCGATGGATGATGTGTCCCACCGATAT  
TGCTGCATGTGCCAAGATTTAGCACGGTACAGTGCTAGAA

>RXA00259

ATGAGCGGACTGTTTACCCCATTTTCAGATGCGGCAAAAAACAACACGGTAAAAACTGAT  
GGAGATTCAAGTATCTGGTCGAGACTTGCCCTATTACTAAGATCTCTGAGGATCGTTTTCGAG  
CGTTCTGCGTATTACAGCCAGCTGGCAAATATAATCTGCGATGTGGCACCTTGGGGAGCG  
AGCACTGTTTTAGTCTTACTGGTCAGTGGGGCAGTGGTAAGACATCTCTTGTTAATTTG  
ATTCGCTCGGAAGAATCTCTATCGAACGAAAAATGGACAATCGTTGATTTCAACCCGTGG  
GTGGCCTCTGACCCGCAATCTTTGATTGAGGAGTTTTACCGAGTAATCGTTGGGACGGTA  
CCTGATGATAAGACCGGCCAAAAGATCAAAACTGTTCTGCAGAAAACCTTTAGCACGATT

GGGTCAATTGCAGGTGGGGTCGGAGGGTTTGGTGTCTAGAACGACTTGCGCTCTCAAAA  
GGAGTAGATGCTGCAAACGCTGTATATAAGACATGGAAACAGGAGCAAGATTTCGTGGCCA  
ACGCTGTATACACGTGCTGCGAACCATTTTAAAGATCTGAACAAGCGAATTCTCATTGTC  
GTCGATGATATTGATCGCCTCCATACTGATGAATTGGCGCTGTTAATGAAAGTAATACGC  
TTGCTTGGACGATTCCCGCAGGTGAATTATCTTTTGGTTTATGAAGAAGAATCACTGTTA  
ACGACGCTAGCCAGATCGACAGCTGTAGGTGGTAGCGAAGATGATGCTTTGCGTTTCATG  
GAGAAAATCGTGCAGTATCCTTTTCGATGTTCCGCCTCTGACATCATTTCAAATAGAGAAA  
GAGCTCAGTGCATTATTTGACAAGCTTTTCCAGGGTGTTCGCTATCGGGTGATCCTGAA  
GACTTTGCACTAGTGAAGTCGAGAATGTTTCGATGTCTGGGAAAAGACTCTGGTCACGCCG  
AGGCTGTTGCACCGTTTTGCTGCTCTACTAACCAACTGGACTCGGATATATGGATCAGGT  
GAAGTTAACGGCGTTGATCTCACAATACTTGCAGCATTCGAATTGTTTTTCCGTCTGTG  
TATAAACGTCTTTCTCGAGCGAAGGAAGTATTGCTTCAAGGAGGTGCAACGACAGGCTCG  
CAGAAACCCGGTTGGGAAAAGCAATTATGTGAGGGGATGAACAACGAGCAGATGGATCTT  
TTAAAGACCATGCTTTTGTTCCTTTTCCACGTCTTTTCGGATCACCTAGTACGAGAATG  
CATCGTGAGAGGGGGATCTCGACGGAAGTTTATTTTGACACGTACCTCATGTTTCAAAGA  
CCTGGACATGTCATAAGTGATGAACAGTTGGATAAGTATCTATCTAATGCGGACGATGCT  
ATGGGTTTCGTCGATTTAATTAACCTCCGATGACAATGACATGGTGGCATCAGTGATGAAA  
AAGCTTCCTCTAGCAATTGATCGACTTGATGGAGAGGGTGTAGGCACATGGCAGTTGAG  
GTGTTATTCACCGCTGCTAATGGTATGCATGATAAAGGTCGTCAGTGCGTATGAGCGGC  
ATATTCAGTGACCTGTATTCCCATGCGTGCTCGATTCTTGGTGCATTGCCTCAATTACCA  
GTGGAACAACCTCTATGAGAAATCTTTTCTGAGATGACGCTTAATGAGGCTGCTTTCTGG  
TTAAACCAGGTGGGGGAAAGGGCTAGAGCCTGTGGTAATGATGTAAGTGGCCTTGAGCTT  
TTTCGTAAAGTTAATATAAAGACCGAAGCTAGAATTTTAAGTGTATTGAAGAATCAGGAC  
CCCTCAGATTGGGATTTAGGTCCATATTCGCTTGGTATTTTGGCGAAAAGCTCGAATTTT  
TCTTCAGTGCTGAAGTCTCTGCAAAGTGGTATAGAGGAACATCAGTTTGATGTGATAGAT  
ATTGGAGTGCTTTTCTTAACGACTGTGTATTCTTCGCGACAGGGACCAAGCGGTGGTGCA  
TGGATAGATTCTTTTCAGCATAGTCTGTTTTACGGTACGTACCTGATTCTCTACGGGCT  
ATAACCAAGTCTGAAGTAGATGTAGAAGTGGTAAGATACAGTTCACGGATTTTAGCTGG  
GAAGGGAAGCGAAAAGTTGTGCGCATATGCACTGGAGACTGGAAGAAGTGATTTCACTCGA  
GAACGATTAGGGGGCTACAGTATCGCAGATTCTATAGTCGAT

>RXA00259-downstream  
TGATGAGGCTGAGGTCATGACTT

>RXA00269-upstream  
TGCGATCTTGGTGGTTGTGCGCCATGCTGCTGCCGAGGTGGCGTGCGAAGTTCTCCAAGGC  
ACCGAAGCCTAAGCAACCAGTAGCAGTGGAGGCTTAAGAC

>RXA00269  
ATGTTATCCATCAACGGAATTTCTAAGACGTTCTTCCCCGGCACTGTGAATGAGCGCCGC  
GCGTTGCAGCAGCTCAAACCTCGATATGGCTGAGGGCGATTTTGTACCGTCATCGGTTCT  
AACGGTGCGGGTAAATCCACGCTGCTCAACGCTGTTTCTGGCCGTTTGCTTGTGATTCC  
GGCGAGATTTCCATCGACGGCAACAAGGTAAACAAGATGTCAGAGCACAAGCGTGCCCGC  
TACATCGGCCGCGTTTTCCAGGATCCTCTGGCCGGCACCGCGCCGAATCTCACCATTGAA  
GAGAATCTGGCCATCGCGTTGCTGCGCGGCAAGCGCCGTGGATTGGGCTTTGCACTGACC  
TCGAAGCGCCGTGAGCAATTCAAGCAGGAACCTTGAGCGCCTTGAGCTGGGTCTGGAAAAC  
AGGCTCACTGCCAAAGTTGGTTTGTCTCTGCGGGTCAGCGTCAGGCATTGTCCCTGCTG  
ATGGCTGGTTTTACTCAACCTAAAATCATGCTGTTGGATGAGCACACCGCAGCGCTTGAT  
CCACAGCGTGCAGAGCTTGTGACCACCTTGACCGAAAAGATCGTGGCAGATGGAAATCTG  
ACTACGCTTATGGTCACGCACAACATGGAACAGGCAATTCGCCTGGGCAATCGCCTGATC  
ATGATGCATGAAGGCCAGATTGTCTACCAGGCAGATCAGGCTACCAAGTCGAAGTTGACT  
GTGCGCGATTTGCTGCAGGAGTTCGCCAACATCAAGGGCGCAACATTGTCTGACAAGGCG  
TTCCTCGGC

>RXA00269-downstream  
TAAAAAGAGCTTGCTTTACGACG

>RXA00281-upstream  
GGTTGACTCTTTGGCTTTGATGCCAGCATTCGCCAAAGCGTGGCCCTCTTTAAGAAAGCT  
ACTGAACACAACAGAGTAGGTTTATGCGACACTGGTGCGC



>RXA00281

ATGATCAACGTTGAAGGCCTCACCAAACAATATGGTCAGGTCCGCGCAGTCGATGATCTG  
AGCTTCGAAGTAAAACCCGGAATAGTCACCGGATTTCTCGGCCCCAACGGCGCCGGAAAA  
TCCACCACGATGCGGCTGATCCTTGGCTTAGATAATCCAACCTGCAGGGCATGCCACGATC  
GAAGGACAACCCTACCGATCGCTCAAAAATCCCCTGACCAAAGTGGGAGCACTGCTTGAT  
GCCAAAGCAACACACCCCAAATAGAACAGCAGAAAACCACCTCAAGTGGATCGCCCGTGCA  
AATGGGCTGTCCACCAAAGAGTCGATGAAGTTCTCACCCCTCGTGGGACTGACTGGTGTT  
GGGTCAAAGAAGACCGGTGGGTTTTCACTAGGCATGGGCCAACGTCTAGGACTTGCTGCA  
GCATTGCTCGGCGATCCGGAATACTTAATTCTCGACGAACCCGTCAACGGCCTTGACCCA  
GAAGGCATTCACTGGGTGCGCACCTTGTTGCAAAACATCGCCAAGCAGGGCAGAACCGTG  
CTCGTGAGTTCCACCTGCTGTCCGAGATGGCGCAAACCTGCGGAACATTTGATCGTGATT  
GGGCGTGGCAAGCTGGTCCCGATATGCCCATGCATGAGTTTGTGCGCTCCCATTCCGCT  
TCCACAGTTGTGGTGCGGGCAGCA

>RXA00298-upstream

TTTAGACAAGTTCTGGTTAAAATTCTTCATGAAGGTGAGAATCTGGGAATTTCTCGGTAC  
TCTTTCAGATTCGTAGTTATCCACTGATTGGAAGAATGAG

>RXA00298

ATGAGCTCAAATATAGCTATCACGACCGAGCCTGAAGGGAAAAATAAAAAGGGTCTCAAA  
TCAGACCCGTTCAATTTTTTCCATTTCTGTGCGTTTTATCGTGGTGTTTGTTCATCGCCACA  
ATTGCGCTAGGCGAGAAAGCTCGAACAACCTTTTCCGCGATTGCCGGCTGGCTCTTAGAA  
AATTTAGGGTGGATGTATATCGGGGGTGTCTCCTTGGTTTTCAATTTTCCTCATGGGTATC  
TTTGCGTCCCGGTATGGCCGGGTAAACTTGGTGATGACGATGATGACCCCGAGCACACC  
CTAATCGTGTGGTTCTGTATGCTTTTTGCTGGCGGTGTGCGTGCAGTCTTAATGTTTTGG  
GGTGTGCGGAACCGATTAACCACGCGTTCAACGTGCCAATGGCTAATGAAGAATCCATG  
AGTGAAGCCGCAATTGTGCAGGCTTTTGCTTATACTTTCTATCACTTCGGTATTCACATG  
TGGGTAATCATGGCACTCCCAGGATTATCATTGGGATACTTTATTTACAAACGTAAGCTA  
CCTCCCCGTCTATCCTCTGTGTTTTCTCCGATCTTGGGTAAAGCACATTTATTTCCACACCC  
GGCAAGCTCATCGATGTACTGGCCATCGTAGGCACCACGTTTGGTATTGCTGTGTGTCAGTA  
GGTCTTGGTGTGCTGCAAATCAATGCAGGTATGAACAAACTATGGAGCACCCCGCAAGTA  
TCGTGGGTTCAGCTTTTGATCATCTTGATCATCACCGCGGTTGCATGTATTTCCGTTGCT  
TCCGGTTTGGATAAGGGCATTAAGTTACTGTCCAACATTAATATTGCAATGGCCGTTGCG  
TTGATGTTCTTCATCTTGTTCACTGGTCCAACCCCTCACATTGCTGCGCTTTCTCGTAGAA  
TCCTTCGGAATCTATGCATCCTGGATGCCTAATCTGATGTTTTGGACTGACTCTTTCCAA  
GATAACCCAGGCTGGCAGGGCAAATGGACGGTGTCTATTGGGCATGGACTATTTGTTGG  
TCGCCATATGTCGGCATGTTTCGTGGCGCGTATTTTCGCGTGGACGTACCGTCCGTGAATTT  
ATCGGTGGGGTTCTAGCTCTGCCAGCGATCTTTGGCGTAGTTTGGTTCTCTATCTTTGGT  
CGTGCAGGCATCGAAGTGGAAGTGAAGTAAACCCAGGTTTCTTGACCCAGCCAACCTGTTGTT  
GAAGGTGACGTGCCAGCAGCGCTTTTTAATGTGCTGCAAGAGTATCCGCTGACTGGAATT  
GTCTCCGCGTTTGCACCTTGTAATTATTGTGATTTTCTTTATCACCTCCATCGATTCCGCA  
GCGCTAGTTAACGATATGTTTCGCTACCGGTGCAGAAAATCAAACACCGACTAGTTACCGC  
GTGATGTGGGCTGCACCATTTGGGGCGGTGCGAGGTTCTTGCTGATCATTTCCCCATCC  
TCTGGTATTGCCACGCTGCAAGAAGTGGTTATCATCGTGGCTTTCCCATTTCTTCTCGTG  
CAATTTGTTCATGATGTTTTCTTTGCTTAAAGGCATGAGTGAAGATGCTGCTGCGGTTCTG  
CGTGTGCAGACTCGTCAGTGGGAAAAGACTGATACACCAGAAAAACTTGAAGAGCATTCG  
TCCCAACCAGCCCCGGGCTATGATGACGAGGGCAACCCCTTGCCAATGCCTGCCCTCGAA  
CATGATGAGGACGGTAACATTGTTATCCAGGCAACGTAGTCATTGAAGGTGATCTTGGG  
GTAGTTGGTGATGTGGTGCAGCATCTGAGGAAGCCCAAGAGATGGGGTCTCGTTTTAAG  
ATCGTCGAGCAAACCTCGGCCCCAGTCCAGGGACGAATACGATATT

>RXA00298-downstream

TAAACGATTGCTTTTCGACGCAC

>RXA00346-upstream

ATCTATGAGACCCCTCAAACACCGAGAATTTCTTCGATGCATTCACCAAGGCAGTTGAT  
GATCTCACCGCTGCCACTAACCAGGTTTAGAATTATTTAA

>RXA00346

ATGCTGTTGACTTTCAATGATGCTGCGGTGGATCCCCCTCTGGAGGGGCCTGAATTTAGAG  
CTCCGACAGGGGGAATTTCTTGCGGTTTTAGGCCCAACGGCGTGGGAAAATCCACGCTC



ATCGGTACGATTTTGGGCACCCGAAAACCTCACCCACGGTTCGGTTAAAACTGATGCCCCG  
GTGGGTATATTTCCGCAACAACGAATTTTCGATGTCCCGTTGCGTGCCCGCGATATGGTT  
TCGCTGTCCGCGGCGCATGGCGTGGTTTCCAAAAGGGGACCCGCGAAGGGTGACGTCGAT  
AAGCTTCTTGCCCGCGTGGGCGCTTCCGGAATCGCCGATCGACGCGTCGGCGAGCTCTCC  
GGCGGGCAGCAGCAGCTCGTCCGCCAAGCCCAGGCCCTTGCCACGCGCCCGCAATTATTG  
CTTGCCGACGAACCCCTCCTCAGCCTTGACCCCGGCGTCGCGCAGCGCACGGTGTCCCTA  
TTTGGTGAATTGAAGGCCGAAGGCGTCGGCGTTGTTGTGGTCACCCACGATGTCAATCCA  
CTAATGGGCCTGGTAGATCGCATTTTGTACCTCGCCCCAACGGCCACACCATCGGCACG  
GTTGGCGATGTCATGCAGTCCGAAAACCTCAGCGAACTCTACAACGCACCCGTCACGGTG  
GCTCGCATCAACGACAGAATCGTGGTGGTT

>RXA00346-downstream  
TAAGTGGATCTATCCACCTGGCT

>RXA00368  
TCCCTCATGTTATCCCTGGGTGCAGCCCTAATCTGTGGGGTGCTGGGATGGCTGATCGGA  
GTGCTCATCACCCGAACCCAGCATTTCGCCAACGTACCGTTGACACTCACTGTGCTGCTT  
CCCACCGCACTGCCGGGCATGATCATCGGCGTCGGCTGGCTCATTTTGGGCAGATACACC  
GGAATTTACAACACACCTTGGGTGATTTTGGGTGCATATGTGTGTGCTTTTACCGCGCTG  
GTTGTCCAAGCTGTACGCGGACCACTCAGTCAAGCACCCGAAGCAATCGAAGAAGCCGCA  
CGAATCAGCGGCGCAGGCAGATTACGATCCATCATGGACACCACCGGAGCGATGGCAATT  
CCCGCAGCTTTCGCCGGCGCAGTGCTGGTTGCGGTAACCTGCGGTTTCGAGAGTTAACCGTG  
TCCATTTTGTCTCATCGCGCCGGGCACCACCACCCTGGGTGTGCAGGTGTTCAATTTGCAG  
CAGGCGGGAAATTACAATCAGGCATCGGCGTTGTCGTTGATGTTTGCATTATCGGTATC  
GTGGCGCTCGCGTTGACGGTGCGCAGCCAGAAGGAGTTT

>RXA00368-downstream  
TAGGTGTCATCGATCAAATTGCG

>RXA00369-upstream  
GGCGGGAAATTACAATCAGGCATCGGCGTTGTCGTTGATGTTTGCATTATCGGTATCGT  
GGCGCTCGCGTTGACGGTGCGCAGCCAGAAGGAGTTTATAG

>RXA00369  
GTGTCATCGATCAAATTGCGCGATTTAAGCGTGAGCTTCCGCGACGGAACCTTCGGGCTG  
CAAGATATCAATTTGAAAATTGAGCCGGAAGAATTTGTGGTGCTCATCGGGCCGTCGGGG  
TCCGGTAAAACCACCATGTTGGGCACCATCGCGGGGTTTGTGGAGCCAAGTTCCGGCAGT  
GTGCTCATCGCCGGCGAAGAAATGACGCATGTCCCGCCGGAGCGCCGTCGCATGGGCATG  
GTGTTTCAGCAGCATGCGGTGTGGCCGCATATGTCGGTCGCCAAGAATGTGGGATACCCG  
CTGGCGCGAAGTGGTCAGAAGGGGGCGTCGATAAGCAAACGCGTGAGCGCACGCTCGCG  
CTGGTGGGGCTTGAGGGGTTTCGGCAGTCGCAGACCGGCCAGCCTGTCTGGTGGTCAACGT  
CAGCGGGTGGCGCTTGCGCGCGCCATCATCGCCGACCCACCGTGCTGCTTCTCGACGAG  
GCCCTCTCCGCCCTCGACGAACCGCTGCGAGACGCTTTACGACGCGAACTCGTATCTTTG  
ACCCGGCGCGAAGGCCTCACTACTGTGCACGTGACGCATGACCGCGCCGAAGCGATCTCC  
ATCGCTGACCGCATCGTCTGACTCGGCAACGGTTCGAATCCAACAGGTAGCCACCCCTACT  
GAGCTCCTTTCCGCCCCCGCTACTGCCGATGTTGCCCGATTATCGTCGACGCCACC

>RXA00370  
GGCAAAGCCCTATGGAATTCCGCCTATACAACAGTGCTTTCTGCGGTGGGCGCGACCATT  
ATCGGCACGATCATGGCTCTCACGCTGGACCGAACTGATGTTTTCGGGCGCACCGCGTTG  
CGGTATTTTTTGTATCCCCGCTGTTGATCCCTCCGTTTATTGGGGCTATTGCGTGGTTG  
CAGCTGTTTCGGGAAGAACCAGGGCATCAACCGGTTTTTCGGCACGGAAGTGTGGGATATT  
TACGGCGCTGATGGTGTGACATTTTTTGTGATTGTGCACTCCTATCCCACTGTGTACATC  
ATTGTTTTCGGCAGCTCTGAGGCAACTTCCTAGTGATTTGGAGCAAGCTGCACGGATCGCG  
GGGGCGGATACTTTTACGGTGTGCGCACCATCACACTCCCACTGCTCAAACCTGCATTG  
TTGTGCGCGTTTACTCTTACCACAGTGGCGAACCTCGCCGACTTTGGCATTCCAGCTCTG  
TTGGGATCGCCAGCGCGTTTTTGAAACCTTAGCCACCATGATTTATCGCTTCATGGAATCC  
GGCACCGTGAGCAATCCATTGCAGGTGGTATCCACCATTTGGCATCGTGTGTTGTTCTG  
GGAATCGCAGCAGTAACCGCGGATTATCTGGTGTCTTTGTACGCGGCATCAAAGTTGCAA  
GACGCAGGAACACCGCATCGCTTTACTCTCAACAAATCACGAATCCAGTCAGCGTGATC  
ACGTGGATCATCGCGTTGATCATCACCGCCGCCCCGCTGCTGGGTCTGGCATAACAGAGCA

TTACTGCCTGCCCCAGGT

>RXA00410-upstream

GTGTTGATGCGTTAGTCCACCCACGCAGCTACGCCCCAAAGGAATAATCTTGAACCCTGC  
CACAGATAACGCTCCGCCGGTCTTTCAGCCCAAGATCTC

>RXA00410

ATGATGATCTATGGAAAAGGATCAACAGAAGTTCGGGCTCTCGATGGCATTCTGTACAG  
ATTCAGTCCGACAAATGGACCTCCATCATGGGGCAATCAGGCTCTGGCAAAACAACTCTG  
TTGCAGTGCCTTTCCGGATTGGCGCAGCCAACCTCAGGCAGAGTGACACTGAACAAAAAC  
AACATCACGTTGAGCTCCCTGTCAGAAAATAAGCGTGCCAAGCTGCGTCGCACGCACATC  
AGCATGGTGTTCAGGATTTCAACTTGGTGCCTATTTTGTTCGGTGAAGGACAATATTTTG  
CTGCCGTTGCGTCTTGCAGCATCGCAGGGTGGATAAGCAGTGGTTTGAACACATCACCAGT  
GTGTTGAAGATTGATAATCGTATGCGCCATTTGCCTGGGGAGCTGTCTGGCGGTCAGCAA  
CAACGCGCCGCGATTGCCCGGGCGTTGATGTCTAGGCCCGATATTGTCATTGCGGATGAG  
CCAACAGGAAGTTTGGATTCCGTCACCAGCGATGCAGTGTGAATTTGTTCCGCAGCATT  
GTTGATGATTTTGGGCAGTCACTTGTGTTTGTACCCACGATAAAGATGCTGCTCACCCT  
GGTGACGTGTTGATCACAATGCGTGATGGCAAGATCATCGATACGGCAGATTTGCGGGTG  
GGGCGT

>RXA00410-downstream

TAATGTTTCAGGCTTGCTTTCGCT

>RXA00419

GACAACGAAGCACAGTGGCGCGACCAAGCACTAGCAGTGGAAGCAACCACCGTGAACCTAC  
ACCGCCGGCGTTTCCGTAGGTGTACTGCTGGGCCAGAAATTTGAGCAGCAGGGCCACGGC  
ACCATCGTGGCATTGTCTCTGTGGCAGGCCAGCGAGTCCGCCGCTCCAACCTTGTCTAC  
GGCTCCGCCAAGGCAGGTTTCGACGGTTTCTACACCCAGCTCGGCCGAAGCCCTGCGTGGA  
TCCGGTGCCAACGTATTGGTGGTTCGCCAGGCCAGGTACGCACCAAGATGTCCGCAGAT  
GGTGGCGAAGCCCCACTGACCGTCAACCGCGAAGACGTGGCAGATGCTGTTTATGATGCA  
GTGGTGAACAAGAAGGACATCATCTTTGTCCACCCACTGTTCCAGTACGTCTCTTTTGC  
TTCCAATTCAATCCGCGAGCAATCTTCCGCAAGCTGCCGTTC

>RXA00419-downstream

TAACGGAAGTTACGGAAGTTACG

>RXA00421-upstream

GCTGGTTGAAGACTCGAAATGAGATCGACCCAACCGGAGTCTTTGCATCTGACATGTCCC  
GCCGACTTGAGCTTTCTTAAGAAAGGGCTTGAACATAACA

>RXA00421

ATGCTTAACGCAGTGGGCAAAGCCCCAAAACATTCTCCTTCTTGGTGGAACCTCTGAGATC  
GGTATTTCCATTGTCTCCCGCTTCCTCAAGCAGGGTCCATCCCATGTGACCTTGGCAGCG  
CGTAAAGATTCCCCACGCGTGGACGCAGCAGTCGCAGAG

>RXA00432

TTGTCTGCGCTGGTTATTTTTGGCGGCGTGCAGCGTATCGCAAACGTGACGCAGTGGATG  
GTTCCGTTTCATGGCGGGTGCCTACATCATTTGTGGGTGTGGTGGTGATTGTGATTAACATT  
CAGCAGGTTCCGACCATGATCAACGACATCATTTGCTGGTGGCTTTTGGTTTCCGTCCGGTT  
GCTACTGCGTCGGTGTGGGGCGCGTTCTGGTTGGCGTTTATGAACGGTATGCGCCGTGGA  
CTGTTCTCCAATGAGGCTGGTGAGGGTTCTGTCCCGAACGCTGCTGCTACCGCGACTGTG  
TCTCACCTGTGAAGCAGGGTTTGGTTCAGACTCTGGGCGTATATTTTCGACACCCTGCTC  
GTTTGTAGCATTACCGCTTTTGTTCATCCTGCTGTCTGGAGTGGAGTACGCGACCGGCGAT  
ATTCAGTCTTCTTCTTGTACTCAGTCCGCGCTGGCTAGCGTTGTTGGTGGTTGGGGAACC  
CACTTCATTACCGTAGTGATGTTCTTCCCTGGCGTTTCTTCCGTGCTGGGTAACTACTAC  
TTGGCACAGGCGAATATTCACTACTTCACCGATTCAAGACTGTCATGACTGTTTTCCGA  
CTCTTGGTGCTGCTCAGCGTGTCTCTGGCGCGGTTGCTTCGGTGCCGTTGATCTGGGCT  
TTGGGTGATACTTTTCGCTGGCATCATGGTGCTCATTAACCTGGCGGCGATCATTCCGCTG  
GGTGGCGTTGCAGTGAAGTTGCTTAAGAATTACACCATTCAGAAGAAGGCTGGTCTGGAT  
CCTGTGTTCCACCGCGACATGATGCCAGAGGTTTCGTAATATTGCGTGCTGGAACGGCAA  
GATGCAGCTACATCCAATATCACGAAGCGATGGAAGTGATCAAGAAGAGC

>RXA00432-downstream  
TAGTCATCGAAGGAACAGTGGTA

>RXA00436-upstream  
GGGATTTACTAAAAATCGGGTAACACGCGCGTAGTATTTTTCGC

>RXA00436  
ATGGAATTATTGGAGACCTTCATCACTGATGTCATTAATGACAATTTGTGGATGATCTTG  
CCCTTCTTGCTCGTTGCTGCTGGCCTCTATTTTCGGTGGGCGTACGTTGCTGGTTCAGATT  
CGGATGATTCCGGAGATGTTCAAAGCGGTCGTCGAGAAGCCTGCGAAGGATGGGGAGTTC  
GCGGACAAGCAGGACATTTTCGGCTTTTAAGGCGTTCACGATTTCTGCGGCGTCGCGAGTT  
GGTACGGCGAATGTTGCGGGTGTGCGCTGGCGATCACTCTGGGTGGACCGGGTGCAGTG  
TTCTGGATGTGGATCATTGCGCTGGTTGGCGGTGCGACATCGTTCATTGAGTCGACTCTT  
GGACAGTTGTGGAAGGTGAAGGACGGCGACAGCTATCGCGGTGGCCCTGCGTACTACATG  
ACGCTTGGTTTGAATGCTCGGTGGCTTGGCGTGTGTTTTCGGTGTGCGCCATCACGTTGACC  
TTTGGTTTTGTGTACAACGCTTTGCAGTCCAACGCGGTGTTGAG

>RXA00449  
CTGGCACTGACCGCTGAGACTGTGGGCGGAATGAAAAACCAAAGAAATTCGCCACTGGA  
CTCATGCTGTCCATTGCTTATTCTGCTTCCATCGGTTCACTCGGCACCTTAATTGGCACG  
CCACCCAATGCCTTGCTTGCTGCGTATATGTCTGAATCGCATGATATCCACATCGGATTT  
GGTCAGTGGATGATTCTTGGTGTACCAATTGCTGTGCTCTTACCATCATCGCGTGGCTT  
GTGTTGACCACCGTGTCAAGCCAGAAATGAAAGAAATCCCTGGCGGACGTGAACTGATC  
AAACGTGAAATCGCTGAAATGGGGCCGTGGACTGCACCTCAGGTACAGTGGGTGTTATT  
TTTGGCGCAGCTGCACTGGCTTGGGTCTTCATTCCATTAACCTCTAGATTGGACCGGTTCC  
CAGCTCTCTATCAATGACTCCCTCATTGGCATCGCTGCCGGCCTGCTGATGTTTATCGTT  
CCCGCTAACTTTAAAACCGGCGAACGCATTCTTGATTGGCGTACTGCAGGCGAACTTCCA  
TGGGATGTTCTCTTGCTTTTTGGTGGCGGGCTTTCACCTTCTGCGATGTTTACCAGCACG  
GGACTTTCCCTATGGATCGGTGAAGTAAAGGACTTATGATGCCCTTCCAATCTTCATT  
CTCATCTTCGCCATTGCTGTCCTGGTGTGTTGTTCTGACCGAGTTCACCTCCAACACCGCA  
ACAGCGGCAACCTTCCTGCCAATCATGGGTGGCGTCGCCGTAGGTATCGGACTGACCGCA  
GGTGGCGAGCAGAATGTTCTGCTGCTGACCATCCCAGTCGCACTGTCCGCAACCTGTGCG  
TTCATGCTTCCAGTGGCAACGCCTCCAAACGCGATTGCATTGCGCTCCGGCTACATTAAG  
ATCGGCGAAATGGTCAAGGGTGGTCTGTGGCTGAACATCATCGCAGTCATCCTCATTACG  
ATTTTCACCTACTTCGTAGCGATCCCACTCTTTGGCATCATGCTT

>RXA00449-downstream  
TAAAAGTTAACAGGCCCGCAGTC

>RXA00456-upstream  
CTCACCAACCCGGAGATCGTCACAGCGGTGCTAACGGATCATGCCTAGCTTATGGCGTGC  
TCGTGCGCAGACTTTTGCTCATTGCCCTAGGTGTAAGT

>RXA00456  
GTGCTGCAGGCACTGCTGGCGATCATGGTGTGCTTGAGCGTAGCCGCCATACTTGAGGGA  
AACCGAGCACTTGTTGGATTGCTGCTTGCTACCACGTTGGGTTTGGGGGTGGCGCAGTGG  
ATTCAAAAAGTAGTGGCAGAAGATCTAGGCCAGCATTATGTGCATGAGGTGCGTCGTGAA  
TTGGTGGGTGCTGCGCTGGTGCCTGGAAATACGGCCTCGTTGGGCGTGAAGTGTACCCGA  
GCCAGCAATGATCTCACCGCGGTGCGCAATTGGGTGGCTTTGGGCATTGTTCCGATGGTC  
ACCGGGCTGCCG

>RXA00459-upstream  
AGGCGTGGCTGTTACTGTGCCACTGCTCAT

>RXA00459  
GTGTGTACCCGTGCTGCCGGTGGTGGCGCGGTGACTTTGAAAAGAGCACGTGAACTACGC  
AAAAACGTGGACGCATGGCTGCGCGGATCGCAGATTCTGTCATGGCTGGAGAATTACTG  
CACGCAACAGGAGCAATAGACCGTGAGCTCAATGCAGTCACCCGAGATTCCGACCGAGTG  
GTGATAGCTGCTGTAAGACGTTCTGGGCCACCGGTTTGTAGCCGCGCATTGATGGCCATG  
GCAGCCTCGCTTGGCACTGTCAGCATTTGTGATTTCTGGCCACCTGGAAGTAAGTGAGGT

GCGGGAATAATGATGCTTCTTGGCGTTCTTGCCACTCCAGTTGCAGAACTTGGCCGCGTG  
 GTGGAATATCGCCAAAATTATAAAGCCGCGACACGCATCCTGATTCCACTTCTGCAACGA  
 GGCTCAGAATTTAAACACTCCCAACAAAACTACCCGGGTGCAAGCAACAGAAGGAATC  
 CCCGGTGTCTATGTCAAAGGTATTTCCGCCCTTCTGGAGAACGGATCTACCTCCACGGC  
 TCTGCAGATGCGACGAGAAAATGGGTACCTCGTTGTCTGCAATGGAGGAAGGCACAGAT  
 GTAATAGTCAACGGTCAAAGGCTTTTCGCAGCTTCCTTTGAAACAACGACGCGCCCTCATC  
 GGAATCGCCTCAGCACACCACCACTTAAGCCGTGGTTCAGTATCGCGCCTGGTTGGTTTG  
 CGAGTGCCGGATGCCACCGTGGAAGAAATTGAGCAAGCACTGGAACAAGTTGGTCTGAAC  
 AACACCGGGAAACAACGCTTGAAAAACGGCGGACACCCCTGGAGTACTTCGCAGATCAAC  
 AAATGAAAATTGCCAGCGCCACCCCTTCGAACCCACCGCTTTTGGTACTTGAAGGCATC  
 ACCCCTGAAAACCTCCTCAACTATCCCGGAGTGATCATCTCCACCGTTCAGGAGAACCA  
 TCCGAAACATGGCGGCAAGTGAACATC

>RXA00459-downstream  
 TAATCTAGAAACATGGCAGGACG

>RXA00477-upstream  
 TGCGGGAGCGAATCAGAGTTCCACTTCATATCAAACCTCTCTACACTCGCTAGAGCCACGA  
 TGAAAGGTCTATCTATGAGCATCTACAGAAAGAATTTCGTG

>RXA00477  
 ATGAAGGTCTCGACTAAAACCTCCACGCTCCTCAGGTACCGCCGTAGTCATAGGCGCAGGT  
 GTTGCTGGTTTAGCCACTTCTGCACTTTTAGCACGTGATGGCTGGCAAGTAACTGTTTTG  
 GAAAAAATACTGATGTCGGTGGCCGAGCTGGATCGCTTGAAATATCAGGCTTTCCTGGC  
 TTTTCGATGGGATACCGGACCTTCTTGGTACCTCATGCCCCGAGGCCTTTGACCATTCTTC  
 GCACTTTTTTGGTGCATGTACTTCTGATTATCTCGATTTGGTAGAATTAACGCCTGGTTAT  
 CGAGTTTTTTCTGGCACACATGACGCTGTCGATGTCCCCACTGGGCGTGAAGAAGCAATT  
 GCGCTATTTCGAATCCATCGAACCCGGCGCGGGTGCAAAACTAGGAAATTATCTTGATAGC  
 GCGGCAGACGCCTATGACATTGCCATTGATAGATTCCCTTTATAATAATTTCTCCACGTTA  
 GGCCCGCTGCTTCACCGGGATGTACTGACCCGAGCTGGCCGACTGTTTTCTCTACTGACC  
 CGTTCTTTACAAAAGTACGTAAATAGTCAATTCAGTAGCCCGGTGTTGCGCCAGATCCTA  
 ACCTATCCAGCAGTCTTCCTGTCTTCCCGACCCACTACTACCCCATCGATGTACCACTTG  
 ATGAGTCATACCGATTTGGTGCAGGGAGTGAAATACCCTATAGGTGGTTTTACTGCAGTG  
 GTTAACGCTCTGCATCAGTTAGCGCTGGAAAACGGGGTTGAGTTTCAACTCGATTCTGAG  
 GTCATTTCCATCAACACTGCTTCATCGAGGGGCAACACAAGCGCCACAGGTGTGAGCTTG  
 CTTCAACAGAAAAGTGCAAAATCTAGATGCGGATCCTTGTGGTTTTCAGCAGGCGACCTA  
 CACCATACAGAAAATAATCTGCTTCCCCGGGAACTTCGAACCTATCCCGAACGATATTGG  
 TCCAATCGCAATCCTGGAATTGGAGCGGTATTAATCCTCCTGGGCGTAAAAGGAGAGTTA  
 CCCCAGCTCGACCATCACAACTTTTCTTCAGTGAAGATTGGACAGATGATTTTGCTGTA  
 GTTTTCGACGGGCCTCAACTTACCCGCCCCACAATGCATCAAATTCATTTATGTCTCC  
 AAGCCTTCAACGTCCGAAGACGGCGTTGCACCTGCTGGATACGAAAACCTTTTTGTTTTA  
 ATTCCGACCAAGGCCTCTAGCAGCATCGGCCACGGTGATGCGTATATGCAGTCGGCTTCA  
 GCATCCGTGGAAACAATCGCGTCACATGCAATCAATCAAATTGCTACGCAAGCCGGCATC  
 CCTGACCTCACTGACCGAATTGTGGTCAAACGCACCATTTGGCCCTGCGGATTTTGAGCAC  
 CGCTACCATTCTATGGGTAGGAGTGCCTGGGTCCAGCACATAACCCTCAGACAGTCCGCT  
 TTCTTAAGAGGGCGCAATAGCTCCCGCAAGGTCAATAACCTCTTCTATTCCGGTGCCACC  
 ACCGTCCCGGGTGTAGGAATACCCATGTGTTTAATTTCTGCCGAGAATATTATTAAGCGT  
 TTACATGCCGATACCAGTGCAGGACCACTGCCCGAACCATTGCCGCCTAAAACGACACCA  
 TCTCAAAAGACCTCATACGATCAT

>RXA00477-downstream  
 TAAATTTTGATCCCTATCATCGA

>RXA00478-upstream  
 ACCAGAAGCAGCCTCAGCTATGACACACCAAAATTCGCCTCTCTTCCTTAAAAGTGCACT  
 GAGACTTTACAATCGGGCCTCATTCAAGGCTTCACATAAA

>RXA00478  
 GTGATCGAAGAATATTCCACGAGCTTCAGTCTGTCTACGTGGTTGCTATCCCCACGCATA  
 CGAAATGACATACGAAATCTCTATGCAGTAGTTCGTATCGCCGATGAGATTGTGACGGC  
 ACTGCACATGCCGCTGGTTGCTCAACTGCCAAAATCGAAGAGATTCTCGATGCCTATGAA



ATTGCGGTTCTTGCAGCACCACAACAACGCTTCAACACAGATCTTGTTTTACAAGCTTAT  
GGTGAAACTGCCCCGACGCTGTGATTTTCGAACAAGAGCATGTAATAGCCTTCTTTGCATCA  
ATGCGTAAGGACCTCAAAGCTAATACACACGACCCAGATAGCTTCACAACGTATGTCTAT  
GGCTCCGCGGAAGTTATAGGCCTGCTTTGTCTCAGCGTTTTCAACCAAGGTAGAACGATT  
AGCAAAAAACGGCTAGAGATTATGCAAAACGGAGCCCGCTCATTGGGAGCGGCATTCCAG  
AAAATTAACCTTTCTCCGTGACTTGGCAGAAGATCAGCAAAATTTGGGCCGATTTTATTTT  
CCCAAAACCAGCCAAGGAACCTTTACTAAAGAACAAAAAGAAGATCTCATCGCTGATATC  
CGTCAAGACCTAGCAATTGCCACGATGCATTTCCAGAAATACCAGTGCAGGCTCGCATC  
GGAGTGATCTCTGCTTATTTGCTCTTTCAAAAACTCACTGACCGAATTGAGGCTACTCCT  
ACCGCCGATTTATTGCGGGAGCGAATCAGAGTTCCACTTCATATCAAACCTCTCTACACTC  
GCTAGAGCCACGATGAAAGGTCTATCTATGAGCATCTACAGAAAGAATTTCG

>RXA00478-downstream  
TGATGAAGGTCTCGACTAAAAC

>RXA00480-upstream  
TTTATGGACCCAAATTCACACTTTCTGTACTTCATCAAAATAAAGCGCCATATACAACGA  
TTGGGAATTTTTGCGAGATAACTGGCCGTGTGATACTCGA

>RXA00480  
ATGGACAATGGCATGACAATCACCACAGAACATTCAACTCATCCTGATCTTGATTTCAAT  
GATGAGATTTATCGGGAACATAACCGCATCTGCGCTTCGCTATCTCAACAGTGCAGCACA  
TATCAACCAGAGTTCCGTACCTGCCTAGATGCTGCTTTCCAAGCTTTGCGAGGTGGCAAG  
TTAATCCGCCCTCGAATGCTACTGGGGCTATACAACACGCTTGTAGACGATGACATTGAG  
GTCAAACCTCAACACCGTTTTACAGGTAGCAGTGGCTTTAGAACTACTGCATTTTTCCCTT  
TTGGTTTCATGACGATGTTATTGACGGAGACCTCTATCGCCGAGGCAAACCTTAATTTTATT  
GGGCAGATTCTCATGCATCGCACACCTGAAAGTTTTGCACAAATCCAGCGCGATCCAGAG  
CATCTAGATTGGGCACAATCTAATGGACTGCTTATGGGAAATCTTTTTCTTGCTGCCACC  
CATCAAATCTTCGCGCGCCTTGACCTTCCACATCACCACGGGTTCGACTTTTAGATTTA  
CTCAACCACACGATAAATGACACTATTGTGGGTGAGTTTCTTGATGTGGGATTAAGCAGC  
AAAGCCATCAGCCCCAATATGGACATTGCTCTAGAAATGAGTCGGCTAAAAACAGCCACA  
TAACTTTTGAACCTCCAATGAGAGCAGCGGCAATTCTCGCGGAACTACCTCAGGAGATT  
GAAACAAAGATAGGTGAGATAGGCACAACTTGGGCATCGCTTATCAATTGCAGGACGAT  
TACTTATCTACTTTTGGTGACGCAGCCGAACACGGCAAAGATGCCTTTTCTGACCTTCGA  
GAAGGAAAAGAACTACAATTATCGCCTTCGCTCGAGATACTGCTAAATGGACTGATATT  
CAAGACAACCTTCGGCTCCGCGAGATCTGAGCACCTCTCAGGCAGAGCGAATTCAACATCTT  
CTCATACAGTGTGGAGCAAAGAATCACTCCTTGAATGCCATCTCCGACCACTTAAATATC  
TGCCGTTTCGATGATCAAAACACTAAGCCCCCAGGTAGATCCCAAGGCTCAAATTTATTA  
CTTAAACAAGTTGAGCAACTAGCCAGCCGCAAATCT

>RXA00480-downstream  
TAGAACTAACCTTTACGCCTTTA

>RXA00524-upstream  
TCCTCGGCACCCGCTACCCCGTCGGAGTTGTCACCGGCGCATTCGGCGCCCCATTCTTA  
TCTATTTACTCATTCGTTCCAACCGCGCGGGAGTAACCT

>RXA00524  
GTGACCACCAACCATCAACTATCCGCCGAAGAAATTTCCCTGGCGTACGGCGAGCGCACC  
ATCATCGATTTCGCTCAGCGTCGACATCGTCCCCGGCAAATCACCTCCATCGTCGGCCCC  
AACGGATGCGGCAAATCAACGCTGCTGCGCGCCTTTGCGCGCCTCCTTAAACCTAGCGCC  
GGGCAAGCGCTTATCGACGCCACCCCTTCTTCACTGCCAGGCAAAGAACTAGCTCGC  
ATGCTCGGGCTGTTACCGCAATCCCCACCGGACCTGAAGGCATCGTCGTCGCCGACCTC  
GTGGGCCGCGGCCGCCACCCCAAGGACTC

>RXA00526-upstream  
GGTGGAGCAGGCGGCGGCTCCTTTTAGTCCTGCGGCCCTTTTGACCCTGCAGCCCCTGC  
CGTTTCTGCCAAGCAAACCGTGGGCCAGGTGATTTAGCCT

>RXA00526  
ATGAGCCTCATCGAAATGCGAAATATTGTCAAGACCTACAACATTGGATCTGAAGGTGAA



CTCACCGTGTGTCACGGTGTGGATTTCATGTGGACCGTGGCGAATTCGTGTCGGTTGTG  
GGTACGTCCGGCTCAGGTAAATCAACGATGATGAACATCATTGGGTTGTTGGATAAGCCA  
ACTGATGGCACGTACACCTTGGATGGCGTGGATGTGTTGGATATCAGCGATGATGCTTTG  
GCGAGCCACCGCGCTAAATCGATTGGTTTTGTGTTTCAGAACTTCAATCTGATTGGCCGG  
ATCGATGCGTTGAAGAATGTGGAAATGCCCATGATGTATGCGGGCATTCCGGCTAAGCAG  
CGGAGAAGTCGTGCGGTTGAATTATTGGAAATGGTCGGGATGGGTGAGCGTCTCAACCAT  
GAGCCCAATGAGCTTTCGGGTGGTCAGAAGCAGCGCGTGGCCATTGCTCGCGCGTTGGCG  
AACGATCCTGAGATCATTCTTGCTGATGAACCAACTGGTGCGTTGGATTCTGCAACGGGC  
CGGATGGTGATGGATATTTTCCACCAGCTCAACAAGGAGCAGGGCAAACCATCGTGTTT  
ATTACTCACAACCCTGAGCTTGCTGATGAATCTGATCGGGTGGTCACCATGGTTGACGGG  
CGCATCATTGGGTCTGAGGTGAAACACTCA

>RXA00526-downstream  
TGAGCCTTGCAGAATCAATTCTT

>RXA00559-upstream  
CCCTTCAATCCAGTCTTTGACGGCCAATACGGCTTGCCGGGTTTCCAGCGGATCAATCCT  
CATGAAGCATCAGCCTAGTACGAACCGTTAAAGTGTCAT

>RXA00559  
ATGTCTGATAATCCGCATGAGAATCCCCGTGAGAATCCACACCGCTCCCCAGAAGTCGTC  
CTTCGTTTCATGGCTGCCCCTACTGACGTTTTGATGGCTGGTAGCCATGGCGTTGGCGGT  
GGCCGAGTCCTGGAATGGATCGATAAGGCTGCTTATGCTTGTGCTACCCACGGGTCTGGA  
ACCTACTGCGTCACTGCTTATGTTGGTCACATT

>RXA00570  
CCAACCATCGTGATGGCCATGGTCGCAGGCATTTTCCTCCGCTTCGGACTCGACCTCATC  
GACGCCAGCGTGACCGACCCGCTCATTGCACTTCCCATGGTCATAGTTTTTGTGGCATTG  
AGCATGAGTCCCCGCTTGGCAAGCATCGCCCCACCCGTTGCAGTAGCCGCAGTAGTGGGA  
ACCATCGTTGCCATCGCATCCGGCAAACCTAGCGTCCGGAATTCTAGACAACGGAATTATC  
TCCCGCCCCGTCTTTACCGCCCCAGAATTTTCCTTCGCCGCCATCATGGAACCTCGTTGTT  
CCCTTGGCGATCACCGTAGTCATTGTCCAAAACGGCCAAGGCGTCGCAGTGCTTAAAGCA  
GCAGGTCACCGCCCCGGAGTAAACCTTGCCGCCGCGGCCTCCGGACTGTGGTCCCTACCC  
ATGGCGTTGATCGGCAACATCACCACTGCCTCACCGGCCCCACCAACGCGCTGATCGTC  
GCCGGAGCAAATCACAC

>RXA00571  
CAGATCGGTGCGCTCAGCCCAGCAGTCGCCGGCACCCCTTGGTTCCTACGCCATGATCGGC  
GTGATGATCGGTGCTCTATCTGCAGGTGCCGTTGGTGACCGCCTTGGTCGTCGCAAAGTT  
ATGCTCACCGCAATCGTCTGGTTCTCTGTGGGCATGGCGCTGACCGCGTTTCGCGTCCTCG  
ATTGCGCTGTTTCGGTTTCTTGCGCTTCTCACCGGACTTGGCGTGGGCATGATCGTTGCA  
ACCGGCGGCGCAATCATCGCGGAGTTCGCTCCAGCGAATAGGCGCAACTTGTTCAACGCA  
ATCGTGTAATCCGGTGTCCCAGCCGGTGGCGTGCTGGCTTCTATCCTTGCACTGCTCTTT  
GAAGATGTCATCGGCTGGCGCGGACTCTTCTCATCGGTGGATCCCCACTACTGTTCTCTC  
CTGCCACTTGCACTTCTTCTCTCCAGAGTCCCCGCGCTGGCTCACCTCCCGCGGCGGT  
GCTGCGGACGCCAAAGCCCTCTGCGCACGCTATGGGCTGCCGACGGAGGAATTTGTGCTC  
GAAAAGCAGCAGGAACAAAGGGCACCGGATTCGCTGGAATTTTCTCCTCCAAGTACCTC  
ATGGGCAACATTTCTCATCGGCGCAATGAGCTTCATCGGGCTGCTTTCGACCTACGGCCTG  
AACACCTGGTTGCCAAAGATCATGGAATCCAACGGCGCAACCTCACATGATTCCCTGTAC  
TCCCTGCTGTTCTCAACGGCGGCGCAGTGTTTCGGTGGCCTCATCGCATCCTGGTTGCT  
GACCGCATCGGCGCGAAGACCGTGATCACCTCCACCTTCGCTCTCGCCGCGATCTGCCTC  
GGAGTCTTGCCAAACATCTCTCTTGCCAATGATGTACACCGCAATCGCATTCGCAGGC  
GTCGGCGTCTGGGCAACCAAGTTCTCACCTACGGCCTGACCTCGAACTTCTTCGGAACC  
GAATGCCGCGCAGCGGGAGTTGCATGGTGTGCAGGATTCGGCCGACTCGGCGGAATCGTC  
GGACCAGCAATCGGTGGCCTGATCATCGGCGCAGGATTCGGACCAAGCTCCGCATTCCTC  
ATCTTCGCAGCAGCTGCCGCAATCGGCGCGGTCTGCACCTTGCTGATCCCGCGCTCCCCA  
GCAGAAGTAGAGGTCAAGGTGCGCGCAGGAACCACTTGACAGTGTC

>RXA00571-downstream  
TAACCCCAATTAATTCGAAACAA

&gt;RXA00572

CAGTGGCTCAACCGCTACCTCGAGCTGTCTGGCCCTGTTGATGGTCAGTGGATTGATGCT  
TCCTGGGCTGCACGTTTTTGCCAGATGCTGGAGCGTGCCGAGGCGCGTTTTGATCGAGCAG  
GATCATGGCCAATTTGAGCCAAGCCTGACGGTGGAGGATGGCGTCGACAAGCTTGTTGCT  
GCTTACCCGCATGCCGCAACCGACCTGCTCACCCTGGCTGATGTCGCCTGGTTCTTGGGC  
CTGTGCCGCACGCCGGGCAAGCCTGTGAACCTTTGTGCCCGTCATTGATAAGGACGTGCGT  
CGCTGGTGGCGCTCGGACTCCCTGTGGCAGTCCCACGATGATCGCTACACCGCTGATCAG  
GTGGCTATTATCCCTGGTGTCTGCGCCGTTGCTGGCATCACCAAGGCCAACGAACCTGTC  
GCTGACCTGCTTGATCGCTTTGTGCGACGCCACCATCGAGCGCATCGATGAGCACGATTCC  
CGCTCCCGCGACATCATGGGCAAAGTGCTTTCCTCACCTGGCACATTCTGGGCTGGCCGC  
AACATCCCATCGGTGATCCACAGCCTTGGGCATGCTGACAAGTGGTCCCGCTCCGAATTC  
GAAGCATTTCCATAGCCCAACCGGCGCCAACCTTGGTGTACGAAGACGCCGAGCACGCGATG  
CTGACTGTGCCTTTGGCGGGTTCCACCGCATTCGGCACCAACCGCTGAGCTGAAAATCCGT  
TTCACCAGCCCCATCGACGCTCTGCCAAGCGCTGTCCCACTGGTCACCCAGGAAGACGCT  
GAAGCCGCGATGGGTGAACTGACCCGCATCGCAGCTGGCGGCACCCTGGCAACTGTGAAC  
AATGGCACCGCTACCTGGGAAACCTCCGTCGATGCCGGCGTCATCGCTGACTACAACAAC  
GTCACCGCAGGCTACCTGCCAGCATCCGTTGTTCCCTGCACACACCGCACCTGACGTGCTG  
GTTGGCCGCGCATGGCCAGCAGTTTTCTGCTGCCGTAAAGTCCGCAGTCATCCCAGGCACC  
GATTCGCGATCCGTTGTGGAAGGCATGCTGTCCCTGGTTTACCTGGAGCACCATTTGTG  
CTCAAGTCCGATGTCCCAACCGACGGCGCGCTGAAGGTTTCCGCGACTGCCGATGAGGTA  
GTCGATACCGACCTGGGTGCGCTCGTGATCGTGCGCGCAGAAATCGCCGACGCAGAAGGC  
AACCTGATTGCTACGTTGGCTGAGCGTTTCGCGATCCGCGGACGCAAGGGCAACGCTGTC  
GCACGCACCAACACCTCCGCACTGCCAACCACCGTGGACACCCACGCTCAGCTCGCGCA  
GTGGCAACCGTTGTTGCACCTGAATCCATGCGCCCATTCGCTGTGATCTCCGGTGACCGC  
AACCCAATTCACGTCTCTGATGTTGCGGGCTTCCCTGGCTGGTCTGCCAGGTGTGATCGTG  
CACGGCATGTGGACCTCTGCCATCGGTGAACTGATCGCCGGTGCAGCATTCAACGATGAG  
CAGATCCAAACTCCCGCAGCCAAGGTCGTGGAATACACCGCAACCATGCTGGCACCAGTT  
CTTCCAGGTGAAGAAATTGAGTTCAGCGTTGAGCGCTCCGCAGTGGACAACCGCCCAGGA  
ATGGGAGAGGTCCGCACCGTTACCGCAACCGTCAACGGCAACTTAGTGCTTACCGCCACC  
GCTGTTGTGGCAGCTCCATCTACTTTCTACGCATTCCCAGGCCAGGGCATTTCAGTCCCAG  
GGCATGGGTATGGAAGCACGCCGTAACCTCTCAGGCAGCTCGCGCTATCTGGGACCGCGCC  
GATGCACACACCCGCAATAAGCTGGGCTTCTCCATCGTGGAATCGTGGAACCAACCCA  
CGCGAAGTAACCGTGGCAGGGGAGAAGTTCTTCCACCCAGACGGCGTTTTGTACCTCACC  
CAGTTCACCCAGGTGGGCATGGCAACTCTGGGCGTTGCTCAGATCGCTGAAATGCGTGAA  
GCACATGCCTTGAACCAGCGTGCATACTTTGCTGGACACTCCGTTGGTGAGTACAACGCG  
CTTGCTGCATATGCTGGTGTGCTGTCCCTGGAATCCGTTCTGGAGATCGTTTACCGTCGT  
GGCTTGACCATGCACCGCTTGGTGGATCGCGATGAAAACGGTCTGTCCAACCTACGCGCTC  
GCAGCTCTTCGCCCCAACAAGATGGGTCTGACCGCAGACAACGTTTTTCGATTACGTTGCG  
TCTGTTTCCGAAGCTTCCGGTGAATTCCTGGAGATCGTTAACTACAACCTTGGCTGGCCTG  
CAGTACGCAGTTGCTGGAACCCAGGCTGGTCTTGCCGCCCTTCGTGCCGATGTTGAGAAC  
CGTGACACAGGTCAGCGTGCCTTCATTTTGATCCCTGGCATTGACGTGCCATTCCACTCC  
TCCAAGCTGCGCGACGGTGTGGGCGCGTTCCGTGAGCACCTTGATTCCCTGATCCCAGCT  
GAGCTGGATCTGGATGTGCTGGTTGGCCGCTACATTCCAAACTTGGTGGCTCGCCCATTC  
GAACTCACTGAAGAGTTCGTGGCATCCATGGCAGAAGTGGTGGAGTCCACCTATGTCAAT  
GAGATCTTGGCTGATTTCAAGGCTGCTTCCGCCGATAAGCAGAAGCTTGCCCGCACGTTG  
CTTATTGAGCTGCTTGCATGGCAGTTCGCATCACCTGTGCGCTGGATCGAGACTCAGGAT  
CTGTTGATCAAGGGCCTTCAAGCTGAGCGTTTCGTGGAGGTGCGGTGTTGGCTCTGCTCCA  
ACGCTTGCCAACATGATGGGCCAGACCCCTGCGCCTTCCTCAGTACGCGGACGCCACCATT  
GAGGTGTTAAACATTGAGCGCGATCGCCAGTTGTGTTTCGCTACCGATGAGGTTGTGCGT  
GAAGTGGCGGTTGAAGAGACCCAGCAGCTCCTGCAGAAACCACTGAAACCCAGCAACC  
CCAGCAACCCAGCCCCCTGTTGCAGCTGCAGCCCTGCCACCGGCGGCCCTCGCCAGAT  
GACATCAGCTTCACTCCTTCTGATGCCACTGAAATGCTCATCGCTATCTGGACCAAGGTT  
CGCCAGATCAGATGGGTGCCACTGATTCATCGAGACCTGGTTGAGGGCGTGTCTCTCT  
CGCCGTAACCAGCTCCTGCTGGATCTTGGTGTGGAGTTCGGCCTCGGCGCAATTGACGGA  
GCAGCCGATGCTGAGCTCGGTGATCTAAAGGTCACCGTGTCCAAGATGGCTAAGGGCTAC  
AAGGCGTTTGGCCCTGTGCTCTCCGATGCTGCAGCTGATGCCCTGCGTCGCTCACTGGT  
CCTACCGGTAAGCGCCCGGGATACATCGCAGAGCGGTCACCGGCACGTGGGAATTGGGC  
CAGGGCTGGGCTGACCACGTGGTCTGCTGAAGTTGTGATCGGCGCCCGCAAGGCGCATCC  
CTGCGCGGCGGCGACCTGGCGTCACTGTCTCCTGCAAGCCAGCGTCTGCATCAGATCTT  
GATTCGCTTATCGACGCAGCCGTCCAGGCCGTAGCCTCCCGCCGCGGCGTTGCGGTCTCC  
CTGCCTTCAGCAGGCGGCGCTGCCGGTGGCGTGGTTGATTCCGCAGCTCTTGGCGAGTTT

GCAGAGCAGGTCACCGGACACGATGGTGTGCTTGCTCAGGCAGCCCGCACCATCTTGACC  
 CAGTTGGGTCTTGATAAGCCAGCAACCGTTTCCGTGGAAGACACCGCAGAGGAAGACCTC  
 TACGAGTTGGTCTCCAAGGAACTCGGTTCTGATTGGCCACGTCAGGTTGCACCAAGCTTC  
 GATGAAGAAAAGGTTGTTCTGCTTGATGACCGTTGGGCTTCTGCGCGTGAG

>RXA00590-upstream

TACGCTGGCGCACACCGCATGCTGGACTCCGGACGAACCGGCCCAACACGTCAAAGCTG  
 TTTCCAATTCTCTATCACCGGCATCCTGATCACTGGCCTC

>RXA00590

ATGCGCGTGGTGTCTTCCCTCGCGGTCTCGGTGTTGTGCGCAGGTGGCGTCACCCTATCC  
 ACCACGGGCAACCCAGCCGCGGAAGCATTCCAGCACGCTGCAGGCGATATCGGACTACGC  
 ATCTTCGGCGCCGTGCTGTGGGCAGCGTCCATTTCTCAGTCATCGGCGCCAGCTACACC  
 TCTGCAACCTTCCCTGGTGGAAAACAAGCCAGAGAAGAAGCGTCTGCAAACTGGGTGACC  
 ATCATCTTCATCCTGATTTCTTGCTCCGTGTTTCATCATGCTCGGCACGGCACCAAGCAATC  
 CTCTTGGTCTTCGCCGGAGCATTCAACGGTTTGGTCTTCCCGTAGGCTTTACCCTGATG  
 ATCTACGTAGCGATCTTCCGCCAAAAA

>RXA00591-upstream

GCAACGCCACAGGCAAAATCCAAAAGAACATCCTGCGGAGACTTCACCATCCCCGTTTCAT  
 AAACCCCCCAACGTCACTTTGAAAACACTTGGAGAACGCA

>RXA00591

ATGACTACATCTTCCACAGCTTCGCCGATCGCTGAATTACAAAACCTCAGCCCGAAGCAA  
 AGAAAATCAGAATCCCGGCGCGCGATTATATCCAGCTACTTGGGCTCCACGATCGAGTTC  
 TATGACTTCCTGTTATATGCCGCGAGCCTCCGCGACGGTATTCCCCGCAGTGTTCTTTACC  
 AATCTCGATCCGCTGGCTGGAACCATTGCCGCCTACGGAACCTTCGCCGCAGGTTATTTA  
 GCTAGGCCACTTGGTGGAGCAATCTTCGGACACTTCGGTGACCGTCTTGAGCGCAAGAAG  
 ATGCTTGTGTTGTCCATGCTCATCATGGGTGTGGCATCCACATGCATCGGCCTTGTTCCA  
 AGCGCTGAAATGATCGGAAGCATGGGCGCGGTAATCCTGATCATGCTGCGCATCTGCCAA  
 GGCATCGCTGTGGTGGCGAATGGGGCGGAGCTGCCCTCATGGCGCTCGAGCACTCAGAT  
 TCCAAGAAGCGCGGATTTCGCCGCCTCCTTCACCAACGCTGGTGCACCAACCGGCGCTGCA  
 CTGGGAACCTTCGCGCTCGGTACCGCATCTGCTGTTCTCACCCAGGAGCAATTCCTTTCA  
 TGGGGTTGGCGCATCCCATTCCTGCTCTCTTTCTGTTCTGCTGATTGTGCGCTTGTTATC  
 CGCGCGAAAGTTAGCGAATCACCCTGTTTCGCGAGCTGCAGCGGCCGCCGAAAAAGCCAAG  
 CCAACCGAACGTAAAGTCCCCCTCTTGCAAGTTCTTCGCCGACCAAGGCACTGATCTTG  
 ACCATGCTTGGCGGCGCATCAGGATTCGGACTTCAAGTTCTCTTGTTCCACCTTCTCCATC  
 AGCTACGCAACACAATCCGGCATCGAAAGATCCAGCGTCTCTACGCCTTCGCAGTCGCC  
 TCAGTGTTCTCTGTCTTCTTTGTGATCCTCTTCGGTTCGCGTATCCGACCTCTTCGGACGC  
 CGACCCGTCATGATCATCGCGCTCGTACTGTTCTGTTGGCCTACCTGCCGGCATCTTCCGG  
 ATGCTCACCTCAGACAACTGGTTCATCCTGCTCTCGGCATTACCATCGCGCTCGCACTC  
 CACGCCATGCTTTACGGCCCACTAGCAGCGTTTATCTCCGAACAATTCGGAACCTCCGCG  
 CGCTACACAGGCGCATCCCTGGGTACCAGTTGGCCACGCTCATCGGTGCAGGATTCACC  
 CCAACCATCCTGGCTAGCCTCTACGCGGGACAGGCGGCGGAACCTCTGTCACCCAGTC  
 ATCGTCTTCTCGCAACGATGTCCCTAGTGTCCATCATCGCCATCGCAATCACCAGAGAA  
 TCAAAAGACCACGATCTTTCTACTTACGAACAC

>RXA00591-downstream

TAAGGGGACGATAGGGTCAATTT

>RXA00596-upstream

CCGCCACCGACGGCCTCTTGAACACCGATGCATACCAACAGGCTGTGCTCGGTGAAAATG  
 CCATCGGAGTGCCAAGCCCTAGCTACCAGGGAGGAACTA

>RXA00596

ATGCTTAACGCCCTGAAATTCATCCCATGGCTGATCGGCCAGATTTTCTCTCTGGCTTC  
 AGCGTGATCACCGCTGCGGTAAAAAAGGACACCGGCTTCAACCCCGTTGTTATCCGCTAC  
 CCACTTCGAGTGACCACGGACTTCCAGATCGCAGCCCTGTCAACGTGCATCACCGCGACT  
 CCTTCCACCCGTGTCCCTTGGCCTACGCGAACCCCGCAAGCCCGGCGACCCACCATTTTG  
 CTGATCCAAGCAGTGTGTTGGTTCGATCCAGTAGAAGTTTTTGAATCCATCGCCGATATG  
 GAACAACGCCTCGTCCCTTCGGTCGCTTCAATTGACCACGGCGTCCCAGGCCAAGGCCCT

TACAAGGAGATCCGCCCCAGCGATGCTGAGTGGCCAAGTCGCGAGATCGCTGACACCGCC  
CAAAACACCGTCAGCCAAGACAAGAGGGAGTTT

>RXA00596-downstream  
TAAACAACATGACTGCTTTTGG

>RXA00607-upstream  
CACTGCCAGCAACGCCAACGGTTGAACCCGAACCAGAAGGCGATGAAGACTGGCCCGAAC  
CCATCAACCCCGCAGGCGATAACAAAGAGGAGGCAAACCG

>RXA00607  
ATGATTCTCGCACTGACAGTCGCGATACTTTTCGGTGGAGGTGTCTACCTCATTTCAGCAA  
CGCGGAATGGTGCATCGTCTTCGGCATGTCACTGATCGGCCACGCAGCGAACCTGACC  
ATCCTGTACGCCGGTGTGCCACGTGGCGCGGCGAAGCCTTCCCCGACAGGACCCCGCTT  
ACCGACGCCGCCGATCCACTCCCCAGGCCTTCGTCTCACC GCCATCGTCATCGCGATG  
GCCACCACAACCATCATGTTGGCCTTGGCAGCACTGGGACGCAGCGACGACACCCGGTCC  
ATCGAACCAGATGACGATCAATCGCCTTTGACTACTAGCGCTCGTTTCAGTCACCAACCCA  
ACAGATCAGGAGGATAAAGCT

>RXA00607-downstream  
TAAATGGCCATGGATGTTCTCCT

>RXA00623-upstream  
TTTAAGCTTCGTGCGCAACGATCACACCACGTTAAATTTGACCATCAATGACGGTGGCC  
GTTTTTTGGCGAATCCCCAAAAGGTGGAAGAGGAAGTTC

>RXA00623  
ATGGATTCAAACACAGAATCTTCAAGTGTTGAGGTCAAAAACGAACACATTAAAGTTCAA  
AAGCCGCCGAAGAAGGACCGCACTCACTGGCTCTACATTGCGGTCATTATCGCATTGATT  
GGCGGTATTACCCTAGGCCTGATTTACCCGGAGTTGGGCAAAGAATTCAAGATTTTGGGC  
ACCATGTTTGTGTCCTTGATCAAGATGATTATCGCTCCAGTTATTTTCTGCACCATCGTC  
ATCGGAATCGGTTCAAGTCAAGGCAGCGGCAACAGTCGGACGCGCTGGTGGCATCGCCCTT  
GCGTACTTCATCACGATGTCCACATTCGCACTCGCAGTTGGCCTGCTAGTCGGTAACTTC  
ATCCAGCCAGGTAGCGGACTGAACATCTCAGTTGATGAAGAATCTTCATTTCGCATCCACA  
GAGAGCAGCCCTGAAGGACTCTTGGGATTCACTCACTCGATCATCCCTGAAACGTTCTTC  
TCTGCATTTACTGATGGTTTCGGTGTGTCAGGTACTGTTTCATCGCCATCCTCGTGGGCTTT  
GCAGCTCAGTCGATGGGTGAAAAGGGACAGCCCATCCTTGATTTTCGTATCCCATCTGCAG  
AAGCTCATCTTCAAGATTTTGAAGTGGATTCTGTGGCTCGCCCCAGTCGGTGCATTTCGGT  
GCAATGGCCGGCGTCGTGGCGAAACAGGCCTTGATGCCGTTGTTTCAGCTCGGTATTTTG  
ATCCTCGCCTTTTACGTACCTGCGTGATCTTCATCTTTGGCGTGCTGGGCGCCGTACTG  
AAGGTGTTACCGGCGTGAATATCTTCAAGCTGGTCAAGTACCTTGCCAAGGAATTCCTG  
CTGATCTTTGCTACCTCATCCTCTGAATCTGCCTTGCCAAACCTCATGCGCAAGATGGAA  
CACATCGGTGTGGCTAAACCAACCGTCGGAATCGTGGTCCCAACCGGCTATTCCTTCAAC  
TTGGACGGCACCGCAATTTACCTCACCATGGCATCTATCTTCATTGCCGACGCGATGAAT  
ATGCCGATGAGCCTCGGCGAGCAGGTTCGGTCTGCTTGTCTTCATGATCATCGCATCCAAG  
GGCGCTGCTGGTGTCTCGGGTGCCGGTATTGCAACGTTGGCTGCCGGATTGTCTTCACAC  
CGCCCAGAACTTCTGCACGGCGTTGACGTGATTGTGGGCATCGATAAATTCATGTCTGAA  
GCCCCGCGCACTAACCAACTTCGCCGGAACCTCCGTGGCAACACTGCTGGTCCGGCAAGTGG  
ACTGGCACCGTGGACATGAACCAAGTCCATGACGTTTTGAATGGAAAATCTCCATTTGTG  
GAGTTAGAAGAAGACCAC

>RXA00623-downstream  
TAGTTTTCAACAGGACGACAACG

>RXA00660  
CCAGGCCATAACCCCGGAACACTTATCGTTCCTGCTGAAGGACGGCGCGTTTCGCACATGAG  
CCAGGATTCATGCTCACTGGCGATTTTCGTTTTTCGCGGGTGATCTTGGCCGACCAGATTTG  
CTCGATGAAGCAGCTGGGGGAGTGGACACTCGTTTTGAGGGGGCTCGCCAAATGTTCAAG  
AGCTTGAAGGAAAAATTCCTGACATTGCCTGATCACATCCAGATCTTCCCTGGTCATGGT  
TCCGGTTCCGCGTGTGGCAAAGCCTTGGGTTCGGTTCCTTCAACAACACTTGGATATGAA  
CGTCAATTTGCGTGGTGGGGAAAGTATCTGGAGGCAGATGATGAACAAGGATTCATTGAT



GAGCTTCTGGAAGGCCAACCTGATGCACCTGCATACTTCGGCAGGATGAAGAGGCCAAAAT  
 AGGCAAGGGCCCGCAATTATGGGCGCTCGCGAGCTGTTGCCACAGCTGGAAGCTTCTGAT  
 CTGCACGACGTCATTGTTGTTGATACCCGCTCAGCCGATGAAGTTCACCAGGGCACTGTA  
 GCTGGTGCAGTGAATATTCCTGCGGGCAATTCGATGGCGAAATTTGGCTCGTGGACCGTT  
 GATCCCGAGAAGGATTCCCGAGCTTTGGTTCTGCTCGCGGCAAGCCAAATTGGTGCCATG  
 GAGATGTGGGACCACATGGTTTCGCGTGGGAATCGATAATGTTGCTGGTTTTATCACCAAC  
 TTTGATGGGGTGGACCTAGTTGCACCGCAAACCTGTGTCCCCAGATCAGCTGGATGAATTG  
 GAATACGATCTACTTCTTGATGTCCGCAACCGCAGTGAAGTCGAAGAAGGCTACATCCCA  
 GGAGCACTCCATATTAATGGTGCATCCGTGCTGTGGAATCTGGAGAACTGCCACGTGAC  
 GGAAAGATCGTGAGCTACTGCAAGAGTGGAACACGCAGCTCAATCGCCGCAAGCACCTG  
 CGTAATGCTGGTTTTGATGTGGTGGAACCTCAAGGATCCTATGACAACCTGGGTCCGGCAC  
 AAC

>RXA00681-upstream

AAGGGCAAGGTTGTCATTGTTGATCCAGATGCGCCACGCATCGAAGGACCCGGCGCGCAC  
 AGCCATGCGCACTCAGTAGCAGCACATGGGGTGGATACAC

>RXA00681

ATGCCTAGTCCACGCACTGTTCTTATCACTGGTGCCGCTGGCGGTTTGGGTCCGGCATTC  
 GCTGAAGGTTTCGCAGCCCAAGGAGACCGTATCGCGGTGGCGGATATCAATCTGGATGGG  
 GCGCAAGAGACCGTTGACAAGCTGAAAGCATTGGGCGCAGATGCCGCAGCCTTTGAAGTT  
 GATGTCACGTCCTTTGGAGTCCACCGAGGCCCTAGCCGCGGTGCCGCTGAGTTTGGCGGT  
 GGCCGAATTGATGTCCTTATTAATAACGCAGCGATATATGCGACAGTGAATCGTTCACCG  
 TTTGAGGATATTGACCCTGCGGAGTGGGATTTGGTCATGGGAGTCAATCTCAAAGGCCCG  
 TGGTTGGTGACGCGTTCTGTGAGTCCGTTTTTGTCCGATAATGCCCGTGTGGTCAATCTT  
 TCCAGCGCGACTGTGTTTTTCAGGATCTGCACACTGGGCGCACTACGTGGCATCCAAAGGT  
 GGGGTCATTGCTTTAACCAGGGTGCTTGCTAAAGAGCTGGGTGGTTCGTGGGATCACGGTC  
 AATGCGGTTGCGCCTGGGTTTACGCTGACTGAAGCCAGCTTGGGACTCATGGATAGCGCG  
 GAAACGTACGGTGTGATCGCGGATCCATCAAGCGCGCAAGCCAACCGAAAGACATCGTC  
 GGCACCACCATGTTTCTTGATCCCCAGAAGCCGAATACATCACTGGGCAAACACTCATC  
 GTTGATGGTGGCCGACAGTTCATC

>RXA00681-downstream

TAAGTACTAAAAGTTCTAAGGAG

>RXA00690-upstream

ATGGATCATTGGACTCACACTGGCTGTCATTTCCCTTGGTTTCAGCGTCTGCTGTGGCGGC  
 GTGGGCGATTTCGTCTTCAGAGGTCCAGGGTTAAAGCTTC

>RXA00690

GTGAAATGGATTGAGCGATATGTGCTGTCCCGGCGGATGGTTCATCCCTGGGCGTGGTGG  
 GTGTGGGCGTTGGGTATTGCTGGTTGTGCCAGCATGACCAACAATCCTTATATTTTGGCG  
 CTCACTTTTGGCACGTTGTGTTTTGTGGTGTTTAACCGTCGTGGGTTCATCGCCGTGGTCG  
 CGTGCTTTCCCGATCTATTTGATGATCGCGGGTTGGCTCGTGGTGTACCGGTTGGTCATG  
 CACATTGTGGTGGGAGCAAAAATTGGCACCATTGAACTGTTTCGGATCCCGCCGGTGCAG  
 TTGCCGGAATGGGCTGCGGGTATCCACGTGTTTGGCACGGTGTATCTCGAGGGTCTGATC  
 ATCGCGACGACGCAAGGCTTAACGCTTGGAACGATGATCGTGGCGGTGGGTGCTGCGAAC  
 TCTTTGGCGGATCCCAAGAAGCTGCTCAAATCGTTGCCTGGCGCATTTGGGCGAACTGGGA  
 ACTGCGGTGGTCATCGGTATTTCCATTGCACCTCAGATGGCTGAGTCGGCGTTCCGCATT  
 AATCGTGACGAACCTTGCGTGGTGTGATGATGCCAAAGGTGTTTCGTGGTTTCGCGCGGATT  
 TTGATGCCGGTTTTCCAGGACACTTTGGATAGGTCTTTGGCCCTGGCTAATTCCATGGAT  
 GCCCGTGGTTATGGCAGGCAGGCTCATGTATCCAAATTCCAACAGCGTGTGACCTCTATT  
 TTTGGTGCATTCCGAATACTCGGCGTGACCGTTGGTCTGTTTGTGGTCTTAGATGCATCA  
 TCACCGATGTTTCGTTGCCGTTCCGGTGTTTATTACCGGCGTGGGCTTCTTGATCATTTTCG  
 TTGGTTCGTTGCTTCACATAGAAAACATCCACCACCTTTTGATCAGTTGCCTTGGGGTGCT  
 GCGGAATGGCTTGTGTGCATCACAGGTGTGATTCCGCTGCTCATGGCTGCGCTGACACGA  
 TACCTTGATCCAGGTTCCATGATCACCACTGGGTTCCTTTGCATATGCCAGACACCGTT  
 CCGTTGCTCGTTGTGGCAGGACTTGTGTGGCGACGATGCCAGGATTCTTGACGCCCCGC  
 TTGCCGAAGAACAAGTGAGGGTCAAGCGTCGAAAAGCAATAAATAGCCCAGAAAGGGCC  
 GAAGTT

>RXA00690-downstream  
TAATGAGTGCTCCTTTTAGCGCG

>RXA00733-upstream  
ACGGCGAGGTTGTCGGTATTGGAACGCACACGAATTTGCTGAACACGTGCGGTACCTACC  
GTGAAATTGTTGAATCCCAAGAGACTGCGCAGGCGCAATC

>RXA00733  
ATGAGTAATACTGCAGGCCCCCGCGGGCGTTCCCATCAGGCAGACGCCGCGCCGAATCAA  
AAGGCACAGAATTTTCGGACCATCTGCCAAAAGGCTTTTCGGAATTCTAGGCCATGACCGT  
AACACCTTAATTTTTGTTATCTTCCTAGCCGTCCTGAGCGTTGGACTTACCGTCTTGGGC  
CCATGGTTGCTGGGTAAAGCCACCAACGTGGTGTGTTGAAGGATTCCATATCTAAGCGCATG  
CCGGCTGGTGCGTCAAAGGAAGATATCATCGCGCAGTTGCAGGCTGCAGGTAAACATAAT  
CAGGCTTCCATGATGGAAGACATGAACCTTGTTCAGGCTCAGGCATTGATTTTGAAAAA  
TTAGCCATGATCCTCGGACTGGTGATCGGTGCTTATCTCATTCTAGC

>RXA00735  
GGTCCCACCGGTGCGGGCAAGACCACATTGGTGAATCTGATCATGCGTTTCTACGACATC  
AACAGCGGTTCCATCACTCTTGGTGAAACAGCACAAAGACGCCGTGGATATCCGCACCATG  
GCTAGAGAAGATCTGCGATCACGAACCGGCATGGTGTGTCAGGATACGTGGCTGTTTGCC  
GGAACCATCAGGGATAACATTCTTTACGGTAGACCTGAAGCAACTGAGGAAGAAATGCTT  
GCTGCGTCCAAGGCCGCTACGTGGATCGTTTTGTCCGTTCCCTGCCAGAAGGCTACGAC  
ACCGTACTTGATGATGAAGCCATGAACCTATCGGTGGGTGAACGCCAGCTGATCACCATC  
GCGCGTGCAATTCTTGGCTAATCCCCGACTGCTGATTCTGGATGAAGCCACCTCATCGGTG  
GATACGCGTACCGAATTGTTGATTACGCGCGCCATGTCCAAGCTGCGCCAAGACCGCACC  
GCCTTCGTCATCGCGCACCGGTTGTCCACGATTCGTGATGCCAACCTGATTTTGATGATG  
AAAGACGGCGAGATCGTGGAGCAGGGCAATCACCGTGAGTTGATGGCCCTGGAGGGCGCA  
TATTGGGAGTTGTATAACTCCCAATTCAACGCCCCCGCGAAAGAAGAATTACAGGCTGAC  
GGAGATCAC

>RXA00735-downstream  
TGATGATTTCTTCTTAGGCTTTC

>RXA00796-upstream  
CTGGAATCCCAAAGCGCTTGCAATGACGCGGAAAGTTAACATAGGCTAGGTACGTCAAGTT  
GTTGATACATCAACTTAATTAACTTTTAGAGGAGTACACC

>RXA00796  
ATGAGCAAGATCGCCATCATCACCGGTTCCACCCGTCCAGGCCGCGTCAACATTGACGTA  
GCCAACTGGGTTCTCGAGCGCGCACAAAGAGCGCAACGATGCACAGTACGAGCTCGTTGAT  
ATCGCCGATTTCAACTTCCCCGTCCTCGACGAAGCAATGCCAGCCGGCTACGGCCAGTAT  
GCAAACGAGCACACCAAG

>RXA00801-upstream  
GGATAAGTTTGTCTTCTGAGCGTATTGGTCTTGATGATGTTGAAGAGGCTTTCAACACCAT  
GAAGGCTGGCGACGTGCTGCGTTCTGTGGTGGAGATCTAA

>RXA00801  
ATGGCTCACGACGGATTGCGCGTAGAAAACATTGTCACCTCAGGCATCTTTGCCCTTGAT  
GGTGGCGAATGGGAAGTCGACAACAACATCTGGGTTGTGGGAAATGATGATGAGGTTTTC  
ATCATCGATGCGGCACACACTGCAGCACCCATCATCGAGGCTGTCGGTGGACGTGCTGTG  
AAGGGCATTTTGTGCACCCACGCACACAATGACCACATCACTGTCGCACCAGAGCTATCC  
AAGGAATTTGATGCACCAATCTTCGTGCACCCAGGTGACCAAATGCTGTGGGAGGAAACC  
CACGGAAACCTGACCCACGAGGATTTGGCAGATCAGCAGAAGTTCCAAATCGCTGGAACCT  
GAACTGATCGTGCTTAATACCCCTGGACACTCACCTGGATCCAGCTGCTTCTACCTCCCT  
GAAGCAAACGAGCTCTTCTCTGGAGACACTTTGTTCCAGGGTGGGCGGGGAGCAACTGGC  
CGTAAGTACAGCTCCTTTGACACCATCATTTGAGTCCCTCAAGACCTCAATTTTGATCTA  
CCAGCGGAAACCACCGTGCGCACTGGCCATGGTGATCACACCAGTGTGGGGGCTGAGGCT  
CCACACTTGAGGAATGGATTAAACGCGGGCAC

>RXA00801-downstream

TAAGCCCCGAACGATTAGTAGGC

>RXA00802-upstream

GCCATGGTGATCACACCAGTGTGGGGGCTGAGGCTCCACACTTGGAGGAATGGATTAAAC  
GCGGGCACTAAGCCCCGAACGATTAGTAGGCTTGGGCACC

>RXA00802

ATGGATCTTAAACTTGGTGGCCAAGTCATACTTGTGTTGGCGGTGCAGGAACTATTGGT  
TCTGAAGTTGTAAACTCTTAACTGAAGAAGGCGCAACCGCGGTAGCGGCGTCGAGAAGC  
ACGCCCTTATCTATTGACGCTTCGGATGAAGCGTCCGTCCGTGCGGGCATTGATCAGGTG  
ATCGCAGAACATGGTCGCCTGGATGGGCTGGTTGTTTCTTCTGCACCCGCTGCGCAAACG  
CTCAGCGCGGAGACAGCAGATGATCCGGACACTGTGTTGGCTGCTATTGAAGGCAAAGCC  
ATCACGTTTATGAAGGCTGCAACCGTGGCGCTCGAGAAGATGCGTGAGGCTGGACATGGG  
CGCATCGTTGCACTTCCGGCATGAACTCATACAAAACATTGAGTACTACTGCGTCGGCG  
CGAAATGCTGCGCTGAATGTCGTGGTGAAAAATTTGGCGGATCGTCACGCGGGCACCGGA  
ATTACAGTAAATGCGATTAGCCCGGGATTCTGTGGTAGCTGAGCCAGACGCTGAGGTAAAC  
CGCGCAAATGGTGACACCACGTGGAGGAGGTCGCGGAGGCGATCGCGTTTTTGTGTCGC  
CGCGCACCGCATCAATTTCTGGAGAGATTATTTCTGGTGGGACATAAGGCGAAGGGCATCA  
TCCTTCCTTAGCTCGCGTGAGCTTCCCAAGCGTAAGCACCCCGTGTGAGGGCA

>RXA00802-downstream

TAACGGCCGTTCTGTAAAGATT

>RXA00819-upstream

TCTTCCGAACGGCCTGC

>RXA00819

ATGGTTGGTGGCTCCCCGGAGCAGGCGCAGCGATTGGATGCGCAGATCAAATCTGGTGAG  
GTCAAGGGCGTTTTTGCCTGACGGAACCTGATCATGGCTCTGATATCGCAGGTGGTCTG  
GCAACCACGGCCACTAAGGACGCAGACACCGGCGAGTGGATTATCAATGGTGAAAAACGG  
TGGATCGGTGGTGCTTCCACTGCTGATTTGATCGCTACCTTCGCCAGGGATACAGCCGAT  
AACCAGGTGAAATGCTTCCTCGTGGCACCTCAGGCAGAGGGCGTGTCCATGGAGATTATT  
GATCGCAAAGCCTCACTGCGCATCATGCAAAATGCACACATTACCTATAACAATGTCCGG  
GTGTCTGGGGATGCGCGGCTGCACAACATCAATTCTTTCAAGGATGTTTCGGAATGCCTG  
CGCCGTATGCGTTCCGATGTGGCGTGGATGGCGGTGCGTGCAGGCAGGTGCCTATGAA  
GCAGCCGTGAAGTATGTGCGCAGCAGGGAACAGTTTGGCCGTCCGATCGCGGGGTTCAG  
TTGATTCAGGAAAAGCTCGCGCTCATGCTGGGCAATCTCACGGCGTCGCTGGGCATGATG  
GTCAAACCTACCGATCAGCAGCAGGCGGGAATTTTCAAAGAGGAAAACCTCCGCGCTGGCG  
AAAATGTTTACCTCGCTCAAACCTTCGGGAGACCGCTAGTTGGGCGCGGGAAATCTGCGGA  
GGCAACGGCATCATTTTGGACAACGATGTTGCCCGGTTCCATGCCGATGCAGAAGCCGTC  
TATTCATATGAAGGCACCCACGAAATCAATGCACTCATCGTTGGNCGNNCCATTCTGGGN  
CNTCTNTTCTTTTTATATTATNACNCTTTTGAGGAGGATCTTCATGACTACTTCCACCAC  
CCCAAACCATCGTTTCTTTCGAAGACGCACCAACCCTCACCGGCCAGGACCTGGGCTTTT  
CGCAGTGGCGCACTGTCACCCAGGAGATGG

>RXA00819-downstream

TGAACACCTTCGCGGACGCAACT

>RXA00821-upstream

TTAAAAGCTTGCTTCTCGACGCAAAAACCCATCCGGCGCATCCCTTCAATGTTAGGGGTG  
CGCTGCTATTTTTCTCCCCAGTTCTACGAAATGACTTATT

>RXA00821

GTGACTAAGCTTGAGCGCATGGAGCATCCTGCTTACAGCCAATTGCGGCCGGTTACCCCG  
TCCGCATCTGTTGTTTTGTGCCCTAATCCCGGTTACAGCTCGCTGGAAGGCACTAATTCT  
TGGGTTATCCGGGCACCAGAAGACCCCGGAGCATTGTCATCGATCCAGGTCCTGAAGAT  
GAGGGCCACCTTAACGTCTTGCAATTCCAAGGCTGAGGAGGTGGGTTTGATTCTTCTGACC  
CACCGTCACTATGATCATGCTGACGGCGCACAGCGTTTCCGTGAGCTGACCAATGCACCT  
GTGCGTGCGATGGACCCTTCGTACTGTGCTGGTGCGGAGGAGATTCATGATGGTGAGATC  
ATCACGATCGACGGTGTACCCACAGATTGAGGTGGTGCCACACCTGGTCATACCCGT  
GATTCTGTGTCTTATTTTCATCTGGAGTGGAGTCCCTCATGAGTCCACTTTGGAGGGCATC

GTTTCTGGCGACACCATTTGCGGGTCGTCACACCACGATGATTTTCAGAGACCGACGGCGAT  
TTGGGTGAGTACCTGAATTCTTTGGCCATTTTGGAGGAGCGCGGCAAGGATATTCCGCTG  
CTTCCAGGACATGGTCCAGATGGACAGGACGTGTCCTCCTTCGCGCGTAAGTACATTGAG  
CGTCGTGAGCTGCGTCTGAACCAGATCCGTGAGGTATGGGAGACCCGTGGCCGTGACGTG  
TCCATGAAGGATCTCATCGACGCCATCTACGATGATGTTGATCCAGTTCTGCGTGGTGCA  
GCCGAGCAGTCCACTCATGTGGCTATTCTGTTACCTGCAGGCTCAGGAAGCTTCCGCCTCA  
AAC

>RXA00821-downstream  
TAAACACTTTTAACTAAACAACA

>RXA00827-upstream  
TGCGTGAATTAAACAGACAACGGAATCAGCATTGTGTCAGTAACCCATGATCCTGATTTC  
TCGCAGCGCTGGGCGATCACCACATTGAGGTGAGCGCGAA

>RXA00827  
GTGAACCTGCTGATCAAAATTAATCCCGTCACCCGCATCATCGCGTTGATGGTACTGACC  
ACGCCGTTGCTGCTGAGTTTGGATGTGATGTCGGCAGCGATCGCGCTGGTGGCAACCATT  
ATTCTGGCACCATTGCGCGCGTGACCTGGAAGATGCTGCTGAAACGTGGCTGGATGCTG  
TTCCTCATGGCACCGGTGGCTGCATTATCCATGGCGCTTTATGGCAGGCCGGATGGAAAA  
GAGTACTTTAGCTTCCTGCTCATTACGTCCTGATAATTCACTGGCTTTGGCTGCTGCC  
ATTGGGCTGCGTGTCTGGCGATTGGTCTGCCCGTTGTGGTGTGCTGATTGCTCGCATTGAT  
CCCACCGACCTGGGCGATGGTTTGGCGCAGCTGCTCAAACCTGCCTGAAAGGTTTGTCTATC  
GGTGTGTTGGCAGGAAGCCGACTGATGACGCTTTTTCGGGAAGATTGGTACTCCATGTCC  
AGGGCAAGGCGTGCCCGCGGAATTGCTGATCAGGGCAAGATCAAGCACTTTTTCACCATG  
ACTTTTGGTTTGTGGTGTCTCGCTTCGCCGTGGATCCAAGCTTGCAACGGCGATGGAA  
GCACGCGGTTTGGTTCGCACGACTGGCCGCACCTGGGCAAGGGAATCCACCGTCGGCGCG  
CGCGATCTGGTGTCTCTTGGTGTGTGCTGCCATTTCCGCGATCGCTCTAACCGTGTCC  
ATTCAGACTGGTTTCTTTAAGTTCTTGGGCACA

>RXA00827-downstream  
TGATCACAGTTTAAATTGATGGA

>RXA00842-upstream  
CCTTGTCGCGGAGGTAAGCGAGGGTATTTCTGGATGTGGAACAACGCGGATTATGGAAAA  
TCGTGACTTTCATAACGTTGAGCCTACTAAGGTTTGTTC

>RXA00842  
ATGATTATTCAAATCCTAAGAGTGGCATTTCGCTTCGTCGGCATCATTGTTGGCGCCGGT  
TTCGCATCAGGGCAAGAGGTCATGCAATATTTTGTGGCCTTCGGCATAGACGGAATTTGG  
GGAGTCATTGTTTCTGCAGTGATCATGTCGGTGATGGCGTTGATCATTTTGCAGCTCGGA  
AGCTATTTCAATGCAGGTGAACACGGTGAAGTGTTCCGCCGAGTAAGTCACCCCGTTTTC  
TCCAAAATTTTGGACATCGGCGTTGTGGTGACGTTGTTCTCCACCGGTTTCGTCATGTTT  
GCAGGCGCGGGATCAAATCTGAATCAGCAGTGGGGGCTTCCGCTCTGGATCGGTTCTGTG  
ATCATGGTTCTTCTGGTGCTGGCTGCGGGCATGTTGGACGTGGATAAAGTAACCACAGTC  
ATTGGTGCAATTACTCCGTTTCATCATCATTTTTCATCACTGCCGCCTCGATCTACACGCTG  
GTAGGTAATTTTCAGCTCAGTGGAGCAGCTTGATTCTGCTGCTTTAGAAGTCGGCACGACG  
TTGCCTCACTGGGCTGTTGCAGCGGTGAACATATGTGGGATTCAACCTGATGGTTGCGGTG  
TCCATGGCTGTGGTCATTGGTGGATCAATGTTTAAACCCGCGGGTTCGAGGTCGGGGCGGT  
TTGCTGGGCGGATTGATCCTGGGATTCTTGATCATCATCAGTGCGCTAACACTGTTCCGC  
ACCGTGGAAGAAGTTGGCCAAGATGATATGCCTATGCTGACGATCATCAACAATTTGAAC  
CCGCTGGCTGGCCAAGTAATGGCAGTGGTTATCTACGGAATGATCTTCAACACGGCACTG  
GGTATGTTCTACGCATTGGGCCGTCGTCCTCACTGCGAAAAACCCACAGCGATTCCGTCCG  
GTTTATGTGGTACAGTGCTGATTGGTTTTGTGTTGAGCTTTGTGGGATTCAAGAACTTG  
GTGGGCTATGTGTACCCAGTCTTGGGATACATTGGCCTGCTGCTGATTGCAGTGATGATG  
GTGGCGTGGGTGAGGGGACGCGTACGCATCTACAAGGAATCCGAACGCCGCATGCGGATC  
GCAGACTTGTTGCAGATCGGCCATGACGGAGCGTTGAGTGGAGCAGAGCTGGCGGTGCTC  
AACCAGGAAATCCAAGATTCAAACCTTGATGAGGAACAAATTAAAGCAGCGGTTAGGAAG

>RXA00842-downstream  
TAGTACTCTGCAGGGACGAGCT



>RXA00847-upstream

TCTGGCCCGCTGTGTCTCTGGACGCAGCGGGCCAGTAGTATTTTGGGGGTGAGAATAAG  
GTTTGGAATTCTAAGTGTGTGCGCTGCACGGTTTCGTTG

>RXA00847

GTGGCATGTCAGGCTAATCCGGGTCCTGCGCCCGTTGAGGAGCCAACTACAGCCACTGCG  
ACGACCACGGCAACTGAGACGACCACCGTAGAGACTGAAGCCCCCAAACAAGATCGGGAA  
ACCATCAGTATTGGTATCGATCCGATCCGCAACGGTTTCAATCCACATTTGTTGTCTGAT  
GATTCTCCACTGGTGCGCGATACTGCATCGTTGGTGTGCGGAGTGCTTTTGAGGGCAAT  
CAGCTGAACACTGACTTGTGTTGACAATGTTGAGCAGGTGGATGAAACCACGGTGAGGTAC  
ACGATTGCTCAGGAAGCGCAGTGGAGTGATGGCACTCCGATTACTGGGTCTGATTTTGAG  
TACTTGCGCAGGTCCATTGTGGCGGGGACAGGAACGCTGAACGATTCTGCATATTCGGCG  
ATTTTCAGAGATTAGGACCTCAGGCGGTGGA AAAACTGTCGACGTTATTTTGAACATCCT  
GTCGCTGATTGGCATTGCTGTTTAACAATTTGTTGCGGAGTCATTTGATCACTGGCAAT  
TCCACATTCCAGACAGCGTTTTATGATTCCATCCCGGCCTCTGCGGGGCGCTACATGGTG  
CGTTCCATTGATCGTCAGCGCGGCGTGATTACGTTGTGCGCAATGATCGTTTCTGGGGT  
GCAATCCGGCACACGTGGAAGTACTCCAATTCAACACCGTTGCCTCTGCATCCCGGGCG  
GGGGAGTACCTGCGCACCGGGCAGAGTTCGTTTATGAATCTGTCACCGCAGGAAACCCTG  
GTGGACACGTTGAATTTGGTGCCGGACACGGAAGTGCGGGTGTCTGACACGACGCGCACG  
CTGGAGCTGGTATTCAACGCCGAAGCGCTGGCACC GGCGCAGCGCGCCTACCTGACATCG  
CTTATCGACGTCCCCCTCACCGCCAAGTTAGCTGGCGGTGCGCAGTGCAAACCTGGGTGTG  
CCCCAAACGGTGGAGGCGAGCGTCGATAAGCAAGAAATTCCTGCGTTGCGCCTGGCGGCG  
GACCCCGCCGACGATGCTGGTTTGGCAGCTGCGCGGGGCATCGTCGATATGCTGGCTGCG  
GATGGAATCAAGGCTCAGGTCGTGACAACCGATTTGAATTCGGCGATTGCGGGTAATTTT  
GATGCGATCGTGGCGTGGACCAGAACTGCCACGGATTCGATTGCGTTGGCGGACCGAGTG  
GGTTGTGGCGTGAAC TTGGCAAAGTGGTGCGCTGAGGGAACCACGGAATATATCAACGGT  
GTTTTGGCGGGTGAGATTGATTTTCGATCCTGCGTGGGAGCAGCAGTTTAACACCGAGAAT  
CACTTGCGGGTTCCGATCCTGCGGGAGACTCGGGTAGAAGCGAAAAATAACGGTATCCTC  
GGGGCTGCGGATGGCTGGCCTGGGGGAATTTCAAGTGCTGCAAGTTGGAGGAAAAACGAT  
GTTGAAGAA

>RXA00847-downstream

TGATCTGTCTGGTGCTCGAGTTG

>RXA00851-upstream

TTGAGCGGGTCATTTGCATCAATGATCATAAAATCGCTGCTGATGGCCCTCCGCAAAAGT  
CCATTGACCTGTACGTATCGCTTATGGCGGAACCTGCGAA

>RXA00851

ATGAACAGTATTCCTTTAGGTTTTTACGTCGATAAGCAATCTGTTGTTTCATTCTTTTCCT  
GCTTTGTGGAAATTCCCACCTTCTGCTGTTTTTTCATCATCGGCGGCTCCATCGCGGCTTCT  
ACCCCGGTTTCATGGGTTGATTTTGGTGGGGATTGCAGTGGTGTGTTTACGTGCTGGCGAAG  
ATTCCGCTGAAGGTGCGGTGGGAGCAGTTGTGGCCAGTGCTGCCGATTTTGATCATGCTC  
GGTGCGTTTTCAGTGGTGGCAGCGCGGCTTTGATTTTCGCGGCAACCACAGTGCTCACGCTG  
TTTTCCGCGGTGATGGCCGCCATGTTGTTGACGTTGACCACGCGGTTGGAAGCGCTCATG  
AATGCAGTTGAGCGGATGTTGCAGCCTTTTGCACGTTTTGGCCTGCCAGTAGAGACGATC  
ACCTTGCTATTTCTCTCACGATTCGGCTCATTCCGCTGCAATTAGCCACGGTGAAGGAA  
GTCCTCGATGCCCGTAAAGCTCGTGGTGCCGGTTTTTCTATCGCCGCGTTTGGCACGCCT  
GTGATCATCAGATCAATAAAGAGGGCCCGCAATATCGGCGATGCTCTTCTCGCACGTGGT  
GCCGGCGAT

>RXA00851-downstream

TAATTTCTTTCAACACATAGCAA

>RXA00852-upstream

AGATCACCGTCATGGTCATAATCGCCGCTGGAGTTCATGCAGCATTCCTTGACATCCGTA  
AGAAATAGTTCCAACCCACTTTTCTCAGAATTGCAGTTC

>RXA00852

ATGCCCCGAGATCATTTTTGACAACACTGAAGTACGCTACGATGACTCGCTCATTTTAGAG  
 CCCCTATCGTTAAAACTGACAGAACACGCATTGGCATCATCGGGGCTAACGGCGGTGGA  
 AAATCCACGCTCATCAGAATGATCAATGGTCTCGGCGAACCAACCACAGGGCGTGTCTA  
 GTTGATGGCCTTGACGTCTCGCATTCGGGACGGGAAGTTCGCAAGAAGGTTGGATTTGTC  
 TTCTCTGACGCTGAAAACCAGATCGTGATGCCAACTGTGCGTGAGGATATTGCCTTCTCG  
 CTTGCGCCGGCACAAAATGCCACGCGCTGAAAAGGCGCAACGTGTCGACGAGATGATGGCG  
 CGATTCAACTTGAGCGAGCATGCAGATCAATCACCGCACACCCCTATCCGGTGGTCAAAAG  
 CAGTTGTTAGCGCTGGCTGCAGTACTGATTTTGGAGCCAGAAGTGATCATCGCTGATGAG  
 CCCACTACCCTGCTGGATCTGCGCAATAGGCTGATGATCAAAGACGTGTTCAATAAACTC  
 GAGCAGCAATTAATCGTTGTCAGCCATGATTTAGATTTCTCTCAGCGATTTTGAGCGGGTC  
 ATTTGCATCAATGATCATAAAATCGCTGCTGATGGCCCTCCGCAAAAGTCCATTGACCTG  
 TACGTATCGCTTATGGCGGAACCTGCGAAA

>RXA00852-downstream  
 TGAACAGTATTCCTTTAGGTTTT

>RXA00856-upstream  
 GTTTTTAGGAATAGAGTGGGCTCAAGCTTTGTGACAAGTTTTTTGGAGAAATCATTACTA  
 GTCGTAGTCTTCAATTTGGGTGCAGGTAGGGTGGAAACACC

>RXA00856  
 GTGAGTGATGTATCAGCAGGCGTAAATGGCGCACAAAGATCCAAGCAATCAAGCGGTCAAG  
 CCTTCCAACCTGGAACCTTCCGAACCTTCTTGACCAGCTTGCCTATCATTGTCATCCCTTTG  
 TTTGCGTGGCTTACGCTTAAAGGTGAGACGGAAACAATGCTTTTGCCTGGTGGGCGTTG  
 GTTGTTTTTCATTTTGCTCATGATCACCGACAAGCTTGACGGCGATATTGCGCGAGCACGT  
 GGCCTGGTCACTGACTTTGGCAAGATCGCGGATCCGATTGCCGATAAGGCGTTGATGACC  
 ACAGCATTTGTCTGTTTCAACATCATCGGCATTTTGCCCTGGTGGGTCACTGCGTTGATT  
 GTGCTTCGAGAGTTCGGCATTACCATCTGGCGTTTCTTCCAACCTGCGCGCTGGAAATGTT  
 GTGCTGCATCAAAGGGGGGCAAGCTTAAGACTGCTCTGCAGACTGTTGCCGTTGCTCTG  
 TATCTGTGCCCTTTCCCAAGTTGGATGGATATTCCAAGCCAGATCGTCATGTATGCA

>RXA00870-upstream  
 CAAGACGGCGATGTCGCCGCCGCTGTTGATACCGCAGCGCGACTTGTTTACACAGATATT  
 CAACAATTCATTCGCAGAGCATTTAAGGAATTTACACAC

>RXA00870  
 ATGTCTGAACCACAAACCATCTCGCACTGGATTGACGGCGCGATTTCCCCATCCACTTCC  
 GGCAAGACCGCTCCTGTCTACAATCCTGCAACTGGCCAGGTCACCGCCAATGTTGCGCTG  
 GCTAGCCAGGAAGAGATCGATGCCACCATCGCTTCTGCCACCAAGGCTGCTAAGACGTGG  
 GGCAACCTGTCTATCGCTAAGCGCCAAGCTGTGCTTTTCAACTTCCGTGAGCTGCTGAAT  
 GCTCGCAAGGGTGAGCTGGCGGAGATCATCACTGCAGAGCACGGCAAGGTCTTGTCCGAT  
 GCCATGGGTGAAATCCTGCGCGGCCAGGAAGTCGTGGAGCTTGCTACCGGTTTCCACAC  
 CTGCTTAAAGGTGCGTTCAACGAGAACGTCTCCACCGGCATTGATGTGTATTCTTGAAG  
 CAGCCACTGGGTGTTGTGCGGTATCATCAGCCCGTTCAACTTCCCTGCGATGGTGCCGATG  
 TGGTTTTTCCCAATCGCAATCGCTGCAGGCAACGCAGTTATTTGAAGCCTTCAGAGAAG  
 GATCCTTCGGCAGCGCTGTGGATGGCTCAGATCTGGAAGGAAGCTGGTCTTCCAGACGGC  
 GTATTCAACGTGCTCCAGGGCGACAAGCTGGCTGTTGATGGTTTGCTGAACAGCCCTGAT  
 GTCTCTGCGATTTCTTTCGTGGGTTCACCCCAATCGCAAAGTACATCTACGAGACTTCC  
 GCGAAGAACGGCAAGCGCGTCCAGGCGTTGGGCGGCGCAAGAACCACATGCTGGTGCTG  
 CCAGATGCTGATCTGGATCTGGTTGCCGATCAGGCAATCAACGCAGGTTACGGCGCTGCC  
 GGTGAGCGTTGCATGGCTGTTTCTGTGGTCTTGGCTATTGAATCTGTTGCCGACGAGCTC  
 ATTGAGAAGATCAAGGAGCGCATCGACACCCTGCGCATCGGCAACGGTGCCGGCGACGAG  
 CAGGGCGAGCCGCACCTGGGCCCCACTAATCACCGACGTCCACCGCGACAAGGTCGCTTCT  
 TATGTGACATCGCTGAGGCCGACGGCGCCAAGATCATCGTGGACGGGCGTAAGTGCGCC  
 GTAGACGGGCACGAGGAGGGCTTCTTCTTCGGCCCTACGCTTATCGACGACATCCCACTC  
 ACGTTCCGCGCCTACACCGAAGAAATCTTCGGCCCGGTCTCTCTGCTCGTTTCGTGTCGCA  
 TCCTTCGACGAGGCAATTGAGCTGATCAACTCCGGTGAATTCGGCAACGGAACCGCAATC  
 TTCACCAACGATGGTGGAGCGGCACGCCGCTTCCAGCATGAGATCGAAGTGGGCATGATC  
 GGCATCAACGTACCAATCCCAGTGCCTGTTGCGTACCACTCCTTCGGTGGTTGGAAGAAC  
 TCCCTCTTCGGTGACGCCAAGGCATATGGCACTCAAGGTTTTGATTTCTTACCAGGGAA  
 AAGGCGATCACCAGCCGTTGGCTCGACCCAGCAACCCACGGTGGCATTAACCTCGGTTTC

tream  
ACAGGACT

eam  
GCTGGGTGATCGGGGGCCGGTTGTTCCGGGTGTGATTGGTGACTG  
CAACAATGTGTCTAAGCTTAGGGGC

GAAGTGGTTGTTTTAGCTGATTCCGAGGGCAATCCTATTGGTACT  
GTGCACACTAAGGACACGCCTCTGCATTTTCGCGTTTTCCACCTAT  
GGGGAGCTGTTGGTGACGCGTCGTGCATTGTCTGAAGAAGACATGG  
AACTCTATGTGTGGGCACCCTGGTCCGGATGAGACAAACGCGGAT  
GGTGTCTGATGAGTTGGGGCTGGAGGTAGATTCTTTCTTGGATATT  
GATTACCAGTACCGTGCTGTCTGACGCGTCCGGCATTGTGGAGTGG  
CACCTCGTGCGTTTTAGCGGTGGGGGAATTTGTGGAGCCACTGGAT  
TTTCGAGTGGGCGGAACCGCAGAAGCTTTTCGACGCTGTTGATGCC  
TCTCCATGGCTAGTGGATCAGCTTAGCGCCCCTGAGCTGCGCCAA  
TTTGACGCAGAG

tream  
GAAGCCTT

eam  
TTCAGTTGTGGTGGCTCCGAATCTGATGAACAATGATCATTCCTA  
TATCAAAGAGAGCCACCACCTACTA

CGAATTTTAAAAACCACGTCTGCGCTTTGGCCCTACTATCTCGGA  
ATTGTGATCGCGGCGTTGTCTGCTGCTGCGCGTTTATTCTCCGC  
ATTGTTTCTGCAGTAACCGGATCTAACACCGTCGATGCAGTTACT  
TTAGCTTTAGCCCTGTTTGTCTGCAAGCTTCCTCAATACGGTGATG  
TACATCGGTGATGTCATGGCATCTCGTATGCGCCAGATTCTGGCC  
AAGCTGTTGGCGCTGCCTCAGAAGTATTTTGATAATCAGGTCACC  
CGCCTTGATCGATCAATCAACGGCATCACGCAGTTCATGCAGAGC  
TTCCCCATGCTCATCACCATGGTGGCAGTGCTGATTATTTCCGCG  
CTGGCAATTCTGCTGGCCATGTTGTTCCCGATTACATGTGGCTG  
AAACGCTGGCAGAAATATGAGGGCGAGAAAAACCATGAAATCGAC  
TTCGCTGAGGTTGTCTGGCCAGGTCAAGGTTGTTAAATCATTCGTC  
CTGGCTGATTTTCGGTGGGCGTTACGGCAAAACAGTAGCGATTACC  
TGGTGGCACCAGCATGGATACTCTCCGTGGCGCGGCACTAAATATC  
CACCTGCTGATTTTCTACCGCACCTTGACGCGCCATTTACCATC  
CTCATCCAGCTTGTACCATGGCGCAGCAACCGGTGTACATGATG  
TCCGCGCAGCGCGCCATCGCCGGCTCCCGCGACTACTTCGAGGTC  
GAGCCCACCGCCAATAAGGAGCTTGTCGACGCCACCCTCGCCTCA  
AGTGTGGGCACGCCCCGCGCGCTGCCCGCTGGAGAACCAGCGATG  
ACCTTCGCCTACGAAGAAGGCAAGCCGGTTATTTCCGACGTGTCC  
GGCGAGCGCATCGCGTTGGTCTGGTGAATCCGGCGGCGGTAAATCC  
CTGTTAGGTCTGTACAAACCAACAGCGGCAGCCTTGACAGTATGT  
GATCTGACTTCCGAGGAACTTCGCGCATCCGTGGGTGTGGTCTTC  
TTCTCTGGATCTATTGCAGAAAACATCGCCTACGGTCGCCCAGGT  
ATCATCGAAGTGGCTAAGAAAGCCAACGCACATGAGTTCATTTCC  
TATGAAACCGTCGTCTGGTGAACGCGGACTCAAACCTTTCTGGTGGC  
TCTGTGGCACGGGCCATGCTTAAAGATGCCCCACTTCTTGTTC  
GCACTGGATACCAAGTCTGAGCAGGCAGTCCAAGCCGGTTTGGAA  
CGCACCACCTTAATGATCGCCACCGCCTGTCCACCATCGCAGGC  
ACCATCCAAAACGGACGGGTGAAGAGGTCTGGATCTCCTACCGAG  
GGTATCTATTCCGAAGTCTGCGCCTGACCAACTCCACAGCAGAA  
CTGCGCGCCTTTGGTTTCACTGGCGATGCACCAGCTGAAGAAGAG

>RXA00878-downstream  
TAGCCCCGCGAAAGAACAATCCC

>RXA00880-upstream  
TCCATGTGGTTAAAGATATGCCTAAAGATCTGACCAAAAACGTGACTAAAGACGTGACGA  
CACAAGTACAGCCAAATTAAAGGAAAGGTTGAATTTGACC

>RXA00880  
ATGACTTCACCTAATACCCTGCAGGAATACACTGAACCTGCCAAGTACACCATCGGAGAA  
TCTGAAACCTGCCTGACCGCCCTTCTAGATCAGATTAAGACTCGACCTTACGGAGTTTGT  
TTCAGCAAGCCTGCCAACTATGAGTGGGTGAATGTAAGTGCCTAAAGAAATTTTCAGGACGAG  
GTTTTTTCGGTTGCAAAAGGAATTATTTTCAGTCGGCGTAGAGCAGGGAGACCGTGTGCGG  
CTGCTGTCCAATACTCGCTATGAGTGGGCTGTGCTTGATTTTCGCTATCTGGGCCGCTGGC  
GCAGTGAGCGTGCCTATCTACAGCTCCTCTTCACTGTCCCAAATTGAGTGGATCATTGAG  
GATTCGCGCGCTGTTTTGGCCATTACCGAAACCCCTGATCATACCGACTTGATGAAGAAC  
CTGGTCATCGGTGAAGACGGAACCTCCAGCGATTAAAGGGTTCACCTTCCAAGCTGCGCCGC  
ATTCTAGAGATCAACTCTTCGGCGTTGGAGACCTTGAAGTTTGAGGGCCGCGAGCTTTCT  
GATGAGCTGGTGTGGGAACGCATTTCATGCAACCAAGGCCGCTGACCTGGCGTCTTTGGTG  
TACACCTCTGGCACAACCTGGTAGGCCGAAGGGCTGCGAGTTGTCCCACTACCACTGGTTG  
GCTGAGGTCCGAGCGCTGATCACCATTGACATCGGAGCGATCGCGATGCCAGGTTCAAGG  
TTGCTCACCTTCCTTCCTTTGGCGCACGTTCTTGCTCGCGCAGTGCACCTTGGCCTTCGCT  
GTCACCGGTGCAACCCAGTCCCACTGGTCTGATTTTCAGCACCTTACTTTGGAACCTGCAG  
CGTTCCCGCCCGAACCTGATTTTGGGTGTTCCACGCGTGTGTTGAAAAGGTCCGCAACGCC  
GCTGCTGCTAATGCTGCTGACGGTGGCGCAATCAAGCGCATCATGTTTGAGCGTGCCGAA  
AAGGCGGCCATTGAATACTCCATGGCTCTTGATACTGCAGAAGGCCCAAGCAAGTCCCAG  
GTTATGGCACATAAAGCGTTTGACAAGCTGGTGTACTCCAAGATCCGTGCAGCTGTCGGT  
GGCGATGTGCAGTACGCCATCACCGGTGGTTCAGCGATGGGGCAGGAGCTGCTGCACTTC  
TTCCGCGGTGTGGGCATGACCATCTACGAAGGTTATGGTCTGACGGAATCTGCGGCTGCT  
GCAGCGGTGGACTTCACTGATCAAAAGATCGGCACTGTGGGTAAAGCCGATGGGTGGCATG  
ACCATCAAGATCAATGAAGATGGCGAAATCATGCTAAAAGGCGAGATGTTGTTCCAGGGA  
TATTGGAACAACCCAGAAGCCACAGCAGAAGCCCTCCACGACGGTTGGTTCAACACCGGC  
GATCTGGGTGAGCTGTTGGAGTCTGGACACCTGGTGATCACCGGACGTAAGAAAGATCTG  
ATCGTGACCGCGGGCGGCAAGAAGCTTTCCCCAGGACCCATGGAAGACATCATCCGCGCA  
CACCCACTGGTCAGCCAGGCCATGGTGGTGGGCGATGGTAAACCATTCGTTGGCCTGCTG  
GTGACCTTGGATCCAGATATGTTGAAGCGGTGGAAGCTGAACCACAACATTGCGGAATCC  
CGCACGGTTTCTGAGATTGCTACTGATCCTGCACTGCGTGCGGAAATCCAGGATGCAGTC  
AACAACGCTAATGCCACGGTGTCTCATTGAGAGGCGATCAAGCGGTTCTACATCCTTGAT  
CGCGACCTGACCGAGGAAGCCGACGAGCTGACCCCAACGCTGAAGGTCAAGCGCAACGTT  
GTTGTTGCGCGTTACGCAGACGCCATCGACCACATCTACAACCGA

>RXA00880-downstream  
TGAGTAACACAGAGACCCAATTT

>RXA00899-upstream  
TTTGCTGCTCCCCTACGTCGGACTCCCCTGTTTCTGCTTATGGGATCGCCATACATCAA  
CCGGTGACGCCACCGCATCCAACAAGAAATCAACGACCTC

>RXA00899  
ATGGAAGACGTCCACGACGACGTCCCCGACATCCCCACCGGAATGGATGTCTCCGCGGAA  
GTTGAATCTGTTCATCAAACTCAACCGCCGCTCACCCGCATGCCAGCAGTGACCGGCGGA  
AACAACGGCTTCTACTCCGACTACCGTGAATCCCTCAAACGGATGACCGCCGCAATCGAC  
GAAGCCGAAGAATACATCTACGTTCGAGATCTACATCATGGCCTGGGATTCTTACACCCAA  
CCATTCTTCGCAGCACTCGAACGAGCCACAACCGCGGCGTCAAAGTCCGACTCCTTTTC  
GACCACGTTCGGCAGCTGGAAATACCCCGGCTACCACCGCCTCAAAAAGAACTCAACCGC  
ATGGGCTTCGCCTGGTACCTCATGCTCCCCCTCCAACCTGGCGACGCGCTTCCGCCGA  
CCCGACCTGCGCAACCAACCGCAAAATGCTCATCATCGACGGCCACACCGCATTCATGGGC  
TCCCAAAATCTCATCGCCCCGAGTTACCTACAAAAGAAAAACATCAAACCTCGGCCGCGAA  
TGGAAGAGACCTCATGGTTCGAACTCACCGGCCCCATCGTCTCCTCCATGGAAATGATCTTC  
GCCGGCGACTGGTACGTGCAATCCAACGAAGCCCTCGACATCCGCGACACGCGAGAAGCC  
CACGGCTACATCGGCAACACTCAAAAAGACTCCGCCACCAACCTCGTGCAGCTCATCCCC



TCCGGCCCTGGTTACACCACAGAACCCAACCTGCGCATGTTCAACTCCATCGTTCACCAC  
 GCCAAAGAACGACTCATCTTGTGCAGCCCCCTACTTCATCCCCGACGAATCCCTCCTCGAA  
 GCCGTCACCTCAGCCTGCTACCGCGGAGTAACCGTCGAACCTATTCGTCTCTGAACAAGCC  
 GACCAATTCGCCATCGACCACGCCCAATCCTCCTACTACCAGGCACTCCTTGAAGCCGGC  
 GTGAAAATCTACCAATTCGCCAAACCCGACGTCCTCCACACCAAGTACATGATCGCCGAC  
 CCCGACGACACCACCGGCAACGAAGCCCTCGGAGTCCTCGGATCCTCCAACCTCGACATC  
 CGCAGCTTTGGCCTCAACTACGAAATCTCCCTGATGATCGCCAAAGGCAACCTCATCCAC  
 GAACTCAACGCCCTCACCAGCCGTTACCGCACAGTAAGTTTCAAGCTCACCTTGGATAAG  
 TGGAACCAGCGCAGTTGGCGGCGCCGCTACGTGGACAATGTCATGCGTTTGACCTCGGCG  
 CTGCAG

>RXA00899-downstream  
 TAGTTTGGCGCGTTTGGAGTGCG

>RXA00902-upstream  
 TTGTTATTGGTTTGTTCACCTCCCATGCAATGTACGATCGGTTCTAACGTCTACGGCAATT  
 GACACGTCAATTTAATTCAGGAAAGGGGTGGGGAGAATTT

>RXA00902  
 ATGTCTAGTGGTTTTGAATATGTTCAACATCCTCGACGAGCCCTCCCTCCGCCTATACCT  
 GAACGGAAAGGTCCTGCCGAGCATTCTGCGGGAACCTTCCATCCCATTAAATCCAAAG  
 AATATTGCAGCGAGCCACGATCAGGTGCTTCTATCTGGTTGGGGCAAATTTGTGCGTTGG  
 CTCTTGGTATTGTTGTCCATTTTGGTCATCATCATTTGGCATCAACCTCATCTTGGACGGT  
 GTCTACGGATTTGGTACTTTTTCAACCACCCAGATGTACCAAGTTGCGAAAGATCCACTC  
 ATTGGTGTGCTGATCGGTATCTTGGCTACGGCCTTGGTGCAATCATCAACCACCACCACA  
 ACGTTGACGGTGACTGCAGTTGGTACGGGCATTGTGTGCGGTGCCTGTGGCGATTCCGATC  
 ATTCTTGGCGCAAATATCGGTACGACGATCACCGCGATGCTCGTTGCGTTTTCTTATGTG  
 GGTGAACGCAGGGAGTTTAAGCGAGCTTTTACGGTTGCCGCCATGCATGTGTGGTTTAAC  
 GTGCTCGTCATTCTTGTCTATTTGTTGTGGAATTGCTCTTTCATCCATTCCGCACAATT  
 AGTGGTGCGATCGCAACGGAGATCACACTGACAACCTGGTGGCTCTTTGCCTACCAGTGGT  
 GTGATGACCAAGATTTTGTATCCCCCAACCCAACCTTCTGGGTATGAATGGTCTTATCGGT  
 TCGATCGGCAATCCTAGTATTTTCGGCGATTGTATGTCTTGTGGTGGGCACCATTCTTATT  
 CTGATTTTCGGTGCGTGCCATGAGTTCTCAGATCCGAACCATTACGGCAGCGACCGTAACC  
 TCAATTATGGACAAGGTGATCAATCCAGAGAACAGCCCCAAGGCGACGATTCTTTCCAAT  
 TTCTGGAGCTTCATTCTTGGAGTTTGTTCACGCTCATGGTCACTGCCTCGTCAGTGACC  
 GTGGCTTCCATGCAGCCAGTGGCTGCCTCTGGTGTCGTTAAGCAAAAGCCATTGCTGGGC  
 GTCATTTTGGGTGCCAACGTGGGCACCACGGTGACCGCAATGTTTGCTACTTTTCGCGATT  
 GTCAGCGATCAGGGTGAGTTCGCTATTTCAGGCTGCGTTGATCCACCTCATTTGTGAACTTC  
 ACCGGCGCATTACTAGTGCTGTGTATTCCGCAGCTTGCCAATGTGATTATTCATTGGCC  
 GAGAAAACCTGCGAACCTCACTGCCCGCAGTTAC

>RXA00931-upstream  
 CCGTAACCTAATCGTTGAAACATCACCTTATTGCTGGGCTTTGCACGCTACTCTTTGTGA  
 GTAACCTCACCGAAGTGCATAAATTAATTGGGAGTGATCA

>RXA00931  
 GTGAAAACCTATTGAAGATATTTTGACCTTGGAAAGAAATCGACCGCGATATTTACCGTGGT  
 CCCGTTATCGAATCTTATTTAGCCAGGACTTTCGGTGGCCAGGTCGCTGCCCAAGCTTTA  
 GTAGCAGCAACGCATACTGTTGATAAAGCCTTTACTGTGCATTCTTTGCATGGCTACTTT  
 ATAGCTCCTGGTGATCCAACAGCACCCGCAATTTATTTAGTGGATCGAGTTCGCGACGGA  
 AAAAGCTACGTCACCCGCTCGGTGCGTGGCATCCAAGACGGCGAAGTAATCTTCAGCATG  
 CAGGCCAGCTTTCATCGTGGGGATGAAGGCATTGAGCACATGGACAAGATGCGTAAAGTT  
 CCAGCTCCTGATGAGATCAAGGGAACAGTAGAACGTATGCCGATCTCAAGTAGGCGAGTG  
 CTTGATGAATGGGCGGAATGGGATATCCGCGTTATTCCGCAGGATCAATTAGAACTCAGC  
 GATTTACCGCTACTGAGCAAGCTGTGTGGATTTCGGTGACCGCTGATCTTCCGGATAAT  
 CCCACCTTCCACCAGTGCTCACTGACTTATCTGTCCGATATGACTTTGCTGCATAGTGCC  
 CTGGTGCCACACCCAGGTGAGAAAATGCAGATGGCCTCACTTGATCACGCTGTGTGGTTC  
 CTGCGTCCCTTCCGCGTCGATGAATGGTTGCTTTATGATCAGCGCTCTCCATCGGCCTCA  
 AGTGGGCGAGCCTTGACTCACGGGCGGCTTTTCAACCAGCAGGGAGATTTGGTTCGCTATT  
 GTCAATCAAGAGGGAATGACCCGCACACTCCACGAGGGTGCGCAATCAATTCCGATGCGC  
 AAAGAC

>RXA00931-downstream  
TAAAATGCAGCGAACTTGAAGAT

>RXA00941-upstream  
AGCCGGGGTGGCCGTTTGCCTGTACGGGTTTGGCTTATCGACGCCCACTTCTGATTTTAA  
AGGCAAATATTTTGTGTCACAGCGAGTAATCTTTTCGGGC

>RXA00941  
ATGAACCTAACCCGGAATGACAGGCTCGATCGACTGCCCCGTAACCTCCAAACATAAAAAG  
ATTCTTGGCGGCTCAGGTATCGGCTGGGCATTGGATGCCATGGATGTCGGACTGATCTCT  
TTCGTCATGGCTGCGTTGGCCACTCATTGGGGCCTATCCCCTACTGAACTTCCCTGCTC  
GGATCCATCGGTTTTCGTTGGCATGGCCATCGGCGCTTCGCTGGGCGGTTTGTGTCGGGAC  
AAGTTGGGGCGTCGACAAGTTTTTGCCTTGTCTTGTAGTTTATGGCGTTGCCACTGGC  
GCGTCGGCGCTTTCAGTGTGCTGGCAATGTTGATGGCGCTGCGCTTCGTCGTTGGACTT  
GGCCTGGGCGCTGAACTCCCCGTTGCATCCACTCTGATTTCCGAGTTTTCTCCACGAAAA  
GTTTCGTGGCCGCATGGTCGTTATCCTGGAGGCGTTTTTGGGCGCTGGGCTGGATCATGGCT  
GCAATCGTCGGAACCTTTGTCTGTCGAGGATCCGATAATGGTTGGCGTTGGGCGTTAGCT  
CTTGGCTGTGTCCCTGCAATTTACGCGGTGTATGTCCGTCTCGGACTTCCAGAATCAGTA  
CGTTTTCTGGAGAAGAAAGGCCGGCACGACGAAGCAGAAGCCATCGTTGTTTCTTCGAA  
GAAGCTGCCGCTGCCGAAGGTAAAGCTGCCGATGCCACCACCGCTGTGGTTCATGACAAC  
GCTGCCGAGGGTTCCGTATCCATCTGGTCAGCTGCTTTGCGCAAGCGCACCGTCGCGCTG  
TGGATCGTGTGGTTCTGCATCAACTTGTCTACTACGGAGCCTTCATTTGGATTCCATCG  
CTGCTGGTTGCCGACGGTTTACCCTCGTGAAGTCTTTCCAATTAATCTGATCATCACC  
TTGGCTCAGCTTCCAGGCTATGCGGTTGCAGCGTGGTTGATTGAAAAGTGGGGCCGTCGC  
AGCACATTGGCCACGTTCTGGTTGGTTCTGCTATCTCTGCAGCGCTCTACGGCTTGGCA  
AATGTGGAGTGGCAGATCCTGGTCGAGGTTGTTTACTATCCTTCTTCAACCTGGGCGCA  
TGGGGCGCACTGTATGCCATTGGGCGGAGCTTTATCCCACTAATGTCCGTGGAACCTGGA  
ACGGGTGCTGCCGCGGGATTCCGGCGCATTTGCTTCCATCATCGCTCCGCTCATTGTTCCG  
CCAGTGATTGCTTTTGGTGGACCAATTGCTTTGTTTCGCTCTCTTTGCCACCGCGTTTGC  
ATCGCAGCGATTGCGGCGTTTACGCTGCCTGAGCAGAAGGGTAAGTCTCTCGCTGAT

>RXA00941-downstream  
TAGTGAGATCCTTCCACCAGTTT

>RXA00962  
GATAAGGCCATCAAGGCGGATCACGACATTAGAGAAGGCCACGATGAGCCAGCAGGTTTC  
AAGGATCTGCTTGTGATCGCTACCGCTGGATCTCCATTTGGTTTCGCGCTCGCCACATTT  
GTCACCCTGCTCGCGTGGTACGGACTGGGCACATGGTTGCCTCGCCTCATGGAAACTGCA  
GGTTATGAGTTCGGCCATGCATTGATGTTACCCCTGGCTCTGAACCTCGGTGCAGTGATC  
GGATCCGTGGTTACTGCGTGGGCGGCGATCGCTTCGGGCCAATCCGTTCCGGTGTCTATC  
GCTGCAGGTATCGCCGGTATTGCACTGCTCCTGCTGCTCACTTACCCGCCTGTCACCGCG  
GTTTATGTCAATTCTCATTTTGGCTGGCGTGGGCACCCACGGCACTCAGATCCTCATCATT  
GCAGCTGTGCGCAACTTCTACCCAAGCAACCTGCGTGGCACAGCACTGGGCTGGGCGCTA  
GGTGTAGGTCGTATTGGTGTGTTGTGGCCCCGAGCTCGCTGGCCTGCTGCTGGCATGG  
AACTTGGGCGTGAACCTCAACTTCATCATGTTTCGGCACCGCTGCGCTGCTCTCTGCGCTG  
GCTCTCAGCGTGTGCTGCGCCTGCAGAAAACCTACAGCGTCACCCACAAAGTCGAAATC  
CAAGGC

>RXA00962-downstream  
TAACCCCTTTTCAACTCACAG

>RXA01060-upstream  
TTCCATTTACACATCTGTTTCGACTCGCGCCCGAATGATGTGCGCATCAACATGAGAAGCTA  
CTTCCATACTTTTACTGATTGATAAGAATGGACAAAGACA

>RXA01060  
ATGAACCGCACACTCCGAACACTTGGCTGGCTTGTGTCGCGTAATTCAAGAAGATCCGGAG  
CCCTGGTTCACCACTGATCCCGACACCGATTATGTCCCTTATGTAAATAGTTTCTCATTT  
GAATCCCTTTCCCTCGTTCCAGATGCTCTGATGCTGCTCAAACGTTCTCTTCACCTTGCG  
ATGGAGCAACAGGACCTCCAGTGAAGGATCTACAAGAAGCACTGAGGCACGTACTAGTT

TTCAAATTCCTTTCAGGGAAGAATGGGAGCTGGAATTAGCATGGGACTCCGAGCGGACC  
AAGTCTGCGGTGAGAATTATTGAGAGCACAAAAGAATCTCTTGCCGATCAATACAGAGAT  
TACAAATACGCATTCTTGCCCTGAGCTAATTTTCCAGGAATCACGCGGGATCTTTGACTTT  
GAGCTGGAGGGATACACCCTCAAAGTAGGACAAAGCACGCTTTCCATTCTTGGGACATG  
ATCGCCAATGGTTATGTCCCTGCAAGTCTTCGGAATTTTGGAGAATTAATGGACCGTGAC  
ACCGGAGATCTTGATGCAGATCCCATTTCTGAGACCTCGAGAACTCAAATTTGAGATCCAT  
AATTGTCCAGATCTTAATCCTTGGATAATGCGGGAAACTTTTGATTTTCATGATGGAAATC  
GCAACTGAAACAGGATGGTTCCATGCTCTCAACCCCGCATATAATTCCGTCTACACCTAC  
GATCTTATTTCTCGCATGCCAGATTTCTTGTGTAAGGGAGCTTTTCGTCCGCATTTCAGTG  
AAACGATCTTGGGAAAAAATTCAAAAGATAGCTAAAGCTGTTGAGTCTTATGCATCTCAC  
GATTACTGCATGTCAACGCTGACACATGACTACAGGGCAATCGAGTTATCCCTGACGCCT  
ACAAAACTGAGGAACCAAGCACA

>RXA01060-downstream  
TAAGAAAACCTCGCCTGCCCCACT

>RXA01067-upstream  
GGCTTTAAGGCCGAGGTGCCTGGCTGAACTGCAGCCCCTCCAGACCCTGAGATCAGGCTA  
AATGGCAAACACAAATAGTTTGCATGGCAGAATAGCTTAG

>RXA01067  
GTGAGTGAATTCCAAGTACCCGAAATCCCTGCCCAATTCCTACCCAAGCATATTGCGCTT  
GTCATGGATGGAAATGGACGCTGGGCTACCGAGCGTGGCATGAAGCGCACCGAAGGCCAT  
AAGCGTGGCGAGGCAGTCTTGCTTGATGTTGTTGATGCATGCATTGAACTTGGTGTTCG  
TACCTTTCTGCTTATGCCTTCTCTACTGAAAACTGGCGTTCGTTCACCGATGAGGTCCGT  
TTCCTCATGGGATTCAACCGAGATGTGCTGCGACGACAACGCGATGACCTACATGAAAAG  
GGCGTTCGTGTGCGTTGGGTTGGCCGTCGTCCCCGCTGTGGCGTTCGGTTATCCGTGAG  
CTGGAAACTGCGGAAGAGCTAACCAGACAAACACCAACCATGACCTTGGCCATGTGTGTG  
AACTATGGTGGACGCGCCGAAATCATCGACGCAGCCCGCGACATCGCCCGCCTTGCAGCT  
GAAGGCAAACCTGCGCCCGGAACAAATCACTGAGAAGACCTTCCCGAACTTCTCGACGAA  
CCTGACATGCCAGACGTGACCTGTTCCCTGCGCCCATCCGGTGAGAAGCGCACGTCAAAC  
TTCCTGCTGTGGCAGTCTGCCTACGCGGAAATGGTCTACCAAGACAAGCTGTTCCCTGAT  
TTCACGCAGCAAGATCTGTACGACGCGGTCTGGAATACGCCAAGCGGGATCGCAGATTC  
GGAAGCGCA

>RXA01067-downstream  
TAATGCCACCAACCAGCCGACG

>RXA01114  
CGCCTTGCAGAAGCACGCGAAACCGCTGGCGGACGCAACCACCCGATCCCTGGTGGCATG  
ATCGAGACCGCTGAGAACCTGCGTCGCGAATACGGCATCTCCCGCGAGGAGCAGGACAAG  
ATCTCCGCAGCGTCCCAGCAGCGTTGGGGCAAGGCTGCTGATGCGGGGCTTTTCGACGAC  
GAGATCGTGCCAGTCAACGTCCCTGCCAAGAAGCGCGGCCAGGAGCCAACCATCGTTTCT  
CGAGACGAGCATGGTTCGACCAGGAACAACCGTCGAAAAGCTTGCTGCTTTGCGCCCCATC  
ATGGGCGGCCAGGATGCGGAAGCAACCGTCACCGCTGGCAACGCGTCCGGCCAAAATGAT  
GGCGCTGCTGCCGTTCATCGTGACCACTCGCGCCAAGGCCGAGGAGAAGGGCCTGCGCCCA  
GTCATGCGTTTGGCTGGCTGGTCTGTGGCTGCTGTTCCCCCAGAGACCATGGGTATTGGA  
CCTGTTCTTGCCACCAAGAAGGTCCTGGATCGTTTGGGCCCTTACCCTGGAGGACATCGGC  
GCGATCGAACTCAACGAAGCTTTCGCGAGCTCAGGCACTGTCTGTGCTGAAGGAATGGAAC  
ATTTCTTGGGAAGATGAGCGCGTCAACCCACTGGGTTCGGTATTTCCATGGGACACCCA  
GTCGGTGCCACCGGTGCTCGCATGGCAGTAACCTTGGCTCACCGCATGCAGCGTGAAAAC  
ACTCAGTACGGACTGGCCACCATGTGCATCGGTGGCGGCCAGGGTCTTGCAGCTGTCTTT  
GAAAAGGAGAAC

>RXA01114-downstream  
TAAAAATGGCTATTTTGCACAGC

>RXA01136-upstream  
CCCTCGCAACACCGACGGTAGCCTCTTGGAATGGCGCGCATCGTGCGTGAGCTTTCCCG  
CTAGGACCTGTCTACTGCCTTCACTTTGTGCGAACACCGC

>RXA01136

ATGACCTTGGATTACTTCAAGGCATCCGGCACTGACTATGCTTTGGGATTGGCTGCAGAG  
TCGGAAGGGGCACGACGCACTGGTATCACCGGCATGGCGAGTGCATTCAAGGAGTTTGCT  
GGTTGTGGTGAGATCGACCTTGAAGCAACCAGGGTAGAAGGTGGCCTCAAAGTTAGTGGA  
AAGCTTCGTTGGGCTTCCAACCTGTGCGAAGATCCAGTGATTGTGCCTGCTGCAAAGACC  
GCAGAGGGCTTACAACCTACTGTTTCGCATTGGGCGCAGAAACCGAAGGTGTCACCCTCGGT  
TCTTCACTTGTCTACTCGGTTTGAACGCAACTGCTTGCCTTGGGTGAGCTTTGAGGAT  
GTCTTCATTCTTGGGGCTCAGATTCTAAGCCACGATTTCTTACCTTGTGGCATCGGTGC  
GCCCCAACCTTCG

>RXA01136-downstream

TGATCCTACGGATCTCCGAATAC

>RXA01138-upstream

CTTATTCAAGTTTTTGGAAAGATAATTAACCTATGACTTTAAAAACAGTAAACGGAACGCA  
GCTGCGAGACACTGTCGGATCGTTCCCTTCAGGTGTCACG

>RXA01138

GTGGTCACCACTACCGATGGGGAAGTGGACCACGGGTTGACTGTGAGTGCGTTCGTGTCC  
TTGTTCGTTGGAGCCTGCCATGGTGTGGTGAGTATCGATAAGAAATCAAGCGTTGTGCCG  
TTTTTGGAGCAGGGTTCACCACTTGTGTCTGTGTTATCGGAAGAGCAGAGCGATTTG  
GCCATCACATTTGGCCGTCATCTGGAAAACAAATTCGACGGCGTTTCCATTAAGCGTTCA  
ACAAACAGGGCAGCGGTCTTGGAAAGGTGCGTCAGCATGGTTGAGTGGCGCTGTGGTGAT  
AAATACCCAGGTGGAGATCACTTTATTATCACCATTTGCCGTGGAAGAGTGTGCTCACGAC  
GAGGAGCAAAAGCCACTTCTTTACCACCGTGGCAGGCTTTTTTCAGTGGCAAGAAGAT

>RXA01138-downstream

TAATTCTCCACCCCTTCATTTTC

>RXA01172-upstream

TAAATTTTTCTAGACTACCCAGATTAAGTGAGATTCTTTCGTGTCTTCGACAACTTCGAC  
AACTTCGGCCACCCGACAAGAGCCGTTGAGCCCGACGGGT

>RXA01172

GTGCTTGCCTCGTTTAGGTTTCGCGTTTAGTAGCCCGCGGAGGTTTCGCACCGAGGTTTTA  
GCTGGCCTCGTGGTGGCGCTCGCGCTGATTCCGGAGTCGATTGCGTTTTCCGTATTAGCT  
GGCGTGGATCCTAAGATGGGTCTTTTTGCGTCGTGCACCATGGCAATGACCATTGCGCTT  
ACAGGTGGACGCCCTGCGATGATTTCCGCGGCGACAGGCGCTGTGGCGCTGGTGATTGCA  
CCGGTGGTTCGGGATCATGGCGTGGAATATTTCTGGCCACGGTAATTTTGGCGGGCATT  
ATTCAGATTGCGTTGTCGTTGCTGGGTGTAGCCAAGCTGATGCGGTTTCATTCCGCGTTCC  
GTTATGCTCGGATTTGTTAATGCGCTGGCGTGCTTGGTGTTTTTTGCGCAGCTGCCGCAC  
CTGATCGATGTTCCGTGGATGGTGTATCCGCTGTTTCGCGCTGGGTATTGGCATCATGCTG  
TTTTGGCCGAAGCTGACCTCGGTGATTCCGGCTCCGCTGATTGTTATCGTGGCCTTGACT  
GCGATCGTGTGGGTTTTTCGGAATCAACATTCCAACGTCTCTGACCAGGGCGAACTCCCC  
TCTTCCCTACCAGAATTCCTCATTCCCAACGTTCCGCTTACTCTTGAGACTCTAAAAATT  
ATTGGGCCGTATGCGCTTGAATGTCGCTTGTGGGTTGATGGAATCGCTGCTGACCGCC  
AAGCTGGTCGATGATATTACGGAGGTTCACTCCAATAAATCCCGCGAAGCTGCAGGTCAG  
GGCATCGCAAACATTATCACCGCGTTTTTGGGCGGCATGGGTGGCTGCGCGATGATCGGC  
CAGACCATGATCAACGTGAAAACTCAGGAGCCCGCACTCGCCTATCCACCTTCTTGGCC  
GGCGGCTTCTGTGCTCCTGGTGGTTTTGCTGGGCGATGTCGTGGGCAAAATCCCCATG  
GCGGCGCTCGTGGCAGTCATGATTATCGTCTCCATCGACACCGCCGACTGGCATTCGCTG  
AACCCGCGCACCCCTCAAATTCATGCCGCTGAGTGAAACGATCGTCATGTTTATAACGATC  
ATCGCGACCCCTCGTCACCGGAAACCTGGCGATCGGCGTCATCCTCGGAGTGCTCACCGCC  
ATGGTCATGTTTGTCTCGCCGCGTGGCCACCTCGTGTCTGTGGAGCGCACCCACGACAAC  
AACATCAGCACCTATACCGTCAAGGGCCAGCTATTTTGGGCGTCCTCGAACGATATGGTG  
TACTCCTTCGACTACTCCGACGAGGCCGAGCAGATCATCATCGATCTCACCGCCGCGAGAA  
ATCTGGGACGCCTCCACGGTAGCCACGCTGGACAGCATCATCCACAAATACGCCGCGCGC  
GGCAAGAGCGTGGAGATCATCGGGCTCGACGGCCCCAGCCGCGATAGGCTTGAGCGCCTA  
TCAGGCAAGCTGGGC

>RXA01172-downstream



TAAAAATTTGCTTATCGACGCGC

>RXA01191

GTGAGTTTGGATGCGAACACGATTGAAACGGCGGGGCGCGGCGACGTGATTTTCGCGTATC  
GCGGATGATTCGCGGGAGGTGTCCACTGCGGCGAGCACCGTGGTGGCGCTGATGGTGCAG  
GCGGGCTTTACCGTGGTGTATTTCCGCGTTTGGCATGGCGGCGGTTGATTGGCGCCTCGGC  
CTTGTTCGGTTTGGTTCGCGATCCCGCTGTATTGGACCACGTTGCGCGTCTATTTACCCCGC  
TCAGGTCCGCTTTATACGCGTGAGCGCGAGGCCCTTTGGGGTGCGCACGCAGCGGCTTGTC  
GGCGCAGTCGAAGGCGCGGAAACCTTGCGCGCTTTCCGCGCAGAAGATACAGAATTAAAG  
CGTATCGACGCAGCCTCCGGCGAAGCCCGCGACATTTCCATTTCTGTTTTTCAGGTTCTC  
ACATGGGCATTTTCCCGCAACAACCGCGCGGAATGCATCACCTCGTGCTCATCTTGGGC  
ACCGGCTTTTACCTGGTCAACATCGATCTGGTCACCGTCGGCGCAGTCTCAACCGCCGCA  
CTGATCTTCCACCGACTCTTCGGTCCAATCGGCACGCTCGTGGGCATGTTCTCCGACATC  
CAATCCGCCAGCGCATCGCTGATCCGCATGGTGGGCGTTATTAACGCGGCATCGAACCAG  
GTCAGCGGCACCTCGCCGGCGTCTGCCAGCACCGCTTTAACGCTTTTCGACGTCTCCAC  
CACTATCACACTGCACCCGTCATCAAGAATGCATCCGTGCAGCTGGAACCAGGGGAACAC  
ATCGCCATTGTGGGTGCGACCGGCGCTGGTAAAAGCACGCTCGCCCTCATTGCGGCAGGC  
CTGCTCAGCCCAACTTCCGGGCGAGGTGGCTCTCGGCGGATCGAGTTTTTCTAACGTCGAA  
CCGGAAGCATTGCGCCAGAAGATCGCGATGGTCAGCCAAGAAATCCACTGCTTCCGAGGA  
TCTGTTTTAGATAATCTTCGTATCGCACGCCCCGAAGCCACCGATGCGGACATCCACGCC  
GTTCTCGCCGATATTGGTGTATTCCTGGTTGGAGCGCTTACCGCAAGGCATAGACACCATC  
GTGGGTGATGGCGCTTTCCGTTTAACTCTGTGGAAAACCAGATCATGGCGCTTGCTCGC  
GTACATTTGGCCGACCTAGCAATCGTCATCCTTGATGAAGCAACGGCTGAATCAGGCTCT  
GATCATGCAAAACAGCTTGAAGATGCAGCCCTTAAAGTCACTGAAAACAGATCAGCCATC  
ATCGTGGCTCACCGCCTCAACCAAGCGAAAACCGCCGATCGCATCATCGTCATGGACTCC  
GGAGAAATCATAGAATCTGGAACCCATGAAGAGCTTCGAGCGATCGGCGGTTCGATATGAA  
CAACTGTGGACTGCGTGGTCTGCGCGC

>RXA01191-downstream

TAATTAGCCACCCAAGACCACGC

>RXA01205

GTATCGGCCTATCCGCCGGCCATCATCGCAGCGGCTCTCGTAGGAATTTGCGCGGGAGTT  
TTGCCCCATAATTTTGAACCCTCGCGAATATTTATGGGCGATTCCGGCTCCATGCTCATC  
GGCCTGCTGTTGGCTGCAGCATCGACCTCAGCGTCAGGAAAAATCAACATGAGCCTGTAT  
GGCGCAGCTGATTTTATCGCATTTGATCTCACCCATCATCGTTGTTCTCGCCGCCGTGGCC  
ATCCCACTGCTCGACCTCGTGATGGCAGTGGTTAGGCGCGTGGGCAGGGGAGCATCACCC  
TTTTCCCCGGACAAAATGCATCTGCACCACCGACTGCTGTCCATCGGACACACCCATAGG  
CGCGTGGTCTTAGTGCTCTACACCTGGGCGAGCGCCGTGGCATTTCGGCGCAGTGAGCTTC  
TCCGTCGTTCCGCCACTGTTTGCCACCGGATCGAGCATCTGTGGCATCCTCATCGCCGTC  
GCTGTCACAGCCGTGCCAGTGATGAAAAGCCGGCGAGCCGCCAACTTGAT

>RXA01205-downstream

TAAGTGATTGTCACTTTGGATTG

>RXA01212

GGCCTGAATTTCCATGTACAGCGCGGTGAAGTATTTGGTCTGCTCGGCACCAACGGGGCC  
GGCAAAACCTCCACCTTGGAAGTCATCGAAGGACTTTCCGCACCCAGCTCCGGCACCGTG  
CGCATCTCCGGGCTTGACCCCGTTGCCGACCGCGCGATCCTGCGCCCCGAGCTCGGCATC  
ATGCTGCAATCAGGCGGCCTGCCATCACAGCTCACCGTCGCCGAAACCATGGACATGTGG  
CACGGCACCTGCACGTATCCGCGCGCCATTAAAGATGTGCTTGCCGACGTCGACCTCCTA  
CACCGCGAAAACGTCAAGGTTCGGCGCGCTTTCCGGAGGCGAACAACGACGCCTTGATTTG  
GCCTGCGCACTGCTTGGCGACCCCTCAATTTTGTTCCTCGACGAACCCACCACCGGCCTC  
GACCCAGAATCTAGGCGCCACACCTGGCAACTCCTGCTGGACCTGAAACAGCGCGGCGTC  
ACCATGATGCTGACCACCCACTACCTGGAGGAAGCCGAATTCCTCTGCGACCGGATTGCC  
ATCATGAACGCCGGTGAGATCGCAGTGGAAGGCACCTTGGATGAACTGGTGGCCCGCGAG  
AAGTCGATCATCAGTTTCGTGCTGCGTGGCGGGCAGGTGGAGTTGCCGGTCTTGAGTGGG  
GCTGAAATCATCCGCGACAACAACACGTCCGCATCGCCACCACCACCTGCAGCAGCAC  
ACCTTAGAAATACTTACCTGGGCTGCAGAGACCGGGATCGCGCTGGAAGGCTTCGCTGCA  
AAACCCGCCACCTTGGAATCCGTATTCATGGAC

>RXA01219-upstream

CACCATTGTTGGGAAACCGATTCCCCAGTTGATCCGGACCCATACTTGTCTTCCTATGACTG  
GGCCAAGACCACCGCTGCGACTTCCTAAGAGATAAAAATC

>RXA01219

ATGGACATTTTACTCAATCAGCTCGTAGCCGGGCTTTCAGTTGGATCGGTCCTTCTATTG  
GTCGCAGTGGGATTGTCACTGACCTTTGGACAGATGGGCGTTATTAATATGGCGCACGGA  
GAGTTCATCATGGTCGGCGCATAACCCGCATATGTGGTGCAGCTGGTCGTCGGTTCTGCC  
GGTTTATCCCTACTGATCAGCATTCCGCTGGCCTTTATTATCGGTGGGCTTTTCGGAGTT  
CTCCTCGAACAATTCCCTGCTGAAGTATCTTTATCACAGGCCACTAGACACGCTGCTGGCC  
ACATTCGGTGTGCGTTTGATCCTTCAGCAGCTGGCCCGAAACATTTTCGGAGCTCCCGCA  
GTGGATGTCAGGGCACCGGAATTTCTCCGCGGAAACGTCGAAGTTCTAGGCGTCTTGGTG  
CCGACCGCGCGACTATTCATCCTGGCGCTGGCCATCGCATCAGTGAAGTGCAGTGTG  
TTCCTAAATCGCACTGCCTGGGGCCGACGCATCCGCGCCGTGGTTCTGAACCGCGACCTC  
GCGGAAACCGCAGGTATTGATACCCGAGCTACTGACCGAATGACGTTCTTTGTGGGCTCC  
GGTCTTGCCGGAATCGCCGGGGTAGCTATCACATTGATTGGCGCGACCGGCCCCACCATC  
GGTCAGAACTACATCGTGGATGCCTTCCTTGTGTTGCCGCGGTGGCATCGGCCGGGTG  
AAGGGCGCTGTGATCATGGCTTTCGTGCTGGGAATTACTCAAGCATTCGTGGAATATACG  
ACAGGTGCGAGCATCGCGAAGTTCATCGTACTCATCGCTGTTGTTGCCTTCCTGCAGTTT  
AGGCCTCAAGGACTCTTCCAAACCCAAACTAGGAGCCTCGTA

>RXA01219-downstream

TGAGCACTCAACTCAAGCTGAAG

>RXA01220-upstream

CAGGTGCGAGCATCGCGAAGTTCATCGTACTCATCGCTGTTGTTGCCTTCCTGCAGTTTA  
GGCCTCAAGGACTCTTCCAAACCCAAACTAGGAGCCTCGT

>RXA01220

ATGAGCACTCAACTCAAGCTGAAGAAGCCCGCAAAGAAGAAACTACGCCGAAACTTAGC  
GTCGTAAATGCTCCACGCTGCGCACTGCGGCGTTGGGCTGGCCGCGCTCGCTGCGGTA  
TTGCTGTGCGCCCCGCTCTTTTTATCCACATTCCAGCTGACGTTGATGTGCGGCTTGGTG  
TGTTATGCGATCGTCGCGAGTCGGCATCGGGCTGGCGTGGGGCAGAGGCGGCATGCTCACG  
CTGGGGCAAGGCGTGTCTTTTGAATCGGCGCGTACATCATGGCCATGCACATGCTGTAC  
AGCGATTTCGCGAGATTTTGGGACCACAGTTCCGCAATGGTGGTCCATTTTGGCCAACCCG  
GCAGTCGCACTCATCGCAGTTGTGGCGCTTCCCGGCATCGTGGCTTTTGTGCTCGGCTTC  
TCCATTTTCAAACGACGCATCAAAGGCGCCTACTTTGCCATCGTGAACCAAGCGCTCGCC  
GCAGCTGTTGTGGTGTGCTGGTTCGGACAACAAGATTCCCTTGGAGGTTCCAATGGTCTT  
TCCGGATTTTCGATCGTTCATGGGTTTGGCGTCTACGACCCCATCAACCGCATCATGTTT  
TACTTCACCGCAGTGGGAGTTCTCTTGGCTTTGGTGGCTATCTCATATTGGCTCATGCGC  
AGCCGCTATGGAGAAGTGTGCTGGCCACCAGAGATGCAGAAGAACGCGTCCGATTCCCTC  
GGATATGATCCCGCATTGATCAAAACCGCCGCATATGTCATTGCTGCGATGATTGCCGGA  
ATCGCCGGAGCGCTGTTCGTGCCGATCGTGGGCATCATTTACCCGCGAGAAATCGGCGTG  
GTGCCATCAATCGTGTTCGTGATCGCCGTCGCCGCTGGTGGCAGGGCATCCCTATTCGGT  
CCCGTAGTTGGCGCGCTGGTGTGCTGGGCTGGGTGGAATCCACACTTGCTCAAACCTTTCCC  
AGCATGTGGTCTTATTTCCAGGGTGCATCCTGGTTCTCGTGATCGTGTGCTGCCGGGC  
GGAATTGCTTCAATTAAACTTTCCGCGCTCAAAAATAAGGCCAGGAAGGCCACCTCA

>RXA01220-downstream

TGAGCCTTAAATCACCAACCTC

>RXA01221-upstream

TCCAGGGTGCATCCTGGTTCTCGTGATCGTGTGCTGCCGGGCGGAATTGCTTCAATTA  
AACTTTCCGCGCTCAAAAATAAGGCCAGGAAGGCCACCTC

>RXA01221

ATGAGCCTTAAATCACCAACCTCAAAGTCGCTTTCGGGTCGTTTCATCGCCGTGAATGAG  
ATTAGTTTTAGGTGCTGCCCGGTACGTCCACTTCCTCATCGGTGCCAACGGTGCAGGT  
AAAACCACCTGCATTGACGCGATCAGCGGATTGGCGCCGGGGCAGGGATCAGTGCAGTTG

GATGGCACTGAGATTCTGGGAACCCCTGTGCACCGCATTTGCTCGGATGGGTGTGGGGCGA  
ACGTTTCAGACCGCCAGCGTGTGTTGAAGAATTGTCTGTGTTGCAGAATCTGGATATTGCG  
TGCGGGATTCATCGTCCGTTGCGGGCGCTTCTCGGGGTGCGTCATCGGATTGATCCCCGA  
ATTGAACACGCCCTGGAGGTCACGGGTCTTGCTGATCTGGTGAATGCTCAGGCGGGAACC  
TTGTTCGCATGGGCAGAAACAGTGGCTGGAAATTGCAATGTTGCTGGTGCAGGATGCGCAG  
GTGCTCATGCTGGATGAGCCGGTGGCGGGCATGAGTGAGGAGGAGCGTGTGCAACGGGT  
GAGCTTTTGCAGAGGGTTGCGCGGGGACGGGTGGTGTGGTGGTGGAGCACGATATGGAG  
TTCATGCGTCGTTTTGCCACTCGCGTCACTGTGATGAATCGCGGCACGATCTTGTGTGAG  
GGGTCTGGTTCGATGAGATTCAGGCGAATCCGGATGTGCAGTCCATTTATTTAGGTACGGCA  
GGGAAG

>RXA01221-downstream  
TGAGTTAGTCATGTTGGAAATCA

>RXA01222-upstream  
AATCGCGGCACGATCTTGTGTGAGGGGTCGGTCGATGAGATTCAGGCGAATCCGGATGTG  
CAGTCCATTTATTTAGGTACGGCAGGGAAGTGAGTTAGTC

>RXA01222  
ATGTTGGAAATCACTAATTTGTGTGCAGGTTATGGCCGCACGCAGGTACTTCATTCTCTT  
TCAATCTCCACGAGCAGCAACGGCATCCTGTCGATCCTCGGCCACAATGGCGCTGGTAAA  
TCCACCTTGCTGCGAACCGCGGTGGGGTTGATTAAGCCGACTTCCGGAGAGGTCAAACCTT  
TTCGGCCAGGATGTCACCTCGTTGTCCACGCATGAGCGAGTAAAGCGCGGAATGGCTTAT  
GTGCCGCAGGGCCAGCAGTCTTTTACGCAGCTTAGTTGCATGGAAAATTTGCAGGTGGTA  
GCGGATCTGCAGGGACGTGTGGGCAAGGCACGCATCGCGGAGGCGCTTGATCGCTTTCCG  
GCGCTGACCCAGGTGCTGGACCGCCAAGCCGGCCTGTTGTGCGGGTGGTTCAGCGTCAGCAG  
CTTGCCATCGCCCCGCGCGCTGATCACGGCGCCAAAGCTTTTGTCTCTCGACGAACCCACC  
GAGGGTATTCAGCCTTCGGTGGTTGCTGAAATTCAGCAGACCATCATCGATTTGGCTAAG  
GACGGCATGAGCATTGTCCTGGTGGAGCAAAACATTGGTTTTGCATTGGATGCTGCAACA  
AGCTACGCCATTGTGGCGCGTGGTCAGGTCGTGGAATCGGGACAAGGCGCTGAAACCACC  
GCAGAGAAGCAGACTAAAGTGCGGGAATCTCTAGCAATC

>RXA01222-downstream  
TAGCGGCTGTGGATAGCGTTTTG

>RXA01235-upstream  
TTCTGAAGCTGTGCCGGCCGCTGCTTAAGTTTTCTGTGCTGAAGAGAATTTTCCTCAACCC  
CTGGGTGGCTACCGCGTTGTGCGGTAGTCATTTTGGGGTTT

>RXA01235  
GTGGTGCTGTTTTTCAGGTTTTAGCGGTGTTATTGATTTAAGCCCCACAGCAGTGATTAGA  
CATTTGAGTGGGCAGGACACGCTCACCCCTCGAGATCAGGCCATCTTCTTTGATATCCGG  
CTGCCTCGAATTATCGCTGGTGTGTCATTGTGCGGAGCAACGCTGGCTATTTCTGGTGCTGCT  
TACCAAGCGGTATTTAGAAACCCGCTGGCTGATCCTTATTTGTTGGGTGTGTCCGCAGGT  
TCTGGCCTTGGTGTACGGCAGTGATTGTTGGCGGTACCGTGCTGGGATTTTCTGCACCG  
AGCATCGGCGTGATTGGTGCAGCATTTGTAGGTGGTGTGCGCGAGTACTTGCCACGCTG  
ATGGTGAGTCGGGGAGTAGGACAGGGATCATCAACCACCGTGGTTATTTTGGCGGGCGTG  
GCGGTTGCTGCTTTTGCCAGTTCCATCCAGACCTATATTCAGCAACGACACATCGATACG  
GTGGCGCGCGTATATGTGTGGATGTTGGGCAACCTCAATGTCACCAACTGGATGTCGATC  
TTCATCGTGGCTGTGGTGGCGGGACTATGCGCGGCCGTGATCATGTCCTGCGCCAGGTTG  
TTAGACGTGATGGCTGTTGGTGTGTTGGAAGCCCGCACATTGGGCGTCGATCCAGGCCCTC  
GTACGCATTGGCATTGTCATCGTGGCAACCCTTGGTACAGCTGCAGTGGTATCCATTTCC  
GGTCTCATCGGGTTTGTGGGCATCATTGTTCCGCACGCCCTGCGCCTAATTGTTGGCCCG  
GGGCATCGGATTTTACTGCCACTGTCTTTCGTATGGGGTGCCATTTTCTCTCGTGTGGCA  
GATACCGCAGGGCGAACATTGATGGCTCCTCAGGAACCTCCCGTGGGTGTGGTGACAGCT  
GCACTCGGCGCACCGTTCTTCTTATTTATTTTGGCGAGAACCAGCAGACAACGAGTTCCA  
AAAAGGAGTGCT

>RXA01235-downstream  
TAAGTGCGGATCATTGAATGCGA

>RXA01260-upstream  
CTAAACGTGGGCTGCATTCCTTCCAAAGTCTCTGATCAAAAACGCTGAAGTTGCCCATAC  
CTTTACCCATGAGAAGAAGACCTTCGGCATCAATGGCGAA

>RXA01260  
GTGACCTTCAACTATGAGGATGCTCACAAGCGTTCCCGTGGCGTTTCCGACAAGATCGTT  
GGAGGCGTTCATTACTTGATGAAGAAGAACAAGATCATCGAAATTCATGGTCTTGGAAC  
TTCAAGGATGCTAAGACTCTTGAGGTCACCGACGGTAAGGATGCTGGCAAGACCATCACC  
TTTGATGACTGCATCATCGCAACCGGTTCCGGTAGTCAACACCCTCCGTGGCGTTGACTTC  
TCAGAGAACGTTGTGTCTTTTGAAGAGCAGATTCTTAACCCTGTTGCGCCAAAGAAGATG  
GTCATTGTTGGTGCAGGCGCAATTGGAATGGAATTCGCCTACGTTCTTGGTAACTACGGT  
GTAGATGTAACCGTCATCGAGTTCATGGATCGTGTGCTTCCAAATGAAGATGCTGAAGTC  
TCCAAGGTTATTGCAAAGGCCTACAAGAAGATGGGCGTTAAGCTTCTTCCTGGCCATGCA  
ACCACTGCTGTTCCGGACAACGGTGACTTTGTGAGGTTGATTACCAGAAGAAGGGCTCT  
GACAAGACAGAGACTCTTACTGTTGATCGAGTCATGGTTTCCGTTGGTTTCCGTCCACGC  
GTTGAGGGATTGTTGCTTGAACACTGGCGTTAAGCTCACCGAGCGTGGCGCAATCGAG  
ATCGATGATTACATGCGTACCAACGTCGATGGCATTACGCCATCGGTGACGTGACCGCC  
AAGCTTCAGCTTGCTCACGTCGAGAAGCACAGGGCATTGTTGCCGCAGAGACTATTGCT  
GGTGCAGAACTCAGACTCTTGGTGATTACATGATGATGCCACGTGCAACCTTCTGCAAC  
CCACAGGTTTCTTCCTTTGGTTACACCGAAGAGCAGGCCAAGGAGAAGTGGCCAGATCGT  
GAGATCAAGGTTGCTTCCTTCCCATTTCTCTGCAAACGGTAAAGCAGTTGGCCTGGCAGAA  
ACTGATGGTTTTCGCAAAGATCGTTGCTGATGCAGAATTCGGTGAGCTGCTCGGTGCACAC  
CTGGTTGGAGCAAATGCATCAGAGCTCATCAATGAATTGGTGCTGCTCAGAACTGGGAT  
CTCACCCTGAAGAGATCTCTCGTAGCGTCCATATTCACCCAACGCTATCTGAGGCAGTT  
AAGGAAGCTGCACACGGTATCTCTGGACACATGATCAACTTC

>RXA01260-downstream  
TAGAATCCACCTCGTTGGCCCTG

>RXA01261-upstream  
GTGGGTGTTTTTCATTTCTTCCACTCTAAAATTAAGTATGGAAAACCAACCGCACCCGG  
ATGCACGACAATGACCCACTAAACACGTATCCTTGAATGC

>RXA01261  
GTGACTGAACATTATGACGTAGTAGTACTCGGAGCCGGCCCCGGTGGCTATGTCTCCGCC  
ATCCGTGCAGCGCAGCTTGGAAGAAGGTTGCTGTAATTGAGAAGCAGTACTGGGGTGGT  
GTTTGCCTAAACGTGGGCTGCATTCCTTCCAAAGTCTCTGATCAAAAACGC

>RXA01261-downstream  
TGAAGTTGCCCATACCTTTACCC

>RXA01269-upstream  
GATTATCTCTGCGCCGATTACAGCTGGCAATAGCAGCAGTTGTATTGAGAGCTCATGGTCCG  
TCCGATTCTATTTTCGTCAACCACGACCTGGGAAAGACGGT

>RXA01269  
GTGGTATTTGAGATGATTAAGTTTCGAACCATGCTTGAACCAGATGAAAAACATGTAAC  
GATGAACAGCGTCTAACTAAAGTTGGAAAGCTTCTGCGGGAAACGAGTTTAGATGAGTTA  
CCTACACTCTGGAATGTATTTAAAGGTGATATGAGCCTTGTAAGGGCCTCGACCTTTGCTT  
GTTAGCTATCTGGAACATTACTCTTCTGAACAAGCTCGACGCCATGAAGTTCGTCCCTGGG  
ATTACTGGTTTGGCTCAGGTGAATGGCCGTAATCAAACACTTGGGATGAACGACTTAAG  
TTGGATGTCGAATATGTGGATCGCTGTAGTTTGAACACTAGATTTCAAATATTAATCGCC  
ACTGTAAAAACAGTTCTTTCTAAAAAGGGCATTAGTAATGAAGGTCATGTCACGATGCCA  
TCCTTCATTGAAGAAAGAAAA

>RXA01269-downstream  
TAGCAGGTAAAAATTTTACTTTC

>RXA01291-upstream  
AACCCGCAGCGGGTGGAGCGGGGCTGAGGGAGACGTCGAGAAGCGTCCCTTTTCGGTTGTC



TGGATTTCTCGCGGTAAAGTTTCCTGTGAAGGAGGCGAGT

>RXA01291

GTGGCTGATCAGCAAGATTTTTTGGGCCGTTTTGATGCGATGAGCTCAAAGGCGACGGCC  
ACGGTAATCGCCCATTTATTCCTCCAGTTTTACTCTGGCATCGAAGCTGTTGTCGCCGAAA  
ATTCGTCGCGATATTGAGGCATTGTACGCAATGGTGCGAGTGGCCGATGAGGTTGTGGAC  
GGCGCTGCTGCTGCCGCGGGGTGTGCGCCGGACGCCGTTGCGGAGATTTTGGACAATTAC  
GAACGCCAGGTTCTGCTCAGTTTGTCCGTTCTTTTCATACCGATCCAGTGATCCATGCG  
TTTGGCAATACCGCCCGCAAATGTGGTTTTGAGCAGGCTCACATCGTGGCGTTTTTTGAT  
TCCATGCGCCGCGATCTCTCCCAAACCTCCTATGATCCGACTCAGTTGGATGAGTACATT  
TACGGCTCCGCTGAGGTCATCGGGTTGATGTGTTTGAAAATTTTCTCCAAGATTCCACT  
GCCAGCCCGCAGGATCGGGCCACGATGGAACACGGCGCCAGGCGTTTGGGTGCGGCATTT  
CAAAAGGTAAATTTCTGCGAGATCTAGCTGAAGACCGCGAAGGCCTAGGCCGTTCTTAT  
TTGCCGGTATTCACCGAAGAAATGCGCGATGAGATCGTTACTGATATCCGAGAGGATTTG  
GATGCCGCCCCGGCTGAGCATTCCGCTGCTGCCATTTGGCGCGCAACCGGTGTGCGCGCC  
GCGACCGATCTCTACGGTTGCCTCGTGGACAACCTGGAATCCGCGTCCCTCGAAGACTTA  
AAAAACGGGCGGGATTTTGTGCCGTCTTTAAAAAAGCCAGCCTGGCAACCAAAGCAATGT  
GGAAAGAAGTGTTCAAAAATGACAAAAGCAGTGGTCATCGGCGGGGGACTAGCAGGACT  
AGCCACCACCGCACTGCTCTTACGCGAAGGATA

>RXA01291-downstream

TGAAGTCCACCTCGTCGAACAAA

>RXA01292-upstream

TCCGCGTCCCTCGAAGACTTAAAAAACGGGCGGGATTTTGTGCCGTCTTTAAAAAAGCCA  
GCCTGGCAACCAAAGCAATGTGGAAAGAAGTGTTCAAAA

>RXA01292

ATGACAAAAGCAGTGGTCATCGGCGGGGGGACTAGCAGGACTAGCCACCACCGCACTGCTC  
TTACGCGAAGGATATGAAGTCCACCTCGTTCGAACAAAACGAGCACCTCGGCGGGCCGCGCC  
GGGACCTTCGAACCTCGACGGCTTCCGCTGGGACACCGGCCCCAGCTGGTACCTCATGCCC  
GACGCCATGTCCCACTTCTTTAAGCTCTGCGGCACCTCCATCGACGACCACCTCGACCTC  
GTGCCACTTGAACCCGCCTACCGCGTCATCGACGACCACGGCGAATTCATCGACGTCACC  
TCCGACATCGATGCGATGGCCGAGCTTTTCGAATCCCGCGAACCCGGCGCCGGCGCCAAA  
CTGCGCACCTATATCGACTCCGCCACACAGGTCTACAACCTGGCCATCGACGGCTTCCTC  
TACACCAACTTCACCAACTTCATCCCATACTTAAGCCCCGGCATGCTGCGCCTTTTACCC  
AAACTTCTAGCAAGCCTGTCGACCTCGCTAAAAGTCAAGGTCAACACCCAATTCCGCGAT  
ACAAAACCTGCGCCAAATCTTAAGCTACCCCGCAGTTTTCTCTCCTCAGACCCTTCGCAC  
ACCCCGGGCGCTCTATCACCTCATGAGCCACACCGACCTCGTCCAAGGCGTCTCCTATCCC  
CGAGGCGGGCTTCACCGCCTTCATCAAGGCACTAATTTGCTTATCGACGACGCGTCTCCTC  
CACCTCGGCACCCCCGTCAGCGCAATCACCACCAAGGCCGAAACGCCACAGGCGTCCAA  
GTCGGCTCAGAGTTCATCGAAGCCGATATCGTGATCAGCTGCGCTGATCAGCACCACACC  
GAAACCCAACCTCCTACCTGCTTCGTTGTGCGCGAAGCCGGAGACGAGCTGGAAGAACAAA  
CAACCCGGCCTCAGTACTGTGCTGGTTTTTGGCAGGCGTGAAGGGGGAGCACACCCTGCTT  
TTTCTCCGACTGGGACGAAGATTTCCGCAAAGTTTTTCGACGGCTCCACCCCAAGATTCC  
CGGCTTCAGAATCCATCTAGATCTCCAAGACCTCCGCAACAGATTCCGATGCCGACCCCG  
AAGGCCACGAGAACCTCTTCATCCTGGTCCCAGTACCCGCCGATGTCTCCATTGGTACG  
GGTCCGCTTACGGAGAAGAATCTGACATGGTGGGCCGGATCGCAA

>RXA01292-downstream

TAGCAGCAGTGGCTCAAATTGGG

>RXA01293-upstream

CGATGCCGACCCGAAGGCCACGAGAACCTCTTCATCCTGGTCCCAGTACCCGCCGATGT  
CTCCATTGGTCACGGGTCCGCTTACGGAGAAGAATCTGAC

>RXA01293

ATGGTGGGCCGGATCGCAATAGCAGCAGTGGCTCAAATTGGGCGATGGGCTGGCATTGAT  
GGTTTGGAAAGCCGCATTGTTGTGACGCGCACCATCGGCCCTGCCGACTTCGCAGACCGA  
TACAACTCCTGGAGCGGCGGGTCCATTGGCCCCCTCACACACCCTGGCACAATCGGCGTTC  
TTTAGGGGTCTAACAAATCCCGCAAAGTAGATGGCCTGTATGACGCGAGGTGACACCACA

GTTCCAGGGGTGGGCGTATCTATGTGTTTGATCTCTGCAGAAAACGTGCTCAAGCGTCTC  
CGCGGGGACAACAGTGTGGATCGGACT

>RXA01293-downstream  
TAACGGGACTTTTTTCTTTTGCT

>RXA01339-upstream  
GAGAAGGCGGAACCGAAGGAATCGAAGAATATCTCTCCGTGCGTTACCTCGCTTTGCCGT  
GACACATGAGCTGTCCGGTGAATAACCCGAAGGAAAAAAC

>RXA01339  
ATGACTACCGAATCAATAGTTGCGCACAATGCTGCAGGTACAGCACCTCAGAATGTGTCC  
TCTGCTAAGAAGAAGTACCTCAGCGTTGCCCAAGGCGTTGCCCTTATCTACGGAACCAAC  
ATCGGCGCCGGTGTGCTCAGCCTCCCATACGCTGCCCGCAACGGTGGTTTCCTCGCCCTG  
GTTGTTGCCCTGCTCATTGCGGGAACACTGACCACCATCTCCATGCTCTACATCGCCGAA  
GTATCCCTGCGCACCAAGAAGCCACTGCAGCTTTCGGGCTGGCAGAAAAATACCTGGGG  
CAGTGGGGCCGCTGGCTGGTGTTCATTGCCATTGTGGTCAACAGCGTGGGTGCACTGATT  
GCCTACGCATCAGGATCCGGCATTTTGATAGGCAACCTCACCGGCCTGCCACCAATCGTG  
GGCACCTTGGATTCTTTGTTTTAGGCACCTTGATCATGTGGAAAGGCCTGCACACGGCA  
AGCTTCGTGGAGGCATTGATCACCCTGGCATGGCAACGATCATCATCGTGCTGTGTGGA  
TGGACAGTGCTTGGCCCTGGAATTTCCGCAGACAACCTGATCGTGTTCCACCCATTCTTC  
ATCGTTCGGATCATGAACCTCGCGGTCTTTACCTTCCTTGCCCAATATGTGGTTCAGAA  
ATCGCACGAGGAGTTAACCTGCCACCCCGAAGGCAGTGCCACGCGCGATCATCATCGGC  
ATGGTCGCAACTGGTGTCAACCTGGCAGCTGTACCATTGCGGGCACTAGGGCTTCTGGGC  
ACAGGCGTCAGTGAAGTTGTCAACCTCTCCTGGGGCGAAGCACTCGCCCCAGTGGCCTAT  
TACATGGCCAATGCCTTCGCACTATTGGCCATGTTCACTTCATTTCATCGCCATTGGATT  
ACCGCGATGCGCAACGTACTAGATATTGGCCACTGGCCACAACACGGATGGCAGCGATCC  
GTTGCTGTGCGGACTAACTGTTCTTCCACCACTGGCAATTTCACTTGCGGGATTAGGCGGA  
TTCGTGGCAGCACTGAGCTACGCCGGAGGATTTGCCGGAGCAATCATGTCCATCATCCCC  
GTGCTGTTGCTGCGCAACTCCCGCAAGAGTGGCGACCAAGAACCAGTGTGGAAAGCCACC  
TGGCAAGCGCACCCCATCTTCCAGATCCTGTTGATTGTGGTGTACTCCCTGGCGTTTGTG  
TACTCGGTTCTCGCGATCGTCGGATTAATGCCTGCGGGTTGGGCA

>RXA01339-downstream  
TAGTCACTTCCTGTTGTGGCTGC

>RXA01382  
TCCACCTCCACCGCAGCTGGCACCGGAACCTGCAAATGAAGAAGGCACCATCACCGCAGCC  
ATCTCCTACGAACTGGGAACCAACGGCTACGACCCAATGACCACCACCTCGGCTCTCACT  
GTGGCAGCCAACCTGGCACACCCTTGAAGGCTCACCAGAAATCGACCCAGCCACCGGCGAG  
GTCTACGCAGCACTCGCCAGCGCACTGCCTTCAGCCGATGCGACCTCCCTAGACATCAAG  
CTTCGCGACGGCGCCACCTTCCACAACGGCGACGCACTCACCAGACGACGCTAGTCTTC  
TCTTTTGAGCGAGTCTTCGATCCAGCCAACAACCTCCCTTTACGCATCCTTCATCCCATT  
ATCAAGTCAGTCACCAAGAAGGATGACACCACCGTCACCATCGACCTCGACTACGCAACC  
GGCATCATCAGCGAACGCCTCGCAGTAGTAAAGATCGTGCCAAAGTCCGTCGTGGAAGCA  
GACGCATCCGGATTTCGACGCCAACCCAATCGGCTCCGGGCCATACAAGATGACCGACAAC  
GGTGCATCCAAGGTGGTCAAGTTCGAGCGCAACGACGACTACAACGGGCCACGCCCAGCA  
CGTGCCGCCAAGATGGAATGGCAGATCATCCCCGACGCCTCCACCCGCACCAACTCCCTT  
CAGTCCGGCAGCACCATGGCCATCGACTCCGTTCCATACCTGTGATCCACAGCTTGAA  
GCCACCAGCACCGTAGAATCCGTCCAAGGATTCGGCCTCCTGTTGCGCATGTTTCAGCTGC  
TCCGAAGGCAACCCCTTCAACGACGTCCGCAACCGCCAGGCATTCTCTACGCACTGGAC  
ATGGACAAGATCGTTAAGACCGGCATGTCCGACCAGGCAACCCAGCCACCTCCTTCGTG  
CAGAAGGAACACCCCAACTACAACCAGGCATCCACGGTCTACTCCCTCGACGCCGACAAA  
GCCAAGGCGCTGTTGCTGAAACCGGCCTTACCAGCCTCAACCTCCTGTGCACCGACCAC  
GACTGGGTCAAGAAGTGCACCCCACTGATCCAGGAATCCCTC

>RXA01399  
ATTCTCAGCCCCGCAACCGCACTTGTCTGGCGATTGGATTGATTGCTGCTGCAATTATC  
CCTCCCCTGCTTGCTGCTCGCGGAGTTAAAACAGCCGAAGCCCGGCGCGCTGAATCCAGC  
GAAGCCTACTTGAGTTCCTTGGATCAGGTGCTGTCCAACCGGCGCGCTTCGTGTTTCGT  
GGTGAATGCCGGCCGCTCTGTCCAAGGCGGATGTGGCTGCGCGTTCTTCTTCTCA

CTGGAGGCAGGCGCGAAAGACACTGCCATTGGCGCAGCGAGTTCCCTGTGGATTACCGGT  
TTCACGTGTCATTGGTGTGCTCATGGTTTCCGCGTCACTGTATGCAGATGGAAGCCATTCA  
CCGCAGTGGTTTGGTGTGTTGGTGTGCTTTTCACTCGCAGCTTTCGAGGCTGTCTCTGTT  
CTCCCCGATGCTGCGATTGCTCGTACCCGCGCCGAGATGCCACCAGGAGGCTTGCGGAA  
ATCTCGGCGCTGCCAGAATCTGTCTCTCTTGAGCTTCGCACGGCCTCTGACCAGCCCGTA  
TTACGCGCCGAGAATCTAGTTTATGGATGGGACAGCGACCTAGGCACGAGCAACCTGGAT  
CTCACCTTTGGTTCACGACATGAAATCATCGCACCCCTCTGGAACTGGCAAAACGACCCTG  
CTGCTCACACTTGCGGGGCTGTTGGAACCTCGTGGAGGCCAAGTGCTTATCGACGGCACC  
AATCCTTCCGAGTTGAAAAACGCCGTGCTGTTCACTCCAGAAGATGCCACATTTTGGC  
ACCACTGTCCGAGATAACTTAGCACTCGGAGCACCGGAAGCAACCGACGCGGAAATGACA  
TCGATCCTGGAACATGTTGGTTTGTGAGAGTGGGTTCAGGTTTACCCGATGGTCTTGGC  
ACTGTCCTTGATTGAGGTGCCGATAGTCTCTCGGGAGGTGAGCGCCGCGCCTGCTCCTT  
GCCCCGCTACTACTAAGTGATGCACCAATTCTGCTTTTGGATGAACCCACCGAGCACCTC  
GACACTGCAGGCTCCTCTGAAATCTTGTCTATGCTGGCCTCCGATGAACTCCCTGGTAA  
AGAGCTAGGAGAACCGTAGTGATTGTGAGGCATGTGAGG

>RXA01399-downstream  
TAATTTTGCCCCGCTGTCTTCTG

>RXA01419-upstream  
GCGCCCACTCATCGGCGAGCTTCAGGAGATGAGGTTGATGCTCCATTGATAATTTCTTTC  
GCTAATAGTCAAATGATCATTGAGTGTTAGTGTTTTCTC

>RXA01419  
ATGCTTCTTTCCGCCCCGACACACACGAGTTTCCAAGAACTTGGACTCAATGCTAGTCGG  
CGCAAAGCAATCAACTGGACACTGGCACTCACTGTGGTGCTAATTGCCTCCATGTTTGT  
GGCGTGCTCATCGGTGCATCCGGGACCTCAGTGTTTTCCACGTGGACCGTAATTAGCCAC  
CATCTTTTTGGCACTGAGCTAGGTGGCTCCGACACTGCCGACGCCATCATTGGTACATC  
CGCACCCACGCGTCTTGCTCGCT

>RXA01420-upstream  
CGAAGTTCACGACTACAGGCATTACCTGGGTGCTGATTTTGCGCGAGTAAAGCTGTGGCT  
GCGGAATGCGCTGCTCATCCACACGTGGAATCCTGATTGG

>RXA01420  
GTGACGCTGGGTGGATTGAATGTACCATCGTGGTTCGCTGGGCGCGGAAATGCTGTTCTAC  
CTGACGTTCCCGCTGTTTATTCCGTTAGTGCGCAAAGTGAAGGGCGTGGGCAACTGGTGG  
GCATTTGGCATCACCTTTGCCGTGAGCCTGGCGCTGATTACAGTGATTCACTTTTATGCG  
GACGGACCAAAGGGGATTGAGAACTTCTTTGTTTCCTCGCCTGTGGGACACCAATGTGTCA  
CCGGTTCGCGGAAGTTCACGCCGATCCAGTGTTGGTTTATGCAGGAAGAAATCCCGTGCTG  
GAATCTTACTGGCTGTCTTACTACTTCCCGCTGACCAGACTCATCGAGTTCTACCTCGGT  
GTGTTTGGCGCGAAGCTGGTTGCTGAAGGCATGTTTAAAAACACCAACATCACCATCCCG  
CTGATCGCACTGGCTGTTTCTTTTGTGCTACTTGGTTTGTGCCACTGGCATTCAAGATG  
TCTGTCATCATGTCCCTGCCAATGGCTTTTGTGTTGGCAACGCTTGCGGTGAGAGACATT  
GAAGGCAAGAGTGGGGAAATCGCCTCGCCTCGCGCAGTTTGTGTTGGGTAATATTTCTTT  
GCCTTCTACATGGTGCAATTCGCCGTCATGGTGTGTTGTGAGCGCTATTTTATTGCTGGC  
AAAGAATACGGCTTCTTGGCTGGGCATTCTATGCAGTGGTGTGTTTCATCGTGTGCGTC  
ATTCTCGCGTGGGTGCTGTTACCTTCGTTGATGATCCTT

>RXA01420-downstream  
TAATAAGGCCACGGAA

>RXA01467-upstream  
GCGTCATCTTTAGCCTTGCTTTATGAGCTTTTCCCCGCAATGAGCCGCGTTGTGTATCCA  
TAAGTCTTAGCCTACAAGCGCTTTGAGGTAGTTTGGGATC

>RXA01467  
ATGGATTTCAACGACAAAGCCGCTTCAGAAAACGCTGTAAAGACTGGCGCAGAAGGCCCC  
AACGTTTTTCGCGAGCGTGGCCAAGATTTTGCAGGATGTTGGCGGAATTTAGCCGAAGAC  
GTCACCTCCGGAATCTCGTTTTTACTGAGGATTTGGCAGTGAGCTCAATTACATCGAG  
TTGATTGTCAATGCGGAGGACGCATTTGGTGTTCGCATTGAGGACGCCGATGCCAAGGAT

TTGACCACCGTGCAGGATTTGATTGACTTTATTAACACCAATAAGGCTGAT

>RXA01467-downstream  
TAGCGGGAAAATTTGCGCCAAAA

>RXA01538-upstream  
TCTAAACTCACTCTCAACTCACCAAGATTGTTCAACAATCTGCGATTGGTGTGCAATCTA  
CCCCAATCATTTTGAAAGCCCCCACGAAAGGAGCGCGACA

>RXA01538  
ATGGCCGACAACAAAAATGCCGATGACAGCCAGCTAGTCTCAGCCAGCACTGGAACCCCT  
GGGCCTGGCGACATTGCAAAAGCCAATGCGCCATCCCTCAAGCAAGCTGCAGTAACCGCC  
TCTGGCCGAAGCGCTCTGATGGGTGCCATCTTCCTCATGGCAACTTCTGCCATCGGCCCCA  
GGGTTCCTCACCCAAACCGCTGTCTTCACCAACCAGCTCGGCGCAGCTTTCGCATTTGCG  
ATCCTGGTGTGATCCTCATTTGACATCGCGGTGCAGCTGAATGTGTGGCGCATCATCGGC  
GTCTCTGAAATGCGCGCCCAAGAACTCGGCAACACGGTTATCCCAGGTTTTGGTTGGGTG  
CTGGCCGTACTGGTCTGTATTGGCGGCGTA

>RXA01576-upstream  
ATCGGTGATCTTTCGCGATTGATACGTGCGCGATTGCGTGCCCGCCAGCTGCTCAAGATC  
AATGGATTTTCATGACAATCAAGTTATCATCACTGGGGTCTG

>RXA01576  
GTGGCACCTAACAGGAAAATCAGCCATCATGCACTAGGCTCTATTCCTATCATGGATGCA  
TCAAAAAACAGCGACTTTTAAAGACACCTGGCTAGTCGTACCTTGTATATAACGAGGCAACA  
GTTATCCGGGAAGTTTTAGAGAACGCACTCAAAACATTCCTAATATTGTTGCGGTCAAC  
GATGGCTCCCCGGACAACCTCCGCGGAAGAAATCCATGCGGGCCGGCGCACACCTGGTCAAC  
CACCCCGTGAACCTCGGACAAGGTGCCGCGATCCAAACCGGCATCGAATACGCCCCGCAAG  
CAACCCGGTGCAAAATACTTTGTAACCTTTCGACGCCGACGGCCAAACACCAAGTGAAAGAC  
GTTATCCGCATGGTGGAGCGACTGCGTGCCGAGGACGTGGACATTATCGTCGGCACGCGT  
TTTGAGCGCCACGCCAAGCCGATGACCAGGTGCCACTAATCAAGCGCCTTGTGCTGCGC  
ACCGTGGTCTGCTGTCACCGAAAACCCGCCGACTTGGGCTCACCGACGCCCAACACGGC  
CTGCGCGTATTCAACCAAAAAGTGCGCGCAGGAAATGAACATCCGCATGAACGGCATGTGCG  
CATGCATCCGAAATCGTCGACCAAATCGATGAACGCGGCTGGCGCATTTTCAGAAGAACCC  
GTAGACATCCTCTACACCGAATACTCCATGAGCAAGGGGCAATCCCTGCTCAACGGCGTA  
AACATCCTGGCCGACGGCTTCCTAGCGAGGAGACTCCCA

>RXA01576-downstream  
TGACGCAGACCACCACCCAAATC

>RXA01580-upstream  
CGGTAAACGCCTCATTTAAAGTCCAATGCCATGCTCATAACACTAACAGTTAACCGTGCGG  
TCAACTTTGCTCCCTATCCTTAAAAAGCCACAGAAAAGG

>RXA01580  
ATGTATAAGAATATGCACATTGTTGCCCATCGCGGTGCGGAAGATCTGCACCTCGAAAAC  
ACCATGACCGCTTTCCAGGCTGCCGCGCCCGCTGACGCTTTTGAGCTGGATATCCACGCC  
ACCGCTGACAATCAGGTCGTCTGTTATCCACGACCGCAGCGCGTGTGCGCGGCCA  
GATTCCTTGACCGCGACACCCCGGTGCGCGCTTAAGCGCCGCGCAAATCAAGGAGATA  
ACGCTTATCGACGGATCCCCCGTACCAACCCTGGAGGAAGTTCTACTCCAGACGAGCCTG  
CCGATCCAAGTGGAATCAAATCTGCCGGTGCAGTTCCAGCAGCCGCGAGCATTATTGCAG  
AAATACCCAGAGCACCTGGAGCGCCTGCTGTTTCATCAGTTTCATCGATGCAGCACTGGTG  
GAAATCGTGGATCGACTGCCAGAAGCTCGCGTGGGAATCTTGCGCGATGCGTCCATGGAT  
GATCTGCGCATTTCTTGATTACATCCCGCTAAAAAATGTGGGCGCGATCTTGCCCTCGTGG  
AAAGCACTAAACGTGGCGTCAATTGCTGATCTACATACCAAGGGAATCAAGGTTGGCTGC  
TGGACAATTCGGGATGAAAATGCGTTTGGGATCGCACAAAGCTGGCGTTGATTACCCC  
ACTGTTAGCGATCCCTCTCGTTTCTCGCGCCCTCCCCTGCTG

>RXA01584-upstream  
CCACCCCTTCCCCGCTACGCGCCATACCGGCTTGGGCGGGCATCGGATCACTA



>RXA01584

GTGGTGTGTTTTGGGCGCACTTCTCGGCGCCGTAATCATGGGCGGGTTTTATCCAGCATTC  
ATTCAAGCCGGATCCACAGTGTTTCGGCGGGCGGCCACGTGGTTTTTGCCACTGCTGGAAAAG  
CTCGTTGTTGCGCCCGGTTTTATTAAAGAAACCGACTTCCTATCCGGCTACTCCGCAGCG  
CAGGCAGTGCCTGGCCCCATGTTTCAGCTTCGCCAGCTACCTCGGCGCAATCTACGGTGGC  
ATCGGTGGTGCAGTGCTGGCCAGCCTGGCGATCTTCTTCCCCGCGCACTCTTGAGCATC  
AGCGGAATGTACTTTTGGGGACGCTGGCGAAAAGCACCGCGCATCCAAGCAGCAGTCACC  
GGCATCAACGCCGGTGTGGTGGGGCTTTTGGGCGCAGCGCTCTACGATCCCGTATTTCACC  
CACGGCATCACCAGCGTTTCCGCATTAGCTATCGCAACGGTGTGTTGGCTGGGGCTAGCC  
CACTGGAAAATTCCGCCGTGGGCCATCGCCGCGGGTGCGGCCCTTGACAGGCTGGGTCTTG  
CTT

>RXA01584-downstream

TAGAAAACGCTCAGACCCAAACC

>RXA01591

GCCTCACTTAACTGGTCAGTCATCGTTCCAGCCCTAGTCATTGTCCTAGCGACAGTGGTG  
TGGGGTATCGGATTCAAAGATAGCTTTACCACCTTTGCTAGTTCTGCGTTGTCAGCAGTA  
GTTGACAATCTCGGCTGGGCCTTCATTTTGTGTTGGCACAGTCTTTGTATTTTTTATCGTT  
GTTATCGCCGCTAGTAAATTCGGCACGATTTCGCTTAGGCCGCATTGATGAAGCACCCAGAG  
TTTCGCACGGTGTTCATGGATTTCATGATGTTTGCTGCAGGTATGGGTATTGGTTTGATG  
TTCTACGGAACACAGAACCTTTAACCTTCTACCGCAATGGTGTACCTGGACATGATGAA  
CACAATGTTGGCGTTGCTATGTCCACGACAATGTTCCACTGGACCTTGACATCCATGGGCT  
ATCTACGCAATTGTGGGCCTAGCCATTGCCTATTCGACCTTCCGAGTGGGCCGTAAACAG  
CTTCTAAGCTCTGCATTTCGTGCCACTCATTTGGTGAAAAAGGTGCAGAAGGATGGTTGGGC  
AAGCTCATCGACATCCTGGCGATTATCGCCACCGTATTCGGCACGGCATGTTCCCTTGGC  
CTTGGTGCCCTGCAGATTGGTGCAGGCCTGTCCGCAGCAAACATCATTGAAGATCCAAGC  
GATTGGACCATCGTTGGCATTTGTTTCTGTTTTGACCCTGGCATTTATCTTCTCCGCTATT  
TCTGGTGTGGGCAAGGGAATCCAGTACCTCTCCAACGCCAACATGGTTCTGGCAGCTCTG  
CTCGCGATTTTCGTGTTTCGTGTCGGACCAACCGTGTGATTTTGAACCTGCTGCCAGGT  
TCTATTGTGAACCTACCTGTCCAACCTTCTTTCAAATGGTAGGCCGCACTGCCATGAGTGCC  
GACGGCACACCAGGTGAGTGGCTTGGTGGCTGCACCATCTTCTAC

>RXA01604

GACACACCCTTCGCCGATGTTGAGATAGCTCCAGACAGCGGACTCACTTTGCTGAGCACC  
GGGCGCGAATCCCAATCCAGTTCCTTTTCTTTGGTACTTTCCGGCCGCATGCGCGCCTCC  
ACCGGAACCATCGAATTAAACGGCGAACCCATCAAGGCAACCAAGCTGGCCAAGCATGTG  
GCTTTGGCGGGCATCCCTGAAATCGATTCACTCGAGCGACTTGTCACTGTGCGCACCGTT  
GTCCGTGAACAACCTCGCCTGGTCAAGCCCTTGGTACCTGATGGTGCCAGGGATATTAGT  
GATTCGGGACGGTGGGTGACGTCGAAAAGCATCTTGGCCTGAACCTGAACCTAAAACC  
TTAATCGGCGACCTCAGCGTGCTCGAGCGTTTTAAGCTGCGCATCGCGCTGGCGCTGCTG  
GCGCGGCCAGAGGCGCAACTGTTGGTTCGTGGATGATCCCGATCAAGTGCGCAGCATGGAA  
TTGCGTGCGGAGGTGTTGCACGCATTGAAAGGCGTTGCAGAGGATCTCCCTGTGGTTCGTG  
GTATCCACCAACCCAGATTTTGATTCTTTGGCCGATACCGCTTTGACCATTAACGGGGGCT  
GGAAAC

>RXA01604-downstream

TAATGGCATTTTTTACACTTTGGC

>RXA01614-upstream

TGCAATTTCGCAAACATGAGTAGTATCGCGGAAGTTTCACCACGTGAACATTTTCAGTCGAC  
TCGCGCACACCACACCAACAATCGACCTATCGTTATACGT

>RXA01614

ATGAATCAGATGCAGCAGTGGAAACCAGACTTCCTGGGAGAGGGCTACCAAAACCTCACC  
ATCGAGCTCGGCGACGACCCGGATAATGAAACAGATGTTGTGACAACGGTTGTGCGCTAC  
AACCCAGACAATCACGCGGACGAGTCTTTTGTGCCCCGCCAGCGTTGCTGTGGGTTTAC  
GGCATGACGGACTACTTCTTCCACACTGAATTCGCGGAGTTTTTCCACAATGCCGGTTTT  
GCTGTGTACGGCATTGATCTTAGAAAATGTGGACGCTCCTACCGTCCAGGACAGCAGTGG  
CACTACACCTCTGATCTTGCCCATTAATTCCCTGACTTAACAGCTGCTGCCGAGGTCATC  
TCTTCCACCCACCCTGAGCTAGTCCCCGTCGCCCATTCCACTGGTGGACTCATCGTTCTT

CTGTGGATGTCCCAGATGCGCACAAAGCAATCCAGCTGCCATTGAGAAGATTCCAGCGCTG  
 GTCCTCAACAGTCCGTGGCTGGACATGATGTATCCACCACTGTTTCATCAAGCTGATCACC  
 CCTATGGTGAGGGTGTGGGCAAACGCTCCCCACAACCATCATCCCAGGCGGAGGTTTG  
 GGAGCATACGGAAAATCGATCCATAAGAACTTTTACGGCGAATGGGACTTTGACACCACC  
 ATCAAGCCTGTAGAAGGACATAAAAAGAGCATCGGATGGCTTCGGGCAGTCATGGCTGGC  
 CAAGCAGAAATCCATCACGACCACGTGAATGTCGGAGTGGACGTGCTCACGCTGTGTTCA  
 AATAAGTCCTGGTTGAAGTCTGAATACACAGAGGACACCAACACTTCAGACGCGGTTTGT  
 GATGTGAAACACATTCAAAAGTGGGCTCCTCATTTGAGCTCGCCATCGTCCAGGGTTGAT  
 GTTGAGATCATCGACAACGCTCGCCACGATATTTTCTCTCAAGGAAACCCGCCAGAGAT  
 CACGCCTCTGAAGTACTCAACAACCTGGCTGCAATCGAAGCTTTCCAGCCTCAAACCATCT  
 CAA

>RXA01614-downstream  
 TAACACCGCGAATTATAGACTGA

>RXA01629-upstream  
 CAGGAAGAAGTTAACACCGCCCCAGGGGTGCGTTGGATGATGATCATCTACAAACAAACAT  
 TCCGTTATGCACTCATAAGATATGACGAGAGGTTTTACTC

>RXA01629  
 GTGAGCCCGATTTCGCTCAAAAAAGAAAATCAAGAACGAACCAAGACTAACAGTCGATGAC  
 GTCAACGTTGTTCCCCCAAAGAAGATCCGTCCGGCCATTAAAGGCACTGTGGTGGGTAAC  
 TTCATGGAGTGGTACGACTTCGGAATTTATGGTTATTTGACGGTCACGATGACCGCAGTA  
 TTTACCCAAGGCCTGCCGCAAGAATGGCAGTTGTTGGCCGTGATGTTTGGTTTCGCGGTG  
 TCTTATTTAGTTTCGCCCCGCTTGGTGGCCTGGTTCTGGGTCCGCTTGGCGATAAGGTTGGC  
 CGCCAGAAGGTTTTGTACGTAACCATGGCCATGATGGCCGTGTCTACGGCGCTGATTGGC  
 TTGCTGCCGACGGCGGCGTCGATAGGCGCTTGGGCTTTGGTGCTTTTGTACCTGTTGAAG  
 ATGGTGACAGGGATTTTCGACTGGTGGTGAATATGCTGGTGCGACCACCTATGTTGCTGAG  
 TTTGCGCCGGATCGTCGACGAGGTTTCTTCGGAGCTTTCCTAGATATGGGTTCTTACCTG  
 GGCTTTGCCGCGGGTGCTTCGGTTCGTGGCGATTACTACCTGGGTGACCACTCACTTCTAT  
 GGCGCAACTGCCATGGAGGATTTTCGGTTGGCGTATTCCTTTCTGACTGCGATCCCGCTG  
 GGCATCATTGCGGTGTACCTGCGTACTCGTATCCCTGAGACCCCTGCGTTTGAGAACAAC  
 CAAGACGAGCCAAATGCAGTTGTTGAAAAGGACACTGAAGATCCTTATGCACGCCTGGGC  
 CTGGCTGGTGTATCCGCCACCACTGGCGTCCACTGCTGATTGGTATTGCGATTGTGGCA  
 GCGACCAACACCGCCGGTTACGCGCTAACCAGTTACATGCCTGTGTATCTAGAGGAGCAG  
 ATCGGTCTGCACTCCGCATCCGCTGCCGCTGTGACCGTGCCGATTCTGGTTGTTATGTCC  
 CTGCTGCTGCCATTTGTTGGTATGTGGAGTGACCGCGTGGGCCGCAAGCCTGTCTACGCG  
 ACTGCTGTTGCGGCAACGCTGATCTTGATGGTTCTTGCCTTCTTGATCATGAACACCGGA  
 ACCATCGGCGCCGTACTGATTGCACTGTCCATGGTTGCTATTCCAACCGGTTTGTATGTG  
 GCACTGTCCGCATCTGCCCTGCCAGCGCTGTTCCCAACCGCGTCACGATTCTCTGGAATG  
 GGTATTTCTTACAACATTTCCGTGTCGTTGTTTCGGTGGTACAACCCCGCTGATCACCAG  
 TTCCTGCTGCAGAAGACTGGCCTGGATATCGTTCCAGCGCTCTACATCATGTTCTTCTCT  
 GCAATCGCAGGTGTGGCGCTGCTGTTTCATGACCGAGTCTTCACAGAAGCCACTGCTTGGC  
 TCATTCCCAACCGTGGAACCAAGTCTGAGGCCGTGGAGATCGTGAAGAACCAGGACGAG  
 GATCCAAATATTGATCTTTCCCATATGCCGTTTCTGATGAGGAAACGTAGGTGCTGAA  
 AAGCAAAACGCA

>RXA01629-downstream  
 TAACCGTAAAGCCCGCTGCAAGG

>RXA01644-upstream  
 GTAGGTAGAGGCTTGTGGTCACTACTTGTGGCCACATTTTAAAAAATGCACAAGAAGAG  
 AAAGCAAAGCATTATGAGTAACGCCGTAGCGCAGGACCTC

>RXA01644  
 ATGACCATCGCCGACATCGTCGAGGCCACGACCACTGCACCCATCCCATTCACATCACT  
 GCCTTCGATGGAAGCTTCACTGGCCCTGAAGATGCTCCCTACCAGCTGTTTGTGGCCAAC  
 ACGGATGCAGTATCCTACATCGCAACAGCGCCAGGAGATTTGGGTTTGGCACGTGCCTAC  
 CTCATGGGAGACCTCATCGTGGAAGGTGAGCATCCCGGCCATCCTTATGGGATCTTTGAT  
 GCGTTGAAGGAGTTCTACCGCTGCTTCAAACGCCCGAGATGCATCCACCACCTTGCAGATC  
 ATGTGGACTCTGCGGAAAATGAATGCCTTAAAATTCCAGGAAATTCCACCAATGGAACAA

GCCCCTGCATGGCGTAAAGCACTGATCAACGGGCTAGCATCCAGGCACTCGAAATCCCGC  
 GACAAGAAAGCCATTAGCTACCACTACGACGTGGGCAATGAGTTCTACTCCCTGTTTTTA  
 GATGATTCCATGACCTATACCTGCGCGTATTATCCAACGCCAGAATCAAGTTTGGAAGAA  
 GCCCAAGAAAACAAATACCGCCTCATCTTTGAAAAACTGCGTCTGAAAGAAGGCGATCGC  
 CTCCTAGACGTGGGATGCGGTTGGGGAGGCATGGTCCGCTACGCCGCCAAACACGGTGTG  
 AAAGCCATCGGAGTTACGCTGTCTGAACAGCAATATGAGTGGGGTCAAGCAGAGATCAAA  
 CGCCAAGGTTTGGAAGACCTCGCGGAAATTCGCTTCATGGATTACCGCGATGTTCCAGAA  
 ACTGGATTTCGATGCGATCTCAGCAATCGGCATCATTGAACACATCGGTGTGAACAACAT  
 CCCGACTACTTTGAATTGCTCAGCAGCAAACTCAAAACAGGCGGACTGATGCTCAACCAC  
 AGCATCACCTACCCAGACAACCGCCCCCGCCACGCAGGTGCATTTATTGATCGCTACATT  
 TTCCCCGACGGTGAACCTCACTGGCTCTGGCACCCCTGATCAAGCACATGCAGGACAACGGT  
 TTCGAAGTGCTGCACGAAGAAAACCTCCGCTTTGATTACCAACGCACCCTGCACGCGTGG  
 TGCGAAAACCTCAAAGAAAATTGGGAGGAAGCAGTTGAACTCGCCGGTGAACCCACTGCA  
 CGACTCTTTGGCCTGTACATGGCAGGTTTCGGAATGGGGATTTGCCCAACAACATCGTCCAG  
 CTGCACCAAGTACTGGGTGTGAACTCGATGAGCAGGGAAGTCGCGGAGAAGTTCCTGAA  
 AGAATGTGGTGGACTATC

>RXA01644-downstream  
 TAAAGAAACAATGTTTCTTTT

>RXA01667-upstream  
 TCTCGGCGTTGATGATCATCCGCAATATCATGCCGCCGCAAGATTCCGCTTTTCCAGACT  
 TTGCTCATTCCTTCCTCTATTACTGCTCGCCATCATCGGC

>RXA01667  
 ATGATTTTGGGGCCTAAGGTGTTGGGTCTGATTGGTTGGTTCGGATCATCTTTCCACTTAC  
 ACTACGGTGCTCATTGCGATTGTGTTTGGTTCGATGCCGTATTCGATGAAGTTTGACCGT  
 GCGGTGCGTACTGGCATGAAGACGATGTGGGCGTATTCGACTGCGATGTTTGTGGGGCAG  
 TGGGGTCTGTTCAATTTTGCTGGGTCTGTTTTTGTTCACCGGTGTGGGGTACCGATGAG  
 TGGTTCGGCATGATGTTGCCGGTTGGTTTTGTGGTGGTTTTGGTACTGCTGCTGCGGTG  
 GGTACTGCGTTGGAGTCTTCGGGTGCGGAGGCTGCGATGTCTTTGGGCTTTACCTCTGCG  
 ACGGTGGGTACTTTTGCTGCGATTGTTGGTGGAAATTTTTCACAACGTGGGGTATTAAG  
 AAGGGCAAGACTGCGGCGATGCCTGCGCAGTTGCCGTGGGATTTGCGTTTCGGGTATATC  
 GATAAGCTGAGTGATCGTCCGTCGATTGGTAAGGCGAGTACGAATCCGTCTGCGATTGAG  
 CCTTTGGCGCTGCATACTGGCATTATTTTGTGACTGTTGCGGTTGCGTATTCCATTAAT  
 CAGTGGTTGGGTAGCATGTTCCCAACCGTGCGAGATTCCGTTGTTTGGCATGTCATTTGTG  
 GTCGGCATTTGTGGGCATGGGAATTATGCGTTTGTGAAGAAGCCTGAGTATTTGGATCGC  
 GACACCGTGAATTCCGTGTCGGGCGCGGCGACGATTACCTCATTGCGTTTGGTATTGCC  
 TCGATTGCTCCTGCTGCGATTGCTGATTACTGGGTTCCTCTTGTTGGTGCTGTTTGT  
 GGCACCATCAACTGTTGTTTCTTCTTTTCTGGGTTCGCTCTGTTTCTTTGGCGAGAAG  
 TGGCTGGAGCGCGCATCTTCGGTTGGGGTGGGCTACTGCCGCGGTTGCTACCGGTATC  
 GCGTTGCTGAAGATCGTGGATCCGAAGTTGAAGTCGGGAGCGCTTAATGAGTACGGCGTG  
 GCTTATATCGGTTTTGCTCCATTTGAAATCGGCATGACCATCATCGCGCCGATCGCGGTG  
 CTCGCAGGCTTTACCATGGGGTGGGTGGGCGTCGTTGATTGTTGCGATCGTGATTTT  
 GGCTCGCGTGGGGTCTGAAGTGGTTGCCGGAGCGCGGACATGTCCGCGGCGAGGGTAAG  
 CCGCAA

>RXA01667-downstream  
 TAAAGGTTGGAAGCGCCGGGTCT

>RXA01722-upstream  
 CTCATTCCCCTCGCTAAAAGCTGCATAAAGTTTCGACGTTTTCAAAGTTGATTGCTTGCA  
 CTGTCGTTGCGTGTGCGATGCCCCGGCTATTGTTGATTGC

>RXA01722  
 ATGCTCAGCACGATGCAGGACGTCCCACTGTCATTAAACCAGAATCCTCGAGTACGGGTCC  
 ACTGTTACGGTGATACTTTGATCACCACGTGGGGCGGTGCCGATGGCATTGAACAAGCA  
 CAGCAAACCTTTAGTGCTGTGGGGGCTAGAGCTGCGGCTTTGGCTCATGCGCTGCATGAT  
 TCTTTAGGTATTACTGGGGATCAGCGAGTGGCGTCGATGCTCTATAACTGCGCGGAACAC  
 ATGGAACTATGTTTGCAGTCGATGCATGGGTGCCGTGTTAATCCGCTGAACAAGCAG  
 TTGATGAATGATCAGATTGTGTTCAATCACTCTGAAGCTGAAGTGGTTATCGCT

GATCCGCGCATGGCTGAACAATTGGGTGAGATCTTAAAAGAAACACCAAAGTTCGTGCC  
 GTGGTGTATTATTGGACCGAATGATTTCTCTAGCGCGGCGGCCACATGCCGGAGGGAATG  
 AAGCTGTATTCTATGAAGCGCTCCTTGACGGCCGTTCCACTGTTTACAACTGGCCCGAG  
 CAGGATGAACGCACTGCTGCTGCAATTTGCTATTCCACCGGTACATCGGGACCGCCGAAG  
 GGTGTGGTGTATTCCCACCGCTCGCTTTATTTACAGTCGTTGAGCTTGCGCACCCACGGAT  
 TCCCTCGCAGTGGAACACGGCGAAACGTTCCCTGTGCTGTGTGCCGATTTACCACGTCCTC  
 AGCTGGGGCGTGCCGATCGCAGCGTTTATGTCCGGCACTCCCCTGGTGCTTCTGGACCG  
 GATCTTTCTGCGCCGACATTGGCAAAGATCATTTCACCCACGCTGCCTCGCGTGGCGCAT  
 GGCGTGCCTACTCTCTGGATTGAGCTGATGGTTCACTACCTGAAAAATCCCCCAGAGCGT  
 ATGTCTCTGCGTGAGCTATACGTGGGCGGTTCTGCGGTGCCTCCAATCGTGATCACCATG  
 TGGGAGCAGCGCTATGGCGTGGATGTTGTCCACGTGTGGGGTATGACGGAAACCTCCACC  
 GTGGGTACTGTGTCTCGCCACCATCAGGTGTTTCTGGTGAAAGCCGGTGGAATTATCGA  
 GTCTCCAGGGCCGATTCCCCGCCTCCCTGCAGTACCGCATTGTCAACGACGGCCAGGTC  
 ATGGCGTCCACCGACCGCAACGAGGGCGAGATTCAGGTCCGCGGTCCGTGGGTGACTGCA  
 AGTTACTTCCACCCCGATGTGGAAAAAGAGGTGGCACCGCCTCAACATTCCGCGACCAT  
 GACGTTGAAGAGGAAAAACGATGAGCTCTTACCCGCGACGGCTGGCTGCGCACCGGGGAC  
 GTTGATCTGTACACGCGATGGATTCTTACCATCCAAGACCGCGCCCGCGATGTCATC  
 CGTTCTGGCGGCGAGTGGATTTACTCCGCTCAGCTGGAAAACCTCATCGTGGCTACSGAA  
 GAGGTTGTGAATGCGCCGTCATTGGCTTCCCCGATGACAAGTGGGTGGAACGTCCCCTC  
 GCAGTACCATGCTCTACCCCGGCATTGAACGCACCCGGGAAACCGCCGAGCGCCTCCGC  
 GATCAACTTCGCGACCGCCTACCCAACCTGGATGCTGCCAGAATATTGGACATTTGTTGAT  
 GAGGTGGATAAAACCTCCGTCGGTAAATATGACAAGAAGGACCTCCGCAACCACCTGCGC  
 AACGGCGATTTTGAAGTAATTAAGCTTAAAGGGCCAGGTGARAAA

>RXA01722-downstream  
 TAACTTCCCTATTTATTCCGGCT

>RXA01727-upstream  
 AGCTTTTGGTGGTTTACCCACCTGCGCTCGTCTTAATTTTGCCTGTTCCAGAGAGACCCT  
 TGAGGAGGGGCTGCGCCGTATCGCCAGCGTGTTGTAAATA

>RXA01727  
 ATGAGTAAAAAGTCTGTCCTGATTACTTCTTTGATGCTGTTTTCCATGTTCTTCGGAGCT  
 GGAAACCTCATCTTCCCGCCGATGCTTGGATTGTGCGCAGGAACCAACTATCTACCAGCT  
 ATCTTAGGATTTCTAGCAACGAGTGTTCTGCTCCCGGTGCTGGCGATTATCGCGGTGGTG  
 TTGTGCGGGAGAAAATGTCAAGGACATGGCTTCTCGTGGCGGTAAGATCTTTGGCCTGGTG  
 TTTCTTATTGCTGCCTATTTGTCTATCGGCGCGTTTTACGCGCTGCCGAGGACTGGGGCG  
 GTGAGCTATTTCGACGGCGGTTGGCGTCGATAATGCGCTTTATTCGGGCTTGTTTAACTTT  
 GTGTTTTTTGCGGTGGCACTGGCGTTGTGCTGGAATCCGAATGGCATTGCAGACAAGTTG  
 GGTAAGTGGCTCACGCCAGCGTTGCTCACGTTGATTGTGGTGCTGGTGGTGTGTCGGTA  
 GCCAAGTTGGATGGCACGCCAGGTGAGCCAAGTAGTGCGTATGCGCAGCAGCCTGCGGGG  
 GCGGGTTTGCTTGAGGGCTACATGACGATGGATGCGATTGCTGCGTTGGCGTTTGGCATC  
 GTGGTGATTTCTGCGTTCAAGTACCAAAGGTTAACAAGGTCCGCACGGCAACTGTCGTG  
 TCGGCGTTTCAATTGCCGGAATTTTGTGGCGCTGGTTTATCTTGGTTTGGGCTCAATCGGT  
 CAAGTAGTAAACGGTGAGTTCGCTGATGGCACCGCAATTTTGAACCTACGCTGCACTGTCC  
 ACGATGGGTGAGGCTGGTCGCATCATGTTCTGGTATTTTGTATCCTTGCATGTATGACC  
 ACCGCAGTTGGTCTGATCAGTGCGACGTCTGAGTTTTTCAATTTCGCTGCTGCCAGGTGTC  
 AAGTACCACGTCTGGGCCACTGTTTTTCGCGCTGATTTCTTTGGCGTTGCCACCATGGGT  
 TTGGATACGGTGTGGCCGTTGCGGCTCCAGTGATTAGTTTCAATTTACCCATCGGCCATC  
 ACCTTGGTGTCTTGTGCTCATCGAGCCCCTGCTGTTCCGCTCTCAAGTGGACCTACCTA  
 TTCGGCATTTGGACTGCAGTTGTGTGGGCGCTGTTTATGTCTATCCCTGCGCTGAATCCA  
 TTCATCGAATGGGCGCCGCTGCACAGCATGTCTTTGGGTGGGTTGTCCCAGTTCTCGTG  
 GCCTCTGCCATCGGTTTGGCTATTGATTGGAACAAGAAAGGTGCCAGTCTGTTGCAAAG  
 AAGGAATCCATTTCCGTC

>RXA01727-downstream  
 TAATCGCTAATTGCGAGGAGTCT

>RXA01737-upstream  
 CTTTGAGCCGAACGATCTGCCGACTCAAGAAGAACTAGCCCGGCTGCTCAGTCAGGAATG



ATGCGCCTAAGATCAAACAAGAATGAAAGGACGGTGAACA

>RXA01737

ATGGGCCGAATGAAAAACGATGGTGAACCTCGCGGATCTGCCGGATCATGCACTTTTGAGC  
ATTATTCGAATCCCGCAGGCGGCGAAAAGAAGCCCCCTGGGCGCTGATCTTAACGCGCATC  
GGATACGCGATGGTGTCTGCTGGTTATCGTCACCATGGTTGTCTATTTTGACCGCAACGGA  
TACTCCGAAGACCTCACGTTTCATCGACGCGTTGTACTATTCCACAGTCTCGTTGACCACC  
GTGGGCTACGGCGATATCACCCCGGTGACGCAATCGGCACGCCTGATCAACATCATCGTC  
CTCACCCAGCACGCATCGGCTTCCTGATCCTCCTGGTCGGCACCACCTTGTCAGTGCTC  
ACCGAAGAATCGCGCCGGGCGCCCTGCAAATCCAACGTTGGAGAAAACGCATGCGCAACCAC  
ACCGTCGTTGTTCGGATACGGAACCAAAGGTCGCTCCGCGGTCGCTGCACTGCTTGGCGAC  
GGCGTCCCCGCCAACCAGATCGTTGTTATCGACACCGATCAAGTCTCCCTCGACGCGCGCC  
AACAACAGCGGACTCGTCACCGTCAAAGGCTCCGCCACCAAAGCAGATGTGTTGCGTCTA  
GCTGGCGTGTACGAGCGCGCGCCGTCGTCGTGGCACCGAACCTGGACGATACTGCAGTT  
CTGGTGACTCTATCGGTGCGAGAAATCGCGCCGCGAGGCAATGATTGTGGCCAGTGTCCGA  
GAATCTGAAAACCAACACCTCCTCGAACAATCCGGTGCGGACTCGGTTGTGATCTCCTCA  
GAAACCGCTGGCCGAATGCTCGGTCTGGCAACAGTTACCCCATCGGTTGTGGAGATGATG  
GAAGACCTCCTCTACCCGACGAAGGATTCTCCGTTGCCGAACGACTAGTCGGTGAGGAT  
GAAATCGGCTCCAACCCACGACACCTCGCTGACATCGTCCCTCGGTGTTGTTTCGATCCGGT  
GAGCTCTACCGCATCGACTCCCCAGAAGCAGAACTGTAGAGCCCGGCGATCGTCTCCTT  
TACGTTCCGCGAGTATTTAGCGAGGAGGTAAATGACAAA

>RXA01737-downstream

TGAGAATTCTTCCCATCGGCCCC

>RXA01755-upstream

TCGTTGGCTTACATGGTTCATTGATGACCGGGCTGAATATGTGAGAAAATCCATCCCTTCT  
TTAAGCAAGGAGTGAATTACAGAAAAGGATTGTTTCAGCA

>RXA01755

ATGAGCACACCTGACATTAAAGAAGGCTCGGCAGAATCACCGGGCGAAGTAATGGTCGTT  
GGAGACAGGCGAGAGTGGCGTCGACAAGCAACCGGCATCATTGCCGGCCTCGTCTTAGCC  
GCCCTGGTCTATCTTCTCTTCCCCCTCGAACTCCGTGGAAACCGTCATGCAATCCAGTGGC  
GTCGATCCAGAACTGAATACACCAACAACGCGATGCGTCTTACTGCTGCAGTCACAATC  
TTGATGGCAGTGTGGTGGATGACAGAAGCAATCCCACTAGCAGCAACCGCACTTATCCCG  
TTGGTTGCATTCCCTGCTTTCCAGGTTGTGGACTTTGGGAAGGCAGCA

>RXA01762-upstream

TGGAGTGATGAATTTTCTTATAGAACGTTTTTTTAAACGATTGACTTTTTTAAACGTTTACG  
CTTTTAAATGACTTCAAACGTGATCTAAAGCACAAAGGAGA

>RXA01762

ATGAAAGTGAACCTCGGAATAGGAAGCTACCCACGACGCAGGGCAACTGTTTCGACCAGAG  
TCCACTGCAATCGAATTCGAAGGCACCAGCATCACCTACGGAGAATTCAGCAAACGAGTC  
AATCGGCTTGGACATGCTCTTCTAGACCTCGGCGTTGCGCACCAAGATCGAGTAGCTTAT  
GTCGGATTCAACCACCCTGCCCTGCTAGAAGTGTCTTTTCAACGAACCTCATTGGGGCA  
ACACCCGTGCTTGTTAACCCTCGCCTATCGGCAAACGAAATCGATTACATCATCCAAGAC  
AGCGGTGCGAGCATCGTGTTTTACGGAATCGACCTCATCGAGCACGCCACTTACCTCCAA  
GAACTCCATCCAGAGATCATCATGGTGGCCGTTGAAGGCGATGAGGGTCCAGGTTTGCGT  
CGAAAAGCGCTTATTGAAGCGGCGAGCGACGCCGACATCGACCTAGAAGTCAGCGATGAT  
GACCTGGTGCTGCTCATGTACACCTCCGGAACCACTGGCCGCCCAAAGGGCGCCATGTTA  
TCCCACCGAAACCTCTTCTTTAACTACTTCAATGCCCTGCTCAGCCAGGAAATTGAACAA  
GGCGCGGTACTTTTATCCACTGCGCCGTTATTCCACATCGCGGGCCTCAACATGACCACC  
ATCCCGGTGATGATGAAGGGCGGAAAGGTGATCATCCACCGCGAATTCCGGGCAGAGCAC  
GTCCTCGACGAAATCGAACGCTCCAAGGTATCCGAATCCTTCATGGTGCCAGCGATGATC  
GACATGTTGTCCAACCACCCATCATTTGCCGAACGCGACCTTTCTTCCCTTCGCGCCATC  
ATGGTGGGCGGCTCTCCCTTAGCGAACGTGCGCTGCGAATCTGGCAAGGACGCGACGTA  
AAAATTGTCCAAGGCTTCGGCATGACAGAAACCGCACCGGGCGCCTGTATCCTCGAGGCA  
ACAGACACAAGCACACACCTTGAACCGCAGGTGAGCCCACTTCTTACCGACATCAAA  
CTAGTGGACCCGAAAACCGGCGAAGAAGTCCCCACCGGAGAGGCCGGCGAAGTTCTCATC  
CGCGGACCACATGTGATGACCGGATACTGGAACCGACCAGAAGACACCGCCAGCGCACTA

CAAAATGGCTGGTACCACTCCGGAGATATCGCCATCAAAGATGAAGACGGCTACTACACC  
ATCAAAGACCGCATCAAAGACATGTACATCTCCGGCGGCGAAAACATTTACCCCGCAGAA  
GTC

>RXA01762-downstream  
TAAGTACCC

>RXA01764-upstream  
TTTTCAAATTAATAGTTGACATTTTCAACGTTATGAGTTTTCATTGGTATCACGCCCCG  
ACGAAGTGTCTGGGATCACAAACCTTCAAAGGAGTTTGAA

>RXA01764  
ATGTCTCTCAATGGAAAAGTCGCCATCGTTACCGGATCTGGTGCAGGACTTGGTCGTTCC  
TTCGCTCAGGAGCTTGCCCGTCAGGGTGCATCTGTCAATGACGTAAACCAGGCA  
GCCGCAGATGAGACTGTCGCAGCAATCACCGAAGCCGGCGGCAAGCCGCCGCCGTTATC  
GCCCCCGTTGGACCCTCTGAAAGCGCCGCATTGCTGGTGCGGGAGGCCGTCGACAAGTTC  
GGTTCTTTGGACATTCTTGTACAAACCGCGGGCATCCTTCGTGATAGGTCCCTGCTGAAG  
ATGACGGACGATGATTTTCGATGCAGTCATTAACGTGCACCTCAAGGGCACTTTACCTGT  
GTTTCGCGAGGCATTTGGATACTTCAAGGAGAATGGAATCGCGGGGCGCATCGTCACGATT  
GGTTCTCCACCGGGCAGCGCGGCAACTTCGGACAGAGCAATTACGCTGCAGCTAAGGCG  
GGCATTGTGGGTATGGTTCGCACGTGGGCGCTGGAGATGAAGCGCGCAGGTGTCACCATT  
AACGCGATCATTCGGAAGCAGCCACCGATATGACCAAGACGGTGCCATATTTCCAGAAG  
GCTGTAGAGGCCGATGAGCGTGGCGAGGCCATGCCAGCATTCCTTCGCGAGACCCTAGGT  
TTTGGCACTCCTCAGGATGTTGCGGGACTTGTGGCCTTCCTTTCTCTGATGAGGCAGCG  
AATATTTCTGGACAGGCCATCGGTGCAGGCGGCGACCGCATGCAGGTGTGGAAGCACCCA  
GAGCCAGCAGTTACTGAATTTAACCAGGTGGCTGGACCTATGAAGCACTGCAGGAACGT  
GGCAAGAACATTATTGAGGGCAACCTGCAGTCCGTCGGTGTGTTTTCCCTGAACTGCCG  
GCAGAGCTTCAGCCACAAATCCCAGTCAAGGCA

>RXA01764-downstream  
TAACACCGCACACCAAGAATTTT

>RXA01766-upstream  
GATGAGGTTCGTCCGGGAATCCTCAAAGACAATGCGGTGAAGGTACTTGGCCTAGCCGCT  
AGCACTGAGCGCGGATCTCAAGCAGAAAAGGTTCGTGCAAC

>RXA01766  
ATGCGTGATCCCATTTCAAGGTGCTGTTATTCCTTCTGATCTTTTTGGTTTCGCAGAAGTT  
CTCACCGAAGCCGAACGCGCAGTTCTTCTGGAAACCCGCAGGGTGCTTGAGGAAGAGGTG  
AAGCCTTATATTAATGAGGCCCTGGGATAAGGCAGTCTTCCCCGATGAGATCGTGCAGCCC  
CTCCAAGATCTGCAATTGCTTGATCCGCCTGCACTTCGGGAAGCAGGGGAGTCGGTTCTGA  
GACATTTTCACTGGTTTCCGCAATTTTGAAGTTCGCGCGCTGTGACATCAAT

>RXA01801-upstream  
TTTGGATTCTTTCCGATTATGTCTTGATCGCCCATCTGTACATCCGGGTGTCTAAA  
CACCCGCGAAGATTTCTGTGATGTGCCACACTGGTTCTC

>RXA01801  
ATGTCTAACGTAGTGAACACTTTTGTCCAGAATTCCACCGGTATGGTGGAGCTTAATCGT  
CCCAAAGCGCTCAATTCTCTTAATCAGGAAATGATCGATCTCGTTCAGGAAGCTCTAACC  
ACTTGGGCTGATGATGATCAGGTGCAGCAGGTTCATTTACTCATCCTCGGAGCGTGCA  
TTTTGTGCCGGCGGTGATGTGCGCGCGGTCCGTGAGAGCGTGTGGAGGGCGATGTTGCG  
GCCGGCGATAAGTATTTTCATCGATGAGTTCGCGATGAACAACACGTTGGGAACCTATCCG  
AAGCCGGTCATTTCTGTGATCAACGGCGTCGCGATGGGTGGCGGAATGGGAATTTCCATG  
CATGGATCGCACCGGATCGTCACGGAAAAAGCGTTCGCGTCGATGCCTGAGATGGCGATC  
GGCTATGTTCCCGATGTGGGCTTTACTTATTTCCGGTCAGCGTGCATCGTCGCTGGCCATC  
GCCACATTTTGGCGGTGACCGGGTGGCGCATGAGCCCTGCCGATATGCTGTGGGCTGGC  
GTCGCAACGCATTTTGTGAGGATGCGCAGGGGTTTATTGATGCGGTCTTGAACGAGTCG  
CTTGATGGCGCGCTGGAGAAATTTCCACGCAACCTACGGGCAGCAGCGAGCTGGCCGGC  
GTCGCCAGCCAGATTGAGGAGACCTTTGGGCACAGCTCTTGGGCGCTTATCGACGCCTCC  
CTCCGGTCTCACCCCGATGCTGAATTTGTTGCCAAGGTGGATGGGCTGATGGCGTCGGCA

GCACCGGCATCGGTGGTGGCTACCGTGAAGCTGATGCATCAAAACAGTGAGGCGACCACT  
CTGCGTGAAGGCTTGGACAATGAATTGGCGATGTCTCTTTATATGATCCGCCAGCCTGAT  
TTTGCTGAAGGTGTGCGTGCAGTGTTGGTTGATAAAGACCGCAATGCAGCCTTCTCCCA  
GCCAACTACGAAGATGTTGATGAGTCACATTTTGTGACCTTGTTCAGCGCAGTTCA

>RXA01801-downstream  
TAAACCGCCAAACTTTTGATAG

>RXA01823-upstream  
GCAACACGTTGATACTGAGCTGCACACGCCCGTTGGCCTGGTGACCAGTTTGCTGGGCGG  
GGTGTATTTGATGTGGCTTTTGAGCCGAAAGGAGGCATAA

>RXA01823  
ATGCTGCAAGCGCATGATCTCACGCTGAGTTACGGCGGGCGAAATATTGTAGAAGGGCTC  
AGTCTGGACCTTCCGGAAAGAGGCCTCAGCATCATCATTGGCCCCAACGGATGCGGGAAA  
TCAACCGTTTTGAAAGCGTTGGGCAGACTGCTGAAACCACAATTGGGGAAGATCACGCTA  
GGTGGGCGAGATATTTCCAGCATGGGCACCAAGCATGTGGCGAAACACATCGGGGTGCTT  
CCGCAACCCCATATGCGCCCGATGGGGTGAGCGTCACGGAGCTGGTCAGCCGCGGGCGG  
TATCCGCACCAACATCTGCTGTCGCAATGGTCGAAAGACGATGAAGCCATTGTGGCGCGC  
TCGCTGGCGGAAGTCGGCATGCACACCCATGCTGAGCATTTAGTGTGCGAACTTTCAGGC  
GGCCAGCGCCAACGGGCGTGGATCGCCATGGCGCTCGCTCAGGAAACAGACATTTTGCTT  
CTCGACGAGCCCACCACGTTCCCTCGACGTAGCCCACCAAATATCCGTCCTCGATTTATGC  
TCCGACCTGCACCAACGTGGTCGCACCCTGGCCATTGTTCTACACGATCTGAACATGGCT  
GCACGGTATGCCACCCACATCATCGCCATGCGGGACGGCACCATCATCGACCAAGGAAAA  
CCCGAAGAAATACTCACTAAAGCGCTGCTCAAAGAAGTTTTTGACCTCGACGCACTCATC  
CTCAAAGACCCCAACAACGGCCGACCACTCATCGTGCCACAGACAGGAGAACTCA

>RXA01823-downstream  
TGAAAGAAACCGACAACCTACTG

>RXA01833-upstream  
AAATATACCCCCAGGGTATCTTGACAGATTAAAGCTCGATGTTTTAGGCTCTACATATA  
CCCCACGGGTATCCCCTCAACTTTGATCTAAGGTGTCAC

>RXA01833  
ATGCTTTTTGAACGCATCTACGAAGAAGGCCTCGCCCAAGCCAGCTATTTTCATTGGCTGC  
CAACGCGAAGGCAAAGCGATTGTTGTTGATGCTCGCCGAGATATCCAGACCTATCTGGAC  
CTTGACGCAAAAAACAACATGGTCATTAGCGCCGTAACCGAAACCCATATTCATGCCGAT  
TATCTCTCCGGTACTCGCGAACTTGCAGCTGCCACCGGCGCCGAGATTTTCTCTCTGGC  
GAAGGCGGAGCTGATTGGCAATATGGCTTTACAGGCACCACCTTGATGCACAATTCCACC  
ATCAAGCTGGAAAATATCACCATCACAGCCAAGCACACTCCCGGACACACTCCAGAGCAC  
CTGTCATTTTTTGATTACTGATGGTGCGGTCTCAAAGGATCCCGGTTTTATGCTCAGCGGT  
GACTTCGTCTTCGTAGGTGACGTGGGACGTCCAGATTTACTTGATGAGGCAGCTGGCGGC  
GTGGACACCCGCTTCGCCGGAGCACAGCAACTCTTCCATAGCCTAAAAGAGCAGTTCCTT  
GCACTCCCCGACCACATTCAGGTTTATCCAGGTCATGGTGCTGGCAGCCCTTGTGGCAAG  
GCATTGGGCGCGATCCCTAGCACCAACCGTGGGATATGAAAAGGCTAATGCGTGGTGGGCT  
CCATATCTGCGCAGTGATGATGAAGCCGGCTTTGTGGAAGAGCTTCTCGACGGCCAGCCA  
GATGCCACGCTTACTTTGCTCGCATGAAAAAGCAGAACAGCAGGGACCTGCAGTACTT  
AGTACATTATCCCCGCTTGTGAAGCTAGAAGCCGAGGAAGTCGTCGAAAAGCTTGGTTCT  
GAAGCAGTATTTGTGGATAACCCGCGAGCAAAACCAAGTCCATCTCGGAACCGTTGTTGGG  
GCATTGAATATTCCGCGCGGCGCCAAGGCGTCCAATTTTGCGGCGTGGGTATTGATCCT  
CAAAAGGATGCTCAGGACCTTATTGTTTTGGCTCCGGACGCCAATACCGCTGCGGATTTT  
CGCGACGCTTTGCTGCGGGTTGGCATCGACACTGTGCGTTATTTACCAACAGTATCGAT  
GGATTGCCTACCTTTGTGCCAGAACTCATCTCCCCGCTGAGCTAGCTGAGACCAACTAT  
GACGCACTGATTGATATCCGTGCAAAGTCCGAATTTGCCGCTGGCAGCATTTCCCGGCGCG  
CAGCAGCTTTCTGGAGGTTTCGGCCATGTGGCGCCTCAATGAGCTGCCTGCGGGTGGCACT  
TTGGTAACCTTCTGCCAATCAGGAGCGCGAAATACCGTGGTAGCCAATGCTTTGCGACGC  
GCCGGATTACCGTTATCGAGCTCGAGGGCAGCTACGCCGCGTGGGAAAAATCAGCTGCC  
AATCCTAAAAACTTGCAGACTGCCGTC

>RXA01833-downstream

TAGTTTTAGATCCGGCGCTGTAT

>RXA01853-upstream

GAATGTCCAACGTCAAAAAAATTCTTTTCTATCCTAACCGTATCTTCACACCTTGAGGGA  
ATGATGGGGGAGCGCCGCTTACGCACTACACTGTTTATTC

>RXA01853

ATGGAGATCCTCGGATTCGCGGCTGGTCCGTATAAAACAAATTGCTATGTGGTGCGCGGG  
GAGAATGAGGTCGCGATCATTGATCCTGGCATGCATGCCCACGATGATTTGGTGGAATAC  
ATCACCACGAATAATTTGAGCGTGGACAAGATTGTGCTCACCACGGACACATTGATCAC  
ACCCGTGATGCTGGTGTGTGGCAAAGCGTTTCAATGCGCCGGTCTATATCCATCCTGAT  
GATGCGTTTTTCCTTGAGGTCTACAAGGGATCTGGAACAAAGACGGCCATGCTTTTCGAC  
GCCGACAACATGGTGTCCCCTGATCCTGAGTCACTGCGTGATCTGGTTGATGGTGAGACA  
ATCACTTTGGCTGGCGAAGAATTCACGTTGAAGCATGCACCAGGGCATTACCTGGTTGT  
ACGCTGATCGTCGGCAAGGAATACTGCTTTAGCGGTGATGTGTTGTTCAAGGGCTCTATT  
GGTCGCACTGATTTTGAGTGGTCTGATGCAGATGCCATGAATGAGTCACTACGCACGGCA  
GTGCTCCCACTT

>RXA01853-downstream

TGATGATGCATTGCAGATTCTTC

>RXA01881-upstream

ACCGGCCCTGCGGCCTCAACCGCCGACCAGCGCGGCGCACACATTTTGACTGTTTCATAA  
TAAAGACAACTTAAGTATCGGAGTCGAAGAAAAACCACA

>RXA01881

ATGGCCAATCTGATTAATCTCGAGAACGTCTCCAAAACCTGGGGATTAAAAACGCTTCTC  
GACGGTGTCTCCTTAGGTGTTCAAACCGGCGACCGCATTGGCGTCGTGCGCCTCAATGGT  
GGCGGAAAAACCACCTGCTGGAAGTACTTACTGGCATCGAAAAGCCGGATCAGGGCCGT  
GTGTCTCACAACCTCTGACCTGCGCATGGCTGTGGTGACGCAGCGTGCTGAACTCAATGAT  
GACGACACCGTCGCTGACGTGGTGTCTTGGACCTTTGGGTTTGAAGTTTTCGAATGGGCA  
TCAAACGCCACGGTGCAGGACGTCTCGGTGGCTTGGGCATTGTCGATCTTGGCCTTGAC  
ACCAAGGTGGGGCAAACCTTTTCCGGTGGGCGAAGCGCCGACGCACCAACCTGGCCGCCG  
CGCTGGTTCGCGACCTTGACC

>RXA01881-downstream

TGATCGTGCTCGACGAGCCCACC

>RXA01894-upstream

AGAATTTTTTCGAAAATGCTGGCACCATCAACAGTGACATTGTTAGAACTTCAAGGAGA  
ACCCATGAATGAACCGGAGCAACATCACCGGTCCATGAGG

>RXA01894

ATGCCCAAACCCAAAAATAATGCGGGTCGAGATCTCAAAGCTGCCATTGCTGTGGGGATC  
GGACTGGGGGTCCTGGTTCTTTTGGGGATTGTCCTAAGCCCATGGGGTTGGTACATCCTC  
GTTGCAGGTTTTATGGCTGCAGCAACATGGGAAGTTGGTAGCAGACTTAAAGAAGGCGGC  
TATCATTTGCCACTGCCGATTATGATCATCGGCGGTGAGGCAATCATCTGGCTGTCATGG  
CCATTTGGCACGATGGGCATTTTGGCGTCTTTTGTGGCCACTGTGTTGGTGCTGATGTAT  
TTCCGAATTTTCTACAATGGCACGGAAAAAGAAGCCCGCAACTATTTGAGGGACACCTCT  
GTGGGCATCTTCGTGCTCACCTGGATTCCATTGTTTCGGAAGCTTCGCTGCGATGCTGTG  
CTGATGCAAAACAATTCCATCCCGGGTACATATTTCAATTTGACGTTTCATGCTGTGTGTG  
ATCGCATCGGATGTGGGCGGGTATATCGCGGGTGTGTTCTTTGGATCGCACCCCAATGGCG  
CCGTTGGTGAGTCCGAAGAAGTCTTGGGAAGGCTTTGCCGGCTCCATTGTCTTAGGATCG  
GTCACCTGGTGCACTCAGTGTTCACTTCCTGCTCGATCACCCTGGTGGATGGGTGTGATC  
TTGGGTGTGCCCTAGTTGTGTGCGCCACGTTGGGTGACTTGGTTGAGTCGCAGTTCAA  
CGCGATTTGGGCATCAAGGATATGTGCAACCTTCTTCCAGGCCACGGCGGATTGATGGAC  
CGTTTGGATGGCATGCTCCCGGCCGCGATGGTGACGTGGTTGATCCTGAGTGTGATCAGC  
AGCTCGTATCCGTCG

>RXA01894-downstream

TAAAGCTTGGGCCAGCTTTAAGT



>RXA01897-upstream  
CTATTTAGATCGTTCCGGAACCGATCCACGCGCCGATATCCACTCCCTGGATGAACTCTT  
TCACTAGGCTGGCCTTTATTGTTTCCGGAAGGGGTTGCT

>RXA01897  
ATGAAAATTGGTGTCATCCTGGGCAGTATCCGCGAAGGCCGCTTCGGCCAAGGCGTTGCC  
GATTGGGTCATGGAACAAATCGGGGCTTATGACGCACCCGATGTGGAATTTGAACTCATC  
GACCTCAAAGCTTTCAACGTGCCCCCTGTTGGAATCCGCGACAGTTCAGGTTCCGCGGAT  
AAACAGTACGACGACCCGCGCGTAACGCTGCTGCTCACAGGCCATTGATGCCTGCGATGCC  
TTCTTTTTCATCACCCCGGAATACAACACGGTGTGCCCGGCGCGTTCAAAAATGCGTAT  
GACATCCTGGGCAATGAATGGCTGAACAAAACCGTCGGTTTTCATTTCTACGGTGCAGTC  
GAAGGGATCCGTGTTGTCGAACAGTGGCGTCAGATCGTCGCCACCTTCAACATGTACGAT  
ATCCGCAGCCAGCTATCCTTTTCCACCTTCACCGAGAACAACAACGGCACTTTTGCGCCC  
AATGATCGACGCCCCGGTGAACATAATCCGCCTCCTTGATAGCCTCCTAACGGCTGTCCGC  
GAT

>RXA01897-downstream  
TAAGGCTCTGAAATACTAATGAG

>RXA01946  
ATCCGCAAGTACTCCAGGCTCGAGGAACAATTCCAGTCGCTCGGCGGCTACGAAGCTGAC  
GCCGAAGCAGCCCAGATCTGCGACAACCTCGGCCTCGAGGCACGCATCCTCGACCAGCAG  
CTTAAAACCTGTCCGGCGGCCAGCGCCGCGCGTTCGAGTTGGCGCAGATCCTCTTCGCC  
GCCACCAACGGCTCCGGCAAATCAAAAACCAACATTGCTTCTCGACGAGCCCACCAACCAC  
TTGGACGCAGACTCGATCACCTGGCTCCGTGACTTCCTGGCGAAGCACGAAGGTGGACTG  
ATCATGATTTTCGCACGACGTCGAACGCTTGGCGCCGTATGTAACAAGATTTGGTACCTC  
GACGCAGTACGCAGCGAAGCCGATGTCTACAACATGGGCTTTAGCAAATACGTCGATGCA  
CGTGCACTCGATGAAGCACGCCGACGCCGTGAGCGCGCAAACGCCGAAAAGAAGGCCGGA  
GCCCTCAAGGACCAGGCTGCACGCCTCGGCGCGAAAGCAACCAAGGCTGCCGCAGCTAAG  
CAGATGATCGCCCGTGCGGAACGAATGATCGACAACCTCGACGAAATCCGCGTAGCTGAC  
CGCGCCGCCAACATCGTTTTCCAGAACAGCACCTGTGGAAAAACCCCACTCAACGCC  
AAGGGCCTGACCAAGATGTACGGCTCCCTCGAAGTCTTCGCCGGCGTTCGACCTAGCCATC  
GACAAAGGCTCCCGCGTAGTCGTCTCGGATTCAACGGTGCAGGTAAAACCAACCCTGCTC  
AACTCCTCGCCGGTGTGGAACGCACCGACGGCGAAGGCGGCATCGTCACCGGATACGGC  
CTCAAATCGGCTACTTCGCCCAGGAACACGACACCATCGACCCCGACAAATCCGTCTGG  
CAAAACACCATCGAAGCCTGCGCCGACGCCGACCAACAAGCCTCCGCAGCCTCCTCGGA  
TCCTTCATGTTCTCCGGCGAACAACCTCGACCAACCAGCAGGAACACTCTCCGGCGGTGAA  
AAAACCCGCTCGCACTGGCCACCCTCGTGTCTCCCGCGCAAACGTCCTGCTTCTCGAC  
GAGCCCAACAACAACCTTGACCCGATCTCCCGCGAACAGGTCCTCGACGCACTGCGCACC  
TACACCGGCGCAGTCGTCTGGTTACCCACGACCCGGGTGCAGTCAAGGCCCTTGAGCCA  
GAACGCGTCATCGTGCTTCCTGATGGCACCGAGGATCTTTGGAATGATCAGTACATGGAA  
ATCGTGGAATTGGCG

>RXA01946-downstream  
TAGGTTCTAAGGCTGTTTATGCT

>RXA01980-upstream  
AGGATCGTACCAAATAAGGCAATAAACTCTTTTTACTTTTCCTCAACTTCCTGAAAAGTC  
GCCGCCCTAGAATTCATAAGTTTCCGATATCTTTAACCC

>RXA01980  
ATGCAGATCATTGATCTCTCTCATGCGTTCGCGCCCCGGACAACCCCACTACCCTGGGGAT  
CCAGATCAAGAAATTAAGACGGTCTCCACGATTGAAAACGATGGCTTTTTAATGCATCAA  
TACAGACTTGTGGTCCCTGGGGAACGCATGTAGATGCACCTGCACATTTGATCCACAA  
GGTCGGACGCTTGATCAGATCCCTGTGGAGGAAACGCATTTACCCCTTTATTGCCTGAGG  
TTTTCTCGCCCCGATCTATGTACTGCTGCTGATATAGAAGCGTTTGAACATACACACGGG  
AAAATCGAACCAGGATCCTTCGTGCGCACTCCACACTGGATGGGAATGGGGTAAACAAGGG  
ATCGCACCCGGCTGGTCTATCGAGGCTTTAGAAATCCTCCATGCCCGTGGAGTCATTGCC  
ATTGGCCACGATCTTCCCGATACAGATCCTTCACTGGAGGCACAGCGCTGGTGGCTGTGC  
CGTGACCATTGGCAGATTGAAAACCTACCAATTTGGACAAGGTTCTTGCAACGGGTGCG

ATGATTGCTTGTCTTGGCCAGTTCCAAAAGATGGTGCTAGTTTCCCAGTGCGTCCAATT  
GCTCTCGTCCCAGAGCACCTATCCCCTACTCGC

>RXA01980-downstream  
TAAAGCGAACGGCAGCACCTTCT

>RXA01983-upstream  
ATATCGCTGCCATGGCAGCCTTGCTGGGCAACCTCAAGCACACTGACCTAGAAGAGCTCC  
CCACCGATTACCAGGGGTGTCCTCCCATGTCCGCTGCGTT

>RXA01983  
ATGGAAGGCTACGGACCTACCCAGATCGAAAAGCTCTTACCTGCATACACACAGGTCAAC  
ACAGCCGGGAATAATCCAGCGACGACGCCTGAGCAAGATCTCCTCGGCGGAGCTGCAACC  
TCGCCGGAAACTACGACCACCAGCTGCAGTACGCAGTCGACGCCAGTCCGGTGTCATCAG  
AATGCGGCACAGGCACCGCCCTTCTGATCATGCACGGCACTGGTGACCGGATGGTCCCT  
CCGGAGCAATCGGCTGCGCTGCACACCCATCTTGTGCAGGCTGGTCGGCAGTCCACCCTG  
GTACTCATTGAGGGCTTTGGCCACGGTTTCTCAATCCCGGGGAAGTCGCGGAGCTGGGG  
CCAAACGTTGACTAGACAATGGTCGGCTCGAGCGGGAGCCTCAGACAAATTTAGCGCG  
CAGCAGAGTCCGGGAAACCCCTTTGAACTACAGGGACTTGCCGCCGACCATGAGATGATC  
AAGCGCTTTTTACCCCTGCACCTTCGC

>RXA01983-downstream  
TAAGACTCTACCTTCACCCAACT

>RXA02020-upstream  
TTGGTCAATCAAGCGTGAATCCGGCTTCCATGAGCCAGTTGCCCGCCTCAAAGCTTGACC  
CATTTTCATAACCAGTGCCATGTGGGTTTACGGTTGATAC

>RXA02020  
ATGGCTAAATCTAATGAAGGGCTGGGAACCGGACTTCGGACCCGCCACCTCACAATGATG  
GGACTCGGCTCCGCAATTGGTGCCGGACTGTTCTCGGCACCGGCGTTGGTATCCGCGCA  
GCCGGCCCCGAGTGCTCCTGGCGTACATCATCGCCGGAGCCATCGTTGTGCTTGTTATG  
CAAATGCTCGGCGAGATGGCTGCTGCCCGTCCCGCCTCCGGATCGTTTTACGTTACGGC  
GAGGATGCTTTCCGGCCACTGGGCTGGTTTCTCCCTCGGTTGGTTGTACTGGTTCATGCTG  
ATTATGGTGATGGGCGCCGAAATGACTGGCGCTGCTGCCATCATGGGTGCATGGTTCGGC  
GTCGAACCGTGGATTCTTTCGCTTGCTGCGTGGTCTTCTTCGCTGTGGTGAACCTCGTC  
GCGGTTTCGCGGTTTTCGGTGAATTCGAGTACTGGTTCGCATTATTAAGGTCGCGGTGATC  
ATCGCTTTCTCATCATTTGGTATTGCTCTTATTTTCGGATGGCTTCCCGGATCCACCTTT  
GTTGGAACCTCAAACCTTCATCGGTGATCACGGATTTCATGCCCAATGGTATTTCTGGTGTT  
GCTGCTGGTTTGCTCGCGGTGGCTTTTGCCCTTGGTGGCATTGAAATTGTCACCATTGCA  
GCTGCAGAGTCCGATAAGCCACGTGAAGCTATTTCCCTGGCGGTGCGTGCCGTGATTTGG  
CGTATTTTCAGTCTTTTACTTGGGCTCTGTTTTGGTCATCACTTTCTCATGCCTTATGAG  
TCGATCAATGGTGCCGACACCGCTGCGGAATCCCCCTTACCCAAATCCTGGCGATGGCA  
AACATCCCTGGCACGGTTGGTTTCATGGAAGCGATCATCGTTCTAGCACTGCTTTCCGCT  
TTCAACGCCCAAATCTATGCCACTTCTCGTTTGGTATTTTCCATGGCGAATCGACAAGAC  
GCTCCGCGAGTTTTTACGTAAGCTCAGCACCAGCCACGTCCCCACCAATGCG

>RXA02029-upstream  
CGCACGTACACTACTTTTAGCAGTTAACCCGCCGAACCTTCTTGATTAAAGTATTCATTGA  
GCGTTCTTGGCATAAATCCCCTGGAGGTGCATCAAACGT

>RXA02029  
ATGGCAGAGGCACGTTTTCGCGCATCTTGAACCCATTGATGTGGAAGAGTGGCCTGGGGTG  
GCGTCAGTGCCCAACCTAGCGTTTGCTGGTGACGCGCACGGCAAGCAGAATATCGATTT  
GCCAAGGCCTGCAGCAACGCAGGTTTAGTTCTGCTAGGAAATGACCCGGATCTCATTATT  
GATCATGAGGAATTATTCTCACGTTTGGCCGCATCGGGCTGGCTGGGGCTCGCTGAGAGC  
TACATGGCAGGCGAGTGGCGCAGCGAGAGGCTTGCCGACGTCTTGACCGCTTTGTTGGGA  
ACTGGGTTTAAACCCCGCGGCAAACCTATCTGGATCGTTTACCCTGCCAGGGCAAGCTGTG  
GATGCCGGAGGCGCACTACCCAATGAACTCATTCGTTTAAAGTTCAGGTGATGGCATGAGC  
GCATTTGGTGGAGTTTTTGCCCTCCGGTGTTCGAACCACTTTACGTACCGCAGTGAAAAGC  
CATGTGCCGGGAGCTGGTCGCAATAGGGAGCCCGCATCTCACTTTGTGGATATCACCAAG

ATCTCGGAGCCTGTGGCCGTGGAGCGTGAAGACCTCGGCGAGGCTCAGCGCCGAGCAGCG  
TCCTTTTTTGCTTGACGGCGCCAAAGTTAAAGCCGGAAGCCATGTGTTGGAGTTTCCCAGC  
AGTGGTGGAGCTTTAGCTATTTTGGCTGCTCGACGCCAGGGAAGTGTGACGCTTTAACG  
GCTGATCCCGCGCAAGTTTCAAGCCTGGAGGAGACGTTTGTGCTCGCCGGTGTGGAGGAG  
GATATTCACATCGAGGTCATTCCCCAGGCGATTCCCTCGCCACGCGAATGGGGTGGCGCC  
TACGATTCGATAGTCGCCATGGAGAAGCTAGAAGTGGTGGGCAAGCACGGTTCCAAGCGG  
TTTATTAAAGCTATCGACAGAATGCTCACCACCGGCGGCAACGTAGCCATGCAATCCTTG  
GTAGCTACTGACCAATGGAGTCCTGTGTGTTCTGAAGCGATTTCTTTGCTCAAGGCCTAT  
ATTTGGCCTGCGCTGCATTACCCAAGTGTGATGAAGTTCATCAGCTTGTGATAGGGAT  
TCTTCTCTGCGCGTGGTGAAGGAAACACACTTTGCGGGCCATTACCTAAAAAGCGTGCAG  
TTGCAACGTGAAGTGTGTTGAAGGCCAGATACGCGAAGCGGCGGCAGATGGCTTTGATGCC  
GTCTACCGCCGCATGTGGGTGTATCACTACGCGCTTATTGAAGCCCTGTTACGCCTGGGA  
TGTCTCAATGCAGTGCAATTTGCGTTGACGACAAGAAACAGAAGGGGGCGTCGA

>RXA02029-downstream  
TAAGCAAAAATCTTTTAGACCTC

>RXA02030-upstream  
GCGCCTAACATCTCATTTGTATGGGATTGACTCTAATAATCTCCTGTGGAAACATCGCAAG  
GGTAATTATTGGAATCTATTATTGTGTGAGGCGATAACTC

>RXA02030  
GTGACCACAACTGATCACTCCACGGAGTTGAATCCTTCTGATCCAGGTGGGCAGACGGCA  
ACCCTAGTGATTGACAAGAAAATAAACGTCGGGTGTCAGCAGCCTCCACCATCGGCACA  
ACCATCGAGTTCTACGATTTTTATGCGTACGCTGCGGCAGCTGTCGTTGTTTTCCCAAGT  
CTGTTTTTCCCTGCCAATGACAACCCAACCGTGAACCTGTTGGCATCGTTTGCCACCTTT  
GGTCTTGCGTTGCTGCTCCACTCGGTTCAATCATTTTCGGGCACTTCGGTGACCGT  
GTGGGACGCAAAGCTACCTTGATCGGTTCACTGCTGACCATGGGCATTGCCACCATCTTG  
ATCGGCCTGCTGCCTACTTATGGTCAGGTCGGAATCATTGCAACCGGCGCTGTTGGCGCTC  
ATGCGTTTCTGCCAGGGCCTGGGCCTTGCGGGTGAATGGTCTGGCGCTGCGTTGCTGGCT  
GGTGAACGCGGAAACACTCACCGCGCTCGTGCTGCAATGTGGCCACAGCTGGGTGCA  
CCGTTTGGTTTCTTCTTGGCCAATGGTTTCATGCTCATTTCTGGTGGTGTGCTTGCCCAT  
CAGGACGGCGATCTTCACGGCGCGTTTCATGACCTGGGGTTGGCGTCTGCCATTCTGTCT  
TCGGCGATCATGATCGCAGTTGGCCTGTGGGTGCGTTTCTCACTGGAGGAACTCCAGTG  
TTCAAGCAGGCTGTTGATCAGGGCAAGAAGGTGAAGTCTCCGCTCAAGGAGCTGTTCAAG  
ACTTCCCTGGCCCTGTTGTGCAAGGCTACTTTGATCATGCTGTCCACTTATACCTTGTTT  
TACCTGGTTACCACGTGGATTCTGTGCTATGGCATCGGTAATCGCAGCACCGGAAACGGC  
CTGTCTATTCCGTACTTTGAGTTCTTGCAAGTTGCAGCTGGCCACCATCGTGTTCTTCGCC  
ATCATGATCCCTGTGTGCAAGGCTGGTTGGCTGATGTGTGGGGTTCGTAAAAACACCCTGACC  
TTGGCTTCTGTGCTGCTTCTCGGCTTTGGTCTGACGTTTAAATCTGCTTCTCGATCCAGAG  
ACCGCCACCAAGACCACCGTGTTCATCTTCTGTTTCGTGGGCATGAGCATCATGGGTCTG  
ATCTTTGGACCCATGTCGGCAATTTTGCCGGAGCTCTTCCCCACCAACGTCCGCTACACG  
GGCTCCGGAATCGCCTACAATGTCTCCTCGATCCTCGGTGCAGCTATTGCACCGTTTCATC  
GCAACGTGGCTGGTGTCCGAGTTTTCAAGTGGCGTACGTCGGCTATTACCTCATCATCGTC  
ACCGCAATTACCTTTGTTGCGGTGCTGACGATGAAGGAAACAAAAACCACGACCTCCGA  
GAGGTC

>RXA02030-downstream  
TAAAGATTTTGGCTTATCGACG

>RXA02073-upstream  
TCATTGTTTTAGAGGATGGCCAATTGACCATGATGGATACACCCAGCAACGTTTCCCAGC  
ACAATGCGTTTTTCCGCACCGCTGTGATGGAGGAAGAACA

>RXA02073  
ATGATTTCCCGACTTCTCCAATTGGCTAAGAAAGTATGGCCGGAAGTGGAGCCTCCACG  
CTCCTGCGACTGCTCAATCAGCTACTCACCGCAGCACTCATTTGTGTTCCCGCCTGGGTG  
CTAAGCCGCAAACCAGACATCTCCCTGCTCGCCGTCGCCATCATCATGGCGCTCATCGCG  
CTGACAGCAGCTGTCTGTGCTGGGGTGGAGCAGGTATGCGGCCACCGCGCTGCCTTTGGG  
CTGCTTGCCACATGCGCGTTATGCTTTACGACGCCCTCGTCCACAAAGGTTCCCCCTCG  
CCGATCCACGGCAGCGGTTTCGATCATGTCTGTTGCCACCGTGACATTAACCTCCATCGAA

GTATTCTTCGCGCACACCATTGGGCCTACAGTCACCGCAGTGCTGCTCAGTGCGGGAGGC  
 GTGATCACGCTGGCAACGCTCGATCCCGTTGCTGGTCTAATTGGTTTACTCGGTGTCCTC  
 ATCGCGTGGTTGATCCCCCTTGATTGGAAAACAATCCTCAAGCAGTGAAGCCACATCACGT  
 GGACACATCGCCCAGCACCTCACCGAAGATGCCGCCGGCAGGCTTGAAATCAACTCACAT  
 GGAGCGCAAGCCACACGGTTAAATGCGCTCGAGGTGAAAGAGCAACAACCTGGAACAAGTT  
 GTGACCCGACAGGGCTTGATCGTCGGTATCCGTCAGGGCGCAGCACTTTTATGGCCGTGG  
 ATATCAGCTGTGTTGTTGGTTGCTCTGGTTCCTCATGTGGGCATTGTTGCAGCCGCGATT  
 ATCCTGGGCATCTCCCCTGCGTTGGATGCAGTTGAGGGATTGCTCGCACCATGCCTACC  
 GCGTTAAACAGTGCGCAGCGGTATTTCCAGATCATCGATGCCCTGTTGCTATCGCTGAA  
 CCTGACGAGCCGAAGCCTTTGCCCAAAGGCCCGCTTAAGCTGCGAATTTCTAGAGTTCCA  
 GTCAGCGCAAAGGGCACCCTGTCTTTAGAGGTTGCAGCTGGTGAACACATCGGCATCATC  
 GGATCCAGCGGTAGTGGAAAATCCACTTTGGCCAAACTCATCCTCAAGCTGGCGCAACTA  
 CGGTCTGGAACCATCACCATCGGTGGTGTGATATCGCAGAGGTTTCATCGGCGGAGCTT  
 CGCAAATCCGTACGCTGGTTGAGCAGAAATCTGTGCTGTTTAGAGCAAGCGTGCTGGAG  
 AATTTACGGATGGGCAATCCAGAGCTGTCTGAAGATGAAGCAAGGGAAGCCTTGAGGTTG  
 GCGTCGATAAGCGAACTGCCTTTAGATGCTGACGCCCTGCGCCTATCTGGCGGACAGCAA  
 CAACGGCTCTGCCTGGCGCGTGCTTTGGCACGCACCCCTCAGGTACTGATTGTCGATGAA  
 GCCACCAGCCACCAAGATGCGCTCAATCAAGCGGATCTTTCCCAGACTCTGGCCACGCTT  
 AAAGACACCACGGTGATCATCATTGCGCACCGCACAGCTGCATTAACCCATGTGGATCGG  
 ATAATTGACCTGGAAGAAATCAAAAATCCC

>RXA02073-downstream  
 TGATCCTTAACGCGGATCAGGGG

>RXA02074-upstream  
 CGGGGGAAGGCCGTGTCGCATGCTCGGGCTAGCCTTGATCTCAAGAAGAATTCGACTGG  
 TTTAAAGTCTGGGCTTTAAGTGCAGAAAGGTTGTGGATTG

>RXA02074  
 ATGCGCTCCCTGCTTCGTGATATCCCTGCGGTGGGTTGGCTAATCACCGCGACGATTGTT  
 GTGCGCACGCTCGTTGTTGCGCTGGTCATCGTTGGGATCGGCTTGCTTATCGACGTCCCC  
 TCGCCCGCTCATTAGCCATGTTGTGGTGGGTTCTGGCAGGTGCCACGGCAGCAGCTGCG  
 CTGCTGTGCGCGGAAGCGGTGCTCCCCAACGTATTCGTGCACGAGTTGAACGATCCTGG  
 CGGCGGCAGTTGGCTGCTAAAAATCTGGAGCTGAATTCCAGTTCGTGAGATGATGCCAG  
 TTGATCACACTGGCAACTGAAGCCACCTCAAAAGCATCCACTTACACAGTGATGTTTCTG  
 GGGCCTTACTTTGCAGTATTTTTGGCCCCACTGACAGTTATTGCCGTTGTGCGCGCGGCT  
 ATTTCTGGCCGATTGCGGGGATACTGTGCCTCGGGTTGTGCGTGATACCTTTCGTTATT  
 TCTTGGGCACAGCGCATGTTGAAAGGCGCTGGCGCGGGATACGGGCGAGCATCTGGGCAG  
 TTGGCAGGCGTGTTTTTGGAAATCGGTGCGCACACTAGGCACCACGATGATGCTGAATGCC  
 GCTGGGCAGCGCAGGCAGATCATCACACAGCGCGCAGAGAATATGCGCTCCCAAGTGATG  
 TCATTGCTGTACCGAAATCAGTTGATGATTCTGGTGACCGACGGCGTGTTTGGAGTTGCC  
 ACCACAATGGTTGCTGCGGTGTTTGCCATTGGAGGATTCTTTTCAGGCTCTCTTACTCTC  
 GGCCAAGCTGTAGCACTCGTATTGCTGGCCAGGCTGCTTATTGATCCCATCAACCGCATG  
 GGTCGCACGTTTTACACCGGCATGGCAGGCAAACCCTCGCTGATCGCCATTGAAAAAGCC  
 CTCGCGACAACCTTTACTGATCAGCCAACCTCAACAGGGACAGCGCCACGATGGGGATCTG  
 GTGGTCAACAACCTTGAAGATCGCCCGCGATCACAGGGACATTGTGCACGGTATCTCTTTC  
 AGCATTTCCCGCGGTTCCACATCGCGGTGGTAGGTCCCAGTGGCGCTGGTAAATCCTCT  
 GTGGCTCTAGCGTTGTCCGGACTTTTAGAGTTTGATGGTGCGATTTCCCTCGGCGGCCAC  
 AACTGTGAGATGTTAGATCTTCGCGCCTCAGTCAGTTTCGTGCCCAATCCCCACGCTG  
 TTTAGCGGAAGCATCAAAAGCAATATCGATCTGGCGCGCACGGGTGTTGATTCTGATCAC  
 ATCCACGCAGCACTTTTAGGCGAAGAACTCCCCGCGGACCTCAAAGTCGGTGAAACCGGC  
 AAAGGTGTCTCCGGCGGCCAAGCAGCAGCATTTCCATTGCCCGAGGTTTAGTAAAGAAT  
 GCTGCCGTGATTGTTCTCGACGAGGCGACCGCACAACTCGACTACACCAACGCCCCGCCAG  
 GTTCGACATCTTGCCAAATCCCTTGAGTGCACGTTGGTTGAGATCACCCACCGCCCATCA  
 GAAGCCCTCGATGCAGACTTCATCATTGTTTTAGAGGATGGCCAATTGACCATGATGGAT  
 ACACCCAGCAACGTTTCCAGCACAAATGCGTTTTTCCGCACCGCTGTGATGGAGGAAGAA  
 CAA

>RXA02074-downstream  
 TGATTTCCCGACTTCTCCAATTG



>RXA02095-upstream

CTCTCTTGGTCCTCTCCCCACCCATTTTTAAGTACTCAAGACCCTTCCAACAGAAAGGAT  
TACTCCCCAACAGGCTCAAAAATACTGAAAGGCTCACGC

>RXA02095

ATGAAAACCTGAGCAATCCCAAAAAGCACAATTAGCCCCCTAAGAAAGCACCTGAAAAGCCA  
CAACGCATCCGCCAACTTATTTCCGTGGCGTGGCAGCGACCTTGGGTCACCTCATTCACC  
GTAATCAGCGCTTTAGCTGCAACGTTGTTTGAACCTACACTTCCTCTTTTGACCGGTGGC  
GCCATCGATATCGCGCTCGGAAATACCGGAGATACTTTAACCCTGACCTGCTGGACCGG  
TTCACCTCCGAGTGGATTAAGCGTGTTGACCAGCGTCATTGCCCTTATCGTGCTTCTCGCG  
TTGCTTCGCTATGCCAGTCAATTTGGACGGCGATACACCGCAGGCAAGCTCAGCATGGGG  
GTACAGCATGATGTCCGGCTTAAAACGATGCGCTCATTGCAGAACCTCGATGGGCCAGGT  
CAGGACTCTATTTCGCACAGGCCAAGTAGTCAGTCGGTCCATTTCCGGATATCAACATGGTG  
CAAAGCCTTGTGGCGATGTTGCCGATGTTGATCGGAAATGTGGTCAAGCTTGTGCTCACT  
TTGGTGATCATGCTGGCTATTTCCCCGCCGCTGACCATCATCGCTGCAGTGTTGGTGCCT  
TTGCTGTTGTGGGCCGTGGCCTATTCGCGAAAAGCGCTTTTTTGCCTCCACGTGGTCGGCC  
CAGCAAAAGGCTGCGGATCTGACCACTCATGTGGAAGAACTGTCACGGGTATCCGCGTG  
GTCAAGGCATTTGCGCAGGAAGACCGCGAGACCGACAAATTGGATCTCACCGCACGTGAG  
TTATTTGCCCAGCGCATGCGCACTGCACGTCTGACGGCAAAGTTCATCCCCATGGTTGAG  
CAGCTTCCGCAGCTTGCTTTGGTGGTCAACATTGTTGGCGGTGGCTATTTGGCCATGACT  
GGTCACATCACGGTGGGCACGTTTGTGGCGTTTTCTTCCTATCTCACTAGCTTGTCCGCG  
GTGGCTAGGTCCCTGTCCGGCATGCTCATGCGCGTGAGTTGGCGCTGTCTTCTGTGGAG  
CGCATCTTTGAAGTCATTGATCTTCAGCCTGAACGCACCGATCCTGCACACCCCCTGTCA  
CTTCCCGACACTCCCCTGGGTCTGTGTTCAACAACGTAGATTTCCGTGGGATTCTCAAC  
GGTTTTGAGCTGGGTGTTCAAGCCGGTGAAACCGTTGTGTTGGTGGGCCCTCCAGGTTCA  
GGCAAGACCATGGCTGTGCAGCTTGCTGGAACTTTTATCAACCAGACAGCGGCCACATC  
GCCTTTGATAGCAACGGCCATCGCACTCGCTTCGACGACCTCACCCACAGCGATATCCGC  
AGGAATCTCATCGCGGTTTTTGTATGAGCCGTTCTTGTACTCCTCCTCCATACCGCGAGAA  
CATCTCGATGGGTTTGGATGTCAG

>RXA02095-downstream

TGATGAGCAGATCGAACACGCAG

>RXA02099-upstream

TAGTTAGAGCTGGTTCAAGGGGTGTCAATCCCAAAAGGCACTCCTTGAACCTCATGAAAAA  
GCTTGACAAAACCTTCAACGTCAAAGGAGGTCATCCACGCT

>RXA02099

ATGGGTGCAGATCAAATTGCAGCAGTCTCCGGCAATTCAGCTTGGATGCTGATGTCCGCG  
TCGCTCGTGCTGCTAATGACACCAGCACTGGCACTTTTCTATGGCGGCATGTCTCGTCAA  
AAGTCCGTGCTCAACATGATGATGATGTCCTTTGGAGCATTGGGCGTCGTTACTGTTATT  
TACCTCTTGTGGGGATGGTCGATGTCTTATGGAACCCAATCAATCGCGGGAATCTTTGCT  
AACCCTTTTGAGTTCTTCGGTCTTAAAGATTCC

>RXA02115

ACCCGCGCAACCAAAAGTGTCGGAACAGTTCTCGCACTCCTGTGGTTCGCAATTGTCCTC  
GACGGCTTTGACCTAGTCGTCCTGGGTGCAACAATCCCGTCCATGCTGGAGGATCCCGCG  
TGGGATCTCACTGCTGGACAGGCCACACAGATTTCCACCATCGGCCTCGTCGGCATGACC  
ATTGGCGCACTGACCATCGGTTTCTTAACGGACCGTCTGGGTGACGCGGTGTCATGCTG  
TTCTCTGTGGCAGTATTTTCTGTATTCACTCTCCTGCTGGCATTACCAACCAACGTCCAG  
CTCTTCAGCCTGTGGCGTTTCTCGCAGGTGTTGGCCTTGGTGGAGCACTCCCCACCGCA  
ATTGCCATGGTGACCGAGTTCCGCCCCGGCACCAAGCGGGCTCTGCATCCACCACCTTG  
ATGACCGGCTACCACGTGCGCGCAGTAGCAACCGCCTTCTTGGCCTCTTCTTATCGAC  
GGCTTTGGTTGGCACTCCATGTTTCATCGCAGGTGCCGTACCAGGACTGATCCTGCTACCA  
CTGCTGTACTTCTTCTTCCAGAATCCCCGCAGTACCTCAAAATCTCCGGCAAGTTGGAT  
GAGGCGCAGGCAGTTGCAGCATCTTATGGACTTTCCCTGGATGATGATCTTGATCGCGAA  
CACGAAGAAGAACTCGGCGAGTCTCCTCACTTTCCCTCCCTGTTCAAGCCCTCGTTCCGC  
CGCAACACCCTGGCGATTTGGGGCACCTCATTCATGGGACTCCTCCTGGTCTACGGCCTG  
AACACATGGCTGCCACAAATCATGCGCCAAGCAGACTACGACATGGGTAACCTCGCTTGA  
TTCCTCATGGTGCTCAACATCGGCGCAGTGATCGGCCTTTATATTGCAGGGCGAATTGCC  
GATAAGAACTCCCCTCGCAAAACAGCACTCGTATGGTTTCGTGTTCTCTGCATTTTCCCTC

GCGTTGCTTGCTGTCCGGATGCCACTGATCGGTCTGTATGGCATCGTGCTGCTCACCAGGC  
ATCTTTGTGTTTCTAGCTCCAGGTACTCATCTACGCCTTCGTTGGTGAGAATCACCTGCC  
AAGATGCGCGCAACCGCCATGGGATTCTCCGCAGGAATTGGTCGCCTCGGCGCCATCTCT  
GGCCCGTTGCTTGGTGGTCTGCTTGTGAGTGCCAACCTTGCTTACCCATGGGGCTTC

>RXA02128-upstream

TATTAGCAAACTTCTTAAAGAGCCTTTTTGTGCCTTTATCCGAGTATCTTTAAAGCAT  
GAGTATTAAGTGGGCGCGCTTTGTACCGGGGATAACCGCG

>RXA02128

ATGCGGGGCTATCAACGATCCTGGTTGAAGGGTGATGTCATCGCGGGTATAACCGTGGCC  
GCGTACTTGGTCCACAAGTCATGGCTTATGCCGTCATTGCGGGGCTGCCAGCTGTCGTT  
GGTCTGTGGGGAGTTCTGGCTCCCATGGCGCTGTACTTTTTCTTGGGCACGTCTCGAAAT  
CTCTCGGTGGTCTGAATCAACCACCGCTCTGATGACGGCTGCAGGTGTGGGAGCTTTA  
GTCGGGGCAGCTGGCGGGCCTGAACGATACGCAGAAGTAGCGGCACTATTGGCTATTGCA  
GTGGGCATTGTATGCGCTGTTGGTTTTATTGGCCGATTGGGATTTCTTACCAGGCTGTTG  
TCTCGACCGGTGCTCGTTGGATATTTGATCGGTATTGCAGTCTTGATGATCGTCAGTCAG  
CTGTCCAAAGTCACCCAGGTGAATGTGGAGAGCGGTGACAGCTGGCAGGAAATAATATCG  
TTTATCAAAGTAGCTGGCCAGGCACATATTCCTACAGTGATTTTGGCAGTCGTGGTGTG  
AGCTTGCTGTATCTGGCAAATTGGTTGACGCCTAAATTTCCAGCACACTCATGGTTCTT  
CTGCTTTCGGCAGCCGCGGTGGGGTTTTTTCATCTGGATAGGTTTGGTCTTGAGGTCATT  
GGTGAGGTGCCCCGTGGCCTGCCTCAACCAAGTATTCCTCGATTGGCGATCTAGAGATC  
TGGTCGTTGTTGCCCTATGCCGTGGGTATTGCCATCGTTGGTTTTTTCAGACAATGTGTTG  
ACTGCTCGTGCAATTCGCGTCGGGAAAAGATGAGGTGATTGATTCCAACCAGGAGCTGCTC  
GCACTGGGAACCGCAAACCTGGCGAATGGGTTCTTCCAGGGATTTCTGTGTATCGAGT  
GGCTCCCGAACTGTTCTTGGAGACACGGCAGGTGCTCGCACTCAGGTGCATTCACTTGTC  
GTGGTGGCGCTGGTGATCATGGTGCTGTTGTTTGCTGGTCCTGTGCTCGAGTCTTTCCCA  
GATGCGGCACTTGGCGCCTTAGTTATTTATGCAGCAACGCAGTTGATTGATATCGCAGAG  
ATCAAAGAGATCGCACGTTTCCGCAAGAGCGAGTTGGTCATCACAGCGGCTACTGCTGCA  
TCCGTTGTGGCTTCTGGCGTGCTCGCGGGGATCGGCGTTGCGGTTACGTTGTCCATCTTG  
GATCTCATCAGACGTATTACCCGACCTTATGCCGATGTCCTAGGATATACGCCGGGCATG  
GCTGGAATGCACAGCTTGGAGGATTATCCTGAGTCGACAGCAGTCGAAGGGCTCGTGGTT  
TTTAGATACGATTCCCCACTGTTTTTCGCCAACGCTGATGATTTTTTCAAACGTGCCATC  
GAAGCCGTTGATGAAGCAACTCAACCCGTGCATTGGTTTTTACTGAATGCTGAAGCGAAT  
ACGGAAGTTGATCTCACGGCCGTCGATGCCATGGAAGCACTTCGCAAAACCCTGGAGGAA  
CGGGGTATCCGATTTGCGATGGCCCGGGTGAAGCAAGATCTACGCCGAAGCCTCGAGCCT  
GCAGGTTTCAATTGAATCCGTGGGGGAGGAGTACATTTTCGCCACACTCCCCACTGCAGTC  
AAGGGGTATTCCGTGGAGTTTCGCGATCGTTTTTGGAACCTATCCAGAAGGCGTTCCGAAA  
GAAATTTTGGAACCT

>RXA02128-downstream

TAAGCTGCCTGGTTGGCGGACTT

>RXA02133

GAAAACCCCTACATTGGCGGAGCTGGATACAACGCAGCAAAATTCGGTGTAGCAGCATTC  
AACCGTGTGCTTCGCTTGGAAACCCACCAGCAGACCCTTCGCGTATCTGAGATCGATCCA  
GGTCGAGTTGCCACGGAAGAATTCTCCCTCGTTTCGTTTCGGCGGAGATAAAGAACGCGCA  
GAAGCAGTCTATGACGACGTCCTCAACCTCACCGCTGAAGACATCGCAGAGTCTGTGCGT  
TGGGTCGCGAGCCTTCCAAAGCACATGAACATTGACCGCATGCGTATTACACCTCGCGAT  
CAGGTC

>RXA02133-downstream

TAAACCCGCACTCTTTTGAAAT

>RXA02150-upstream

GTGTTTTTCGGTGGGCTGCGATGACGCATGTCCACCAAAAGAGCCACCCCTTAAAGAAAT  
TAAAAAGTGGTTTTGGTAGCTTCGCAGCAAAATACACATC

>RXA02150

GTGGGTAAACGTATTCTTAGAAGTTCCTACAGCAGTAAAGCGCGAAGAAGGGGTAAACCCA  
AACATCATGAAAAACAACCTGGTATCGGCTTTTCAAGTATGTGCTAATTGGCCCGTTTTTG

CGTGTGTACAACCGCCCGGAGATCGAAGGCAAAGAAAACATCCCTGCAGAAGGTGCCGCG  
ATCATGGCGTCCAACCACGAAGCAGTGATGGATTCTTTTATTTTCCCCTGCTGTGCCCA  
CGGCAGCTGACCTTCCCAGCGAAGGCCGAATACTTCACATCACCAGGTATTAAAGGCAAG  
ATGCAGAAGTGGTTTTTTTACTTCTGTGGGGCAAGTACCCCTGGACCGCACCGCAGATAAT  
GCCATGGATTCTTTGATGAATACCGCCAAAATGGTGCTGGATCGGGGAGACCTCTTCGGT  
ATTTACCCTGAAGGATCTCGTTCGCCCCGATGGTCGCATCTACAAGGGCAAACCGGAATG  
GCCTATGTTGCGATGGAAACTGGTACGACAGTTATCCCCGTTGCCATGATTGGCAGCCGG  
GACGCGAACCCTATCGGAAGTTGGTTTCCGAAACCCGCAAAGTCAGGATCAAGGTAGGA  
AGCCCAATTGATCCCCTCGCATTCGTCAAAGAACATGGGTTGAAGCCTGGAACCTACGAA  
GCAGCGCGCAAGCTGACAGATCACGTTATGTTTCTTCTGCTGATCTCACTGGTCAGCCG  
TATGTTGATGCGTACTCTAAAGATGTGAAAAACGCTCTGGAGGAAGGAAAAGGATACCCG  
GAGGGCACAGCTCCTTCACAG

>RXA02150-downstream  
TAATCGGGTCTTTTCTGTTAAAA

>RXA02171-upstream  
AACCACATTCGTCATTACTTACATCTATGTCATGTTTGCGAACAAGAACTTGGAGCCTCG  
TCAGGCTGCTATTTCGCCAGAAGATGGAAGGTTAATCAGAT

>RXA02171  
ATGAATTCCACTATTCTCCTTGCACAAGACGCTGTTTCTGAGGGCGTCGGTAATCCGATT  
CTTAACATCAGTGTCTTCGTCGTCTTCATTATTGTGACGATGACCGTGGTGCTTCGCGTG  
GGCAAGAGCACCAGCGAATCCACCGACTTCTACACCGGTGGTGCTTCCTTCTCCGGAACC  
CAGAACGGTCTGGCTATCGCAGGTGACTACCTGTCTGCAGCGTCCTTCCTCGGAATCGTT  
GGTGCAATTTCACTCAACGGTTACGACGGATTCCCTTACTCCATCGGCTTCTTCGTGCGA  
TGGCTTGTGCACTGCTGCTCGTGGCAGAGCCACTTCGTAACGTGGGCCGCTTCACCATG  
GCTGACGTGCTGTCCTTCCGACTGCGTCAGAAACAGTCCGCGTCGCTGCGGCCTGCGGT  
ACCCTCGCGGTTACCCTCTTTTACTTGATCGCTCAGATGGCTGGTGCAGGTTTCGCTTGTG  
TCCGTTCTGCTGGACATCCACGAGTTCAAGTGGCAGGCAGTTGTTGTGCGGTATCGTTGGC  
ATTGTCATGATCGCCTACGTTCTTCTTGGCGGTATGAAGGGCACACATACGTTCAAGATG  
ATTAAGGCAGTTCTGCTGGTTCGGTGGCGTTGCCATTATGACCGTTCTGACCTTCGTCAAG  
GTGTCTGGTGGCCTGACCACCCTTTTAAATGACGCTGTTGAGAAGCACGCCGCTTCAGAT  
TACGCTGCCACCAAGGGGTACGATCCAACCCAGATCCTGGAGCCTGGTCTGCAGTACGGT  
GCAACTCTGACCACTCAGCTGGACTTCATTTCCTTGGCTCTCGCTCTGTGTCTTGGAACC  
GCTGGTCTGCCACACGTTCTGATGCGCTTCTACACCGTTCCCTACCGCCAAGGAAGCACGT  
AAGTCTGTGACCTGGGCTATCGTCCTCATTTGGTGCGTTCTACCTGATGACCCTGGTCCTT  
GGTTACGGCGCTGCGGCACTGGTTCGGTCCAGACCGCGTCATTGCCGCACCAGGTGCTGCT  
AATGCTGCTGCTCCTCTGCTGGCCTTCGAGCTTGGTGGTTCCATCTTCATGGCGCTGATT  
TCCGCAGTTGCGTTTCGCTACCGTTCTCGCCGTGGTTCGAGGCTTTCGCAATTACCGCATCC  
GCTGCTGTTGGTTCACGACATCTACAACGCTGTTATCCGCAACGGTCAGTCCACCGAAGCG  
GAGCAGGTCCGAGTATCCCGCATCACCGTTGTCGTCATTGGCCTGATTTCCATTGTCCTG  
GGAATTCTTGCAATGACCCAGAACGTTGCGTTCCCTCGTGGCCCTGGCCTTCGCAGTTGCA  
GCATCCGCTAACCTGCCAACCATCCTGTACTCCCTGTACTGGAAGAAGTTCAACACCACC  
GGCGCTGTGGCCGCTATCTACACCGGTCTCATCTCCGCGCTGCTGCTGATCTTCCTGTCC  
CCAGCAGTCTCCGGTAATGACAGCGCAATGGTTCCAGGTGCAGACTGGGCAATCTTCCCA  
CTGAAGAACCCAGGCCTCGTCTCCATCCCACTGGCATTTCATCGCTGGTTGGATCGGCACT  
TTGGTTGGCAAGCCAGACAACATGGATGATCTTGCTGCCGAAATGGAAGTTCGTTCCCTC  
ACCGGTGTGCGGTGTTGAAAAGGCTGTTGATCAC

>RXA02171-downstream  
TAAATCTAGTTTCTGAAGTTATT

>RXA02173-upstream  
CTAAATTGGGCTTAGATCTTCCGCCTCTAAATAGGTATGCAGAGACATTCTGAATTAATTA  
ACAAAGCCATTTTTCGGCCGTGGAGAAGCGTTTTCCGACT

>RXA02173  
ATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTCATAGACTCGGTTTTGGACCCT  
GACAGCTTCATTTCTTGAATGAAACTCCCCAATATGACAACCTCAATCAAGGCTATGCA  
GAGACCTTGGAGCGGGCTCGAAGCAAGGCCAAATGCGATGAATCGGTAATTACTGGAGAA

GGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATTTTTCCTTCCTCGGCGGT  
TCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTACCGCGCCACAGAGCTG  
AAACTCCCCTGCTGGTCTCCCCTGCTTCCGGTGGTGCGCGCATGCAGGAAGACAATCGA  
GCTTTTGTTCATGATGGTGTCCATAACCGCGGGTGTGCAGCGTCACCGCGAGGCGCATTG  
CCGTTCTTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCATGGCCTCGTGGGGTTCA  
TCTGGGCATCTCACTTTTGGCGAACCCGGCGCGCAGATAGGTTTCTGGGTCTTCGCGTG  
GTGGAGTTAACCCTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTGGTG  
AAAACCTGGTGTGATTGATGGAATTGTGTGCCACTCCAATTGCGTGCAGCGGTGGCAAAA  
ACCCTCAAGGTTATTAGCCGGTAGAGGCAACGGATCGTTTTTCTCCAACAACCTCCTGGC  
GTGGCACTTCCGGTGTGGAGGCGATTGCGCGTTCTCGTGACCCGCAGAGGCCTGGAATC  
GGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAGCTTTCTGGTGCGCGTGCTGGC  
GCATTGAGCCCGGCTGTGCGCGTTGCCCTGGCGCGCATCGGGGGCCGGCCCGTGGTGCTG  
ATTGGGCAGGATCGCCGCTTACGCTTGGGCCGCGAGGAGCTGCGTTTTGCGCGTCGTGGC  
ATTTGCGTGGCGCGCGAGCTAAACCTGCCGATCGTGTCCATCATCGACACCTCCGGCGCC  
GAATTGTCGCGAGGCGGCTGAGGAGCTCGGCATCGCAAGCTCGATTGCGCGCACCTTGTC  
AAGCTTATCGACGCTCCCCCTCCCCACCGTTTCGGTCATTATTGGTCAGGGCGTTGGCGGT  
GGCGCGCTGGCCATGCTGCCCCGCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCC  
GCATTGCCACCAGAGGGCGCCTCGGCCATCCTCTTCCGCGACACCAACCACGCCGCGGAA  
ATCATAGAGCGACAAGGCGTGCAGGCGCACGCACTTTTAAGCCAAGGGCTTATCGACGGG  
ATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTCGGCACAATCAGCAACGCCCTC  
TCCGAATTGGATAACAATCCGGAGAGGGCGGGACGCGACAGTCGCTTCACACGATTTGAG  
CGTTTAGCGCAG

>RXA02173-downstream  
TAAAGAAAATTATGCGCTGATCA

>RXA02224-upstream  
GCTTCGTCGAGGCCGGAACCGTCGTCATTACGTCGAACCCGACGTGGCACGGCGTCGC  
AAAGCAGATGCAATCTGATTTTTCGGAAGGGGTGAAGTAG

>RXA02224  
ATGGCGCAGCATGAGCGCGTTGCGGATGCGCTGCAGCCGGCGTCGTTGGCGGAGTCGTGG  
CGTGAGCTGAAAACGATGCCTTCGGGGCCCAAGGCCTGGTGGTATGTGAGTTTCGTGGT  
ATTAGCGTGGTCACGGTCGTGGCGATGGTCGGCACGTCCAACCTGTTGGGCTATTCCGTT  
GATCTGATCAATGGGCAGTCGTTGCCGCTGATCGGTTACAGGATCGACCGCAATGATCTGG  
TTGCTTGGTTTGGTGGGCGCTGGAATTTTAGCAGAACTGCCGGTCGCGCGCTGCTGCAA  
TTGGTGATCAACACCTTGGCACGTCGCTGTGCGGTGGATCTGCGGAAAGCTGCGCTGTCT  
TCGGCGTTGCGTGCACCGGTTCTGATGTATGGAATTGGGCACGGGAAACGTGATTAGC  
CGCCTGACGCAAGACATCGATAACACTGTGCGCATCGTCGGCATGGTAGGTGTGCGTTTG  
GTGATCACCATTTTATTCTGCCCAGCTCCTTGTTGCGGTTGATGACCATTCACTGGACC  
TTTGTGATCCTGTTTCATCGCAGTGATTGTGGTGCTGATTTCCAGCGGTCGGAAAGCCGTG  
CGAGCTATTCTTTCGGCAACAAATATTGTGTCCAGTACGGAGGCGCGTCGAAACAATCTG  
CTCCTCGATACGATCCGTGGCATTGAAACACTGCGTGTGCTCAAGCTCGGTGCGTGGGGT  
GTGCAGCGGATGCGCCAAGCGTCGTGGACTGCGGTGCAAGCAACAGCTGATCGCGCGCCG  
ATTTTCACTCGTCTGCTCGCCCTTGGTTGATTGCTTATGGCCTGCTGCTAATTGGCGTG  
TTTGGGCTCAGTGCGTTTTTGGGTGCCCAGGATGCGATGAGCATTGGAGCGGCAACGGCA  
GCAGTTTTTCGTGGTTGTGCGCATGGAAATTCACGTGTTCAACGTGCTGTTCTTCGCATCG  
GAAATTCAGAGTGCGTCTACTTCTTGGTTCGCGCGGTGTCCCTTGCCCAGATGGCTCGT  
CGCACCGAACAGCTGTCTGAGTCTGCCGATTGCACAGAACCACCCTCCGTGACTGTGCAG  
GACGTGACGTTTAAATATCCCGGCGGCGTGGCCATTTTGGAGGATTTCAATCTGGTCTTG  
GAAGCAGGAACAACCACAGCGCTGGTCGGTACTTCTGGTGCGGGGAAATCCACGCTCGCG  
GGCGTCATTGCGGGGCTGCAGCGCCCTGATTCCGGCGCCGTTTTTGGTTCGGGGGCATCAAC  
ACCGCCACCGTCACCGACACGTGGACTACCGCCAGGTTGCGCTGATCAGCCAGGAAGTC  
CACCTTTTTCGAGGCACTCTGGCAGAGGATCTTCGCATGGCCAATGCGCACGCCACCGAC  
GCGCAGCTCCACGCAGCGCTCGAGTCGGTCGGGCTCGGGCAAATGACAACTGCTTTTCGA  
CGTTTCTTTCCATCCGGATTAGACACCAAAATTGGCGCCGGCGCAGAAGAACTCACCCCT  
GAAATCCAACAGCAAATCTCTTGGCCGCATCGTGCTCCGCAATCCACCTGTGTGATC  
ATGGATGAAGCCACCAGTGAAGCCGGCAGCGATGATGCCCGCATGTTGGAAAAAGCCGCC  
ACAGAAATCGCACGAAACCGCACCACTTGGTTGTTGCGCACCGCCTTGACCAAGCAGTT  
GTCGCAGATCGCATCATCGTGATGGAACAAGGCACAATCACCGAAGACGGCACTCACCAG  
GAATTACTTGCTTTTGAGGGCCGCTACGCGCAGCTGTATCAACGATGGAGTGCTCAA



>RXA02224-downstream  
TAGTTCAAATCCACCACAACTC

>RXA02225  
CAAACCTGAGGAGCGCTTTGGCGCAGCGGCTGATGAAGCCTTGGCAATCATGTTGAAGGAA  
GCTCGTCTGCAGTCGTTGCTGACTTTTGTGCGCCAACCTTGTCCCAGCGGTGTTTTCTGTG  
GGTCTTTTGGCTTATGCGTCACTGTTGGCTTTTGACGGTGACATAACTGGTGGTGAGATG  
ATCTCGGTGACGTTGCTGGTGCCACCTTCGTTGACTGTGTTGGGTGTGTCGCTTGGCATG  
ATGACAGAGATTTGGGCTAGGGGACAGGCTTCGACAAAAAGGGTCCAAAACCTTAGTCACT  
GAACTGGATAAGGCGGCCGCTGAGCCACGACCTCAGCCTGCCACCTTTGAATTTGAAGAG  
GGGATCACGGTGTGGGATCCTTCGACACCTGAGGCACGCGATGTGATTGATCGGGAGTTG  
GAGGCGCTTCAGGTTTCGCGAAGATGTCATTGTGGCTCCTCACCGCGTCAGCGTGTTTGAA  
GGTGTGCTGAAGGATAATTTGAATCCGATGGGCACCTATCGCACCGGAGATGCTGCGCGCT  
GCTCTTCATGCTGCAAGTTGTGAGGACATCTTGAGCCGATTGGGTGCTGATCTGAACATG  
CCGGGGGAGTTTGAGCTTCCAGATACCTTGATCGGCGAGGCCGGATTGAATCTCTCCGGT  
GGCCAACGCCAGAGGATTGCTTTGGCACGATTCTTGCTGTTGATCCTGAGGTGCTCATT  
TTGGATGAACCGACCACGGGGTTGGATGCGGTGACCCTGGATGAAGTGGCACATCGCGTC  
GAAAAGCTTCGTCGAGGCCGGAACCGTCGTCATTACGTCGAACCCGACGTGGCACGGC  
GTCGCAAAGCAGATGCAATCTGATTTTTCGGAAGGGGTGAAG

>RXA02225-downstream  
TAGATGGCGCAGCATGAGCGCGT

>RXA02233-upstream  
ATCCCCACCCAATTGGCCCAAGAGCTGCAGAGTTACGTTGTAGAACCCACCTCTGCCTAA  
CTGTGCGATTTCCCAAGAGCCCCCTTGGGAGTCGATAATTA

>RXA02233  
GTGCTCGTGACTTCAACATGGGGATGGACCGTCCACGGAGACGGCAAAAAGATCGAACCC  
GGCGCAGTTGTGCTCCTAAAGAGCGCCTGAGCTGGGGGCGCACAATTGGAATCGGTATG  
CAGCACGTGATCGCCATGTTTCGGCGCCACGCTCCTGGTTCCCACACTCACCGGATTTCCG  
GTCAACACCACACTTTTATTCTCTGGTCTGGGAACAATCCTGTTCTGTTGATCACCAGA  
AACCGACTACCCTCGTACCTGGGTAGTTCTTTTGCTTTTCAATTGCACCTTTAACCGCAACC  
CAAGTCCATGGCATTGGCGTGCAGATCGGTGGCATTCTTGTCGCAGGTCTCGTGCTCGTC  
GCCATTGGATTTGTGGTGAAAGCAGCGGGCAAACGCGTTATTGATGCTGTCATGCCACCC  
GCTGTCACCGGTGCGATCGTGGCACTCATCGGCCTGAACCTGGCACCAACCGCGGCAGGA  
AACTTCTCCAGCCAACCACTGGTTGCCACGGCGACCCCTCTTTGCCATTTTGATCGCTACC  
GTTGCAGGCCGCGGAATGATTGCTCGCCTGGGCATTTTGATCGGTGTGGTGATCGGCTGG  
GTTTTTCGAGCTATCACCGGCAACCTCTCAGAAGGCGCAGCAGACACCATCCGTGAAGCA  
GCATGGTTTCGGACTGCCACAGTTCCACAAGCCGGAATTCAGCTCTCTGCCATTTTGGTG  
ACACTGCCAGTCATCATCGTGCTCATCGCTGAAAACGTCGGCCACGTCAAAGCAGTCTCA  
GAGATGACAGGGGAGGACCTCGACGACCTCGCCGGCGACGCACTTATCGCAGACGGATTC  
GGCACCAACCTCGCAGGTGCCTTCGGTGGATCCGGCACCAACCACTACGCAGAAAACATC  
GGCGTCATGGCGGCCACCCGCGTATATTCCACCGCTGCGTACTGGGTGCGCGTGCAT  
GCCATCGCCCTTGCCCTTCATCCCCAAATTCGGTGCATGATCTTCACCATCCCCGCCGGC  
GTGCTGGGTGGGGCATGTTTGGTTCTTTACGGCCTAATCGGTATGCTCGGCATTTCGTATC  
TGGCAAGACAACAAGGTCAACTTCAACAATCCAGTGAATCTGACCATGGCTGCCGTTGCT  
TTGGTTGCAGGCATTGGTAACCTCACCTCACCGTTTTCGGAGTCACTCTTGAAGGCATC  
GCATGGGCTCTG

>RXA02233-downstream  
TAGGCATCATTTGTGCTGTACCCA

>RXA02253-upstream  
TGAGGACATTTCCCAAGTGAAAGGCTTCGGCCCGAACTTGCGGAGGCTGTCTATGAAGG  
TCTTCACGCGTCAAATAAGTAGATCGCTAGGATGTAACC

>RXA02253  
ATGATTCAATCCACTGGGGTCACGCACACTGATAAGTCTGCACAAGAAAATCCTGTGAAG  
TACAGGGACAATTTACACCTGTCATCATCACCGGTATGTCAGGCGCAGGTCTGAGCACA

GCAGCCCGAGTCCTCGAAGACTTGGGTGGTATGTGGCGCACAAATATTCCACCACAGATC  
ATCCTGGAATTAATTGATATGTGCGCTCGGGAAGATTCTCCCGTCGACAAAGTTGCAGTC  
GTGTGCGATGTGCGCTCCCGTGAATTCCGCGGAAGCCTCACCCAGGTTGTTTCAGAGCTG  
CGTGATAAGCAGCTCGATCCACGGTGTTATTTCTGGAAGCACGCGATGAGGTGCTGATC  
AAGCGATTTCGATAATGTGCGCCGCACCCATCCTTTGCAGGGCAGCCAAACCCTTCAGGTG  
GGTATTGAACGTGAACGAACCGTGCTGTCTCCTGTGAAGGAAGACGCTTCAGTGGTCATC  
GATACCTCGGATCTGTCCGTGCATGATTTGCGCCGCGCCATCGAATCCTCGTTTAGGACA  
ATCGCCACGCGCACCCAGCACGTCACCATTTGAATCATTCGGTTTCAAACACGGCTCACCA  
CGCGACGCCGACTTTGTTGTGGACGTGCGTTTCTTGCCGAACCCATTCTGGGTTCAGAG  
CTGCGCCCATTTAGGGGAGTGGACAAGCCAGTATCTGACTATGTGCTCTCCCAAAAAGGC  
GCAGAAGAATTTTGAACAACCTTTGTGGACATGCTCAAAGACATGCTTCCGGGATACCGC  
CACGAAGGAAAAAATTCATCACAAATCGGTGTGCGCTGCACCGGTGGACACCACAGATCA  
GTTGCGGTGTCTGAAGAACTAGCCAAAAGAATCGCAGATCAGACCACGCTCGACGTGTCT  
GTAGTACACCGCGATATTAACCGCCAC

>RXA02253-downstream  
TAGGAAAGGGGCCAACTAATTGA

>RXA02261-upstream  
GAAATCTATAGAACGATAGGTAAAACTGGACTAGGTTTATCTATAGCGGAATAGAAAAT  
ACTCCGCTCGACAGCATCACTTAGCTGAAAGGCCTTTAAC

>RXA02261  
ATGGACCCCTCAGATCTAGCCTGGATTCTCGCAGCTTTTGGCGTTGGTAAGCCTGATGTTT  
CCCGGATTGTCCCTGCTCTACGGCGGCATGCTGGGTGGGCAACACGTTCTTAACACGTTT  
ATGATGGTTATGAGCTCACTTGGAAATCATCAGCCTTGTGTACATCATTTATGGACACGGA  
CTTGTCTTAGGAACTCCATCGGTGGGTGGGGAATTATCGGAAATCCCCTTGAATACTTC  
GGCTTCCGCAACATTATGGAAGATGACGGCACCGGAGACCTCATGTGGGCGGGCTTCTAC  
ATTCTGTTTCGCTGCAATCTCACTCGCACTTGTTCATCTGGTGCAGCGGGGCGCATGCGC  
TTTGGAGCGTGGCTGGTCTTCGGTGTCTGTGGTTTACCTTTGTGTACGCGCCACTGGCA  
CACTGGGTTTTTCGCTATCGATGATCCTGAGTCCGGCTACGTGGGTGGCTGGATGAAAAAT  
GTGCTTGAGTTCCACGACTTTGCTGGTGGAAACGGCAGTGCACATGAATGCGGGTGCCTCT  
GGACTCGCGCTGGCAATAGTGCTGGGACGCCGCCACTCCATGGCTGTGCGTCCACACAAC  
CTTCCACTGATTTTGAATTGGTGCAGGACTGATCGTTGCGGGCTGGTTCGGATTCAATGGT  
GGTACCGCAGGTGGTGCCAACTTCTCGCAAGCTACGTGGTTCGTTACCTCTCTCATTGCT  
GCAGCTGGCGGAATGATGGGCTTCATGCTCGTTGAACGTGTGTTTACGCGGAAAACCCACT  
TTCTTTGGCTCGGCAACCGGCACAATCGCAGGCCTTGTGGCTATCACCCCGGCCGCGGAT  
GCAGTGAGCCCGCTCGGAGCATTCGCCGTCGGAGCGCTCGGCGCAGTTGTCTCCTTCTGG  
GCAATTAGCTGGAAGAAGGGACACCGAGTCGATGATTCCTTCGATGTGTTTCGAGTCCAC  
GGAATGGCCGGCATTGCAGGTGCACTGTTTGTCTATGCTCTTTGGCGATCCACTAGCACCA  
GCGGGAGTTTCCGGAGTCTTCTTCGGTGGCGAACTCTCCCTGCTGTGGAGGGAACCACTG  
GCCATCATCGTGACCCTTACATACGCATTCGGCGTGACCTGGTTGATTGCCACGATCTTG  
AACAAAGTTCATGACTCTGCGCATCACCTCCGAAGCCGAATATGAAGGCATTGACCGCGCA  
GAACACGCAGAATCTGCCTACCACCTCAATTCCAACGGAATTGGGATGGCAACCCGCACC  
AATTTTCGACCTGAAATCCCCGAGGAAACCGTGCCCGACGCCGTGCAGGTGGGCGTCGAT  
AAGCAAAAAATCGCTGATACTCGAAAGGCCTCAAAA

>RXA02261-downstream  
TGACCGCAACCTACACCACTGAA

>RXA02268-upstream  
TGAATCGTTGGTGCTTCGAGTTGGGATTGTTATGTGGGGAGACGTCGATAAGCAAAACAC  
TTGCCGAGCGCAAGCCGGCCTACGGCGCTAGTGTGAGCAC

>RXA02268  
ATGTCCCAGGAAAATTCTGGTTTGTTCGAAGCGCGGATTACACGTGGGGTGGCTAAGGTG  
CGCCGGAATCCGCGCGAGGATTTTGCAGGAGGAATTCACCCAAGAACTCTACGATCACGCA  
ACAAATATCACCTGCCCTGACGGCGCGGCTGAAGCCGAATGGGTTTTTCCAGGATGAT  
TGGCGGGCGCGACCAAGTGGTGCAGCGACCGTGGCCGATCGTGCTAATTCACGGATCCGGG  
GCCAGCAAGGGTTCATGGGAGGAAATGGGCGCTGAGCTGCGCAGCAAAGGTTGGGCGGTG  
TTTGGCCCTGACTTTGGAACGCGTGCCACCGAGCCAATTGCGGCGTCGGCTGCCCAAATT

GGTGCGTATATTGATGCCGTTTTGTTGGTGACGGGCGCTGCGCAGATTGTGCTGGTTGGG  
 CATTTCGAAGGCGGTGTCGTGGCGCGGTATTGGATGCGCACCTACGGCGGATACATGAAG  
 GTCAGGCACATGATTTCCATCTCTACGCCAAATCACGGAACGCTCATGGGAGGCATTTTA  
 AACCCGATGACGAAGGTGAAATCGGGAGAGGGAACGATCGAAAAGCTGATGCACAGACTA  
 TTCGGGCCCCACTGGTTTTTGAACAGCTGCGCGGACACGACATCATCGAGTTTTTGGCCGAC  
 GGTGGGGACCTCGATCCAGGCGTCACCTACACCTGCATTGGTACCCATTTTGATCCTTTC  
 ATCCAACCTCCGGAGGTGGCCTTTTTTGGAGGTCAACGAGGACGATGATCCAAATCGAGTC  
 CACAATATTTGGGTCTGAAGATGAACACCCGCGCGCAATGATTGCCACAAACGATATGGTG  
 CGCGATCCCAGGGTGATCGAAATCGTACGCGCAGAGCTCGACCGGGTGGCACGCCTCGGC

>RXA02268-downstream  
 TAAGTTGGGGACATGGTTGACGC

>RXA02269-upstream  
 CGCAATGATTGCCACAACGATATGGTGCGCGATCCCAGGGTGATCGAAATCGTACGCGC  
 AGAGCTCGACCGGGTGGCACGCCTCGGCTAAGTTGGGGAC

>RXA02269  
 ATGGTTGACGCCCTCAATGATCTCCGCCGAGAACTCACAAACGCGTTAAGGTCCGTGTGG  
 AAAAACCTCCCCACTGATAACGCCCCGAGGCCGATGCCTTGCCAGACGATGTAGTGGAA  
 GAGATTGCGATAAATTTCTACCGTGATCCCAAAAACGCGGGCAAACCAACGAAGACAAA  
 ACAGATTCCTTGCCGATGCTCGCGCGCATACGTTACGTGGACTTTTTTGAAGACGATTGG  
 CGCGCCCCGCCCCACCGAAGACCGCCCCCTGGCCAGTGGTATTAGTCCACGGAACCTGGATCA  
 ACAAAGGTGATTGGCAAGACTTGGGAGCCGATCTACGCCGCGACGGCTGGGCAGTGTTT  
 GCACCCGAATTTGGCCAACGCGCCACCGGTTTCAGTCGCAGAATCATCCGCACAAATTGGC  
 GCCTATATAGATACAGTATTGCTTGCTACAGGAGCCTCAAAAGTCATTGTCGTTGGCCAC  
 TCCCAAGGCGGCGTGTGTGCTGAGATACTGGATGCGTGTTTTGGGTGGTGATCCAAAGTC  
 AAACACATGGTCTCCCTCGCTGTCCCCAATCACGGCACCAACCATGGGCGGAATCGTCAGC  
 CCGCTAATCCGTAACAATCGTGCGCAAAGTGTGGTTAATTCTGTCGTTCAATCATGGTTC  
 GGCGAAGCTGGATTTGAAATGATCCGCGGACACGACACCATCAACGCCATCAATGAAGGC  
 GGCGATTTGGATCCAGACGTGACATATCTGTGCATCGCCACCCACTTTGACACCGTGATT  
 CAGCCCCCTGAAACCTGCTTCCTAGAGGCCCGGAACCCCGAAGAACTCAAGCGGGTCCAA  
 AACATCTGGGTGGAAAACCTCGACCCCAATTCAGTCGTGCTCCACGAAGCAATGCCTTAC  
 GATCCCCGCGTACGCGCACTGGTCAGGGCGGATTTGAGCAAATTGGTGGAGATTTCCGAG  
 ACTGCGGAGAAC

>RXA02269-downstream  
 TAGGGGTTTTGGTGGTTGTCTAA

>RXA02309-upstream  
 GTGCCTTCCGTCGACTACGGTTAAACAAAAAGCTTTTTGTCCATTTCACTGGATTACCG  
 AAAGAATGAATCCACACTCGATCACCAAAGGTAGCGATGA

>RXA02309  
 ATGAGTAGCGGCCGAACCGTTCCAACCCGTTCCACGGGCTCGGAAAAGAAGGTGTATCC  
 ACCACAGGAGCATCTCAGGTTCGAGTTTGGTGATCCCGAGCTAACGGCCAGGATCAATGAC  
 GCCATGGTGCAGGTAGAAGAACTCCTGCACACTGAACTATCGTCCGGGGAAGACTTCCTC  
 GTCGATATCGTCATGCACCTAACACGAGCCGGCGGCAAACGATTCCGCCCCATGTTTGCA  
 CTGCTGGCCTCCGAGTTCGGTGAAAAACCACTCTCCGAAAACGTCATCAAAGCCGCGGTT  
 GTCGTAGAGATCACCCACCTGGCCACCCTGTACCACGACGATGTCATGGACGAGGCATCC  
 ATGCGCCGCGGCGTCCCAAGTGCTAACGCGCGATGGGACAACCTCCGTAGCCATCCTCGCA  
 GGCGACATCCTCCTAGCACATGCATCAGGTCTGATGAGTCAGCTGGGTACCGACACAGTC  
 GCCCACTTTGCCGAAACATTCGGCGAACTAGTCACCGGCCAAATGCGCGAAACAGTCGGG  
 CCACGCGACACCGACCCGATCGAGCACTACACCAACGTAATCCGTGAAAAAACTGGTGTC  
 CTCATCGCCTCCGCAGGCTATTTGGGAGCCATGCACGAGGCGCCGCACCTGAACACATC  
 GACGCCCTGAAGAACTTCGGCGCAGCCGTCGGCATGATCTTCCAAATCGTCGACGACATC  
 ATCGACATCTTCTCGGAAACCCACGAATCCGGAAAAACGCCCGGCACCGACCTCCGCGAA  
 GGTGTATTACCCCTCCCAGTGCTCTACGCACTCCGTGAAGACACCCCCGTGGCGCAGAA  
 CTCCGCGACATCCTCACCGGCCCTCTAGAAGACGACGAGACCGTCAACCACGTCCTCGAG  
 CTCCTCTCCCAATCCGGCGGACGCCAAGCAGCCCTCGACGAGGTCTACCGCTACATGGAC  
 ATCGCCAACGCAGAA

>RXA02310-upstream

GAAATGGACAAAAGCTTTTGTGTTAACCGTAGTCGACGGAAGGCACTTGAAGCACCTTG  
GGTTAGTCTTCTTGCTCTCCGGACTGAGACAATGGGGTTT

>RXA02310

GTGTCTACAACTTTTGATGTGTTGATCATCGGCGCGGGCCCCCTCAGGTGCCAGCGCCGCC  
GTCCATGCGGCCAGGACTGGGCTTCAAACATTGCTTATCGACGCCTCCTCCTTCCCGCGG  
GATAAAACGTGTGGCGATGGCCTTACTCCCCGTGCGATTACACAGCTAGAACTTCTAGGT  
GTTGCTGATCAGGTTACCGGGGATTATTTCAACAAGGGCTTGAAACTGCATGGTTTTGGT  
GGCTCTGTTGAGGCGCCGTGGCCGGAGACATATTTACGAATAAGGGTTCCGCGATGTCG  
CGGATGGAGTTCGATGATTTGTTATTCCGCTTGCCAAAATCTCATGAGGAAGTAACCACG  
TGGGAGAACGCGAGCGCCCAAGACCCCATTTTGAGGGGGAATTTCTTGGAAGGCGTTGTG  
ATTAATCACGCAGGGCAAGAGAAAACCGTCAAGGCGAAGCATGTGATTATTGCCGATGGT  
GTCCGCTCCCCCTTTCGGTAAGAACTGGGTAGGCAGTGGCAACGCGATGAGGTGTATGGC  
ATTGCGGCTCGTGCTTATTGTGAACTCCGCTGTCTGATGAACCGTGGATTCACTCCCAT  
GTGGAAGTGCAGATGAAGATGGTGTGGTGCAGCCAGGATATGGGTGGATTTTCCCGCTG  
GGCAACGGCACGGTGAATTTGGGTTGTGGCGCGCTCTCGACGGATACGAGACCAGCGAAG  
ATCAATACGAAGAAATTGTTGAGCTTCTATGCGGGTCAGCGTCGTAAAGCATGGCAACTC  
GGGCCCCGAGCACGACGTCGCCTCTGCCCTGCTGCCTATGGGCGGCGCGGTGTCGAATGTG  
GCTGGCGCGAACTGGATGCTGATCGGCGATTCCGCCGCGTGTGTGAACCCGCTGAACGGC  
GAAGGCATCGACTATGGCCTGGAAACCGCGGCGATGGCCGTCGACACGCTTGTGGAAAAC  
CCCAAGCGCGATTTGACCTTGGTATGGCCACATAGGTTGCGCGACGCGTACGGCGAGACC  
TTCATGTTGGCGCGCACGGCTGCTCGACTGCTGACGTACCCGCGAGTTTTTGCCGATGGCT  
GGGCCGCTCGCATTCGCGGGGCGCTGCAAAAGGCCATCATGCCGGCGGCTGCGCGTTTG  
ATGGGCAACCTGATCACAGAGGAGGATAAAGACCTGCTCGCCAGGGGTTGGCAGGCCGCC  
GGATCCGCGATTAGTTGGGCGCGGAAGGGCTCCCCCTCTGTGGGACTCGACTAGTTCTCTG  
GTT

>RXA02310-downstream

TAATCGCCGAGTGCAGCGCGACG

>RXA02320-upstream

GTATGTTACACAAGAACCCTGCACAACGCCTTCAAAGTACGTCGACCACGACCAAGCGC  
ATTATTCACTCTCACCTTCAGGATTTAGACTAAGAAACC

>RXA02320

ATGACTGCAGCACAGACCAAACCTGACCTCACCACCACGGCTGGAAAGCTGTCCGATCTT  
CGCTCCCGTCTTGCGAAGCTCAAGCTCCAATGGGCGAAGCAACTGTAGAAAAAGTGCAC  
GCTGCTGGCAGGAAGACTGCCCGCGAACGTATCGAGTATTTGCTCGATGAGGGCTCTTTC  
GTAGAGATCGATGCTCTTGCTCGTCACCGTTCCAAGAACTTCGGCCTGGATGCCAAGCGT  
CCAGTTACTGACGGTGTGTGACTGGTTACGGCACCATCGATGGCCGTAAGGTCTGTGTG  
TTCTCCCAGGACGGCGCTGTATTCGGTGGCGCTTTGGGTGAAGTTTATGGTGAAAAGATC  
GTTAAGGTTATGGATCTTGCGATCAAGACCGGTGTGCCTTTGATCGGAATCAATGAGGGT  
GCTGGTGCAGCTATCCAGGAAGGTGTTGTGTCTTGGGTCTGTAATCACAGATCTTCTAC  
CGCAACACCCAGGCGTCTGGCGTTATCCCACAGATCTCTTTGATCATGGGTGCCTGCGCT  
GGTGGTCACGTGTACTCCCCTGCTCTGACTGACTTCATCGTCATGGTG

>RXA02321

GAGTACGGTGGCATTCTGCGTCGTGGCGCAAAGCTGCTCTACGCATCGGNNGAAGCACCG  
GTTCCAAAGATCACCGTCACCATGCGTAAGGCTTACGGCGGAGCGTACTGCGTGATGGGT  
TCCAAGGGCTTGGGCTCTGACATCAACCTTGATGGCCAACCGCACAGATCGCCGTCATG  
GGCGCTGCTGGCGCAGTTGGATTCTATCTACCGCAAGGAGCTCATGGCAGCTGATGCCAAG  
GGCCTCGATACCGTAGCTCTGGCTAAGTCCTTCGAGCGCGAGTATGAAGACCACATGCTC  
AACCCGTACCACGCTGCAGAACGTGGCCTGATCGACGCGGTGATCCTGCCAAGCGAAACC  
CGCGGACAGATTTCCCGCAACCTTCGCTGCTCAAGCACAGAACGTCACTCGCCCTGCT  
CGCAAGCACGGCAACATGCCACTG

>RXA02321-downstream

TAAATCGGCGAATCCATAAAGGT



>RXA02335-upstream

TGGTTGAGTTCTTCGGGGTTGAGTGTGCAAGAATATTCACCTATTGGTCAGGCAACTATGT  
GTCTACCCACTGAGTCATCAATTTAAATCAGGAGTTATTA

>RXA02335

GTGTCAGTCGAGACTAGGAAGATCACCAAGGTTCTTGTCGCTAACCGTGGTGAGATTGCA  
ATCCGCGTGTTCCGTGCAGCTCGAGATGAAGGCATGGGATCTGTGCGCCGTCTACGCAGAG  
CCAGATGCAGATGCACCATTCGTGTCATATGCAGACGAGGCTTTTGCCCTCGGTGGCCAA  
ACATCCGCTGAGTCCTACCTTGTCATTGACAAGATCATCGATGCGGCCCCGCAAGTCCGGC  
GCCGACGCCATCCACCCCGGCTACGGCTTCCTCGCAGAAAACGCTGACTTCGCAGAAGCA  
GTCATCAACGAAGGCCTGATCTGGATTGGACCTTCACCTGAGTCCATCCGCTCCCTCGGC  
GACAAGGTCACCGCTCGCCACATCGCAGATAACGCCAAGGCTCCAATGGCTCCTGGCACC  
AAGGAACCAGTAAAAGACGCAGCAGAAGTTGTGGCTTTTCGCTGAAGAATTCGGTCTCCCA  
ATCGCCATCAAGGCAGCTTTTCGGTGGCGGCGGACGTGGCATGAAGGTTGCCTACAAGATG  
GAAGAAGTCGCTGACCTCTTCGAGTCCGCAACCCGTGAAGCAACCGCAGCGTTTCGGCCGC  
GGCGAGTGCTTCGTGGAGCGCTACCTGGACAAGGCACGCCACGTTGAGGCTCAGGTCATC  
GCCGATAAGCACGGCAACGTTGTTGTCGCCGGAACCCGTGACTGCTCCCTGCAGCGCCGT  
TTCCAGAAGCTCGTCGAAGAAGCACCAGCACCATTCTCACCAGATGACCAGCGCGAGCGT  
CTCCACTCCTCCGCGAAGGCTATCTGTAAGGAAGCTGGCTACTACGGTGCAGGCACCGTT  
GAGTACCTCGTTGGCTCCGACGGCCTGATCTCCTTCCTCGAGGTCAACACCCGCTCCAG  
GTGGAACACCCAGTCACCGAAGAGACCACCGGCATCGACCTGGTCCGCGAAATGTTCCGC  
ATCGCAGAAGGCCACGAGCTCTCCATCAAGGAAGATCCAGCTCCACGCGGCCACGCATTC  
GAGTTCCGCATCAACGGCGAAGACGCTGGCTCCAACCTTCATGCCTGCACCAGGCAAGATC  
ACCAGCTACCGCGAGCCACAGGGGCCAGGCGTCCGCATGGACTCCGGTGTGCTTGAAGGT  
TCCGAAATCTCCGGACAGTTCGACTCCATGCTGGCAAAGCTGATCGTTTGGGGCGACACC  
CGCGAGCAGGCTCTCCAGCGCTCCCGCCGTGCACTTGCAGAGTACGTTGTGCGAGGGCATG  
CCAACCGTTATCCCATTCACACCAGCACATCGTGGAAAACCCAGCATTCGTGGGCAACGAC  
GAAGGCTTCGAGATCTACACCAAGTGGATCGAAGAGGTTTGGGATAACCCAATCGCACCT  
TACGTTGACGCTTCCGAGCTCGACGAAGATGAGGACAAGACCCAGCACAGAAGGTTGTT  
GTGGAGATCAACGGCCGTCGCGTTGAGGTTGCACTCCCAGGCGATCTGGCACTCGGTGGC  
ACCGCTGGTCCTAAGAAGAAGGCCAAGAAGCGTCGCGCAGGTGGTGCAAAGGCTGGCGTA  
TCCGGCGATGCAGTGGCAGCTCCAATGCAGGGCACTGTCATCAAGGTCAACGTGCAAGAA  
GGCGCTGAAGTCAACGAAGGCGACACCGTTGTTGTCCTCGAGGCTATGAAGATGGAAAAC  
CCTGTGAAGGCTCATAAGTCCGGAACCGTAACCGGCCCTTACTGTCGCTGCAGGCGAGGGT  
GTCAACAAGGGCGTTGTTCTCCTCGAGATCAAG

>RXA02335-downstream

TAAGTTCTTGATTTCCTGTTAGT

>RXA02343-upstream

TTTAAAACTACCCGCACGCAGCACGAACCTGTTCAAGTGATGTAAATCACCGCGGAAATA  
TTGTGGACGTTACCCCCGCCTACCGCTACGATTTCAAAC

>RXA02343

ATGACCATTTCTCACCTTTGATTGACGTCGCCAACCTTCCAGACATCAACACCACTGCC  
GGCAAGATCGCCGACCTTAAGGCTCGCCGCGCGGAAGCCCATTTCCCATGGGTGAAAAG  
GCAGTAGAGAAGGTCCACGCTGCTGGACGCCTCACTGCCCCGTGAGCGCTTGGATTACTTA  
CTCGATGAGGGCTCCTTCATCGAGACCGATCAGCTGGCTCGCCACCGCACCAACCGCTTTC  
TGCTGGGCGCTAAGCGTCTGCAACCGACGGCATCGTGACCGGCTGGGGCACCATTGAT  
GGACGCGAAGTCTGCATCTTCTCGCAGGACGGCACCGTATTCGGTGGCGCGCTTGGTGAG  
GTGTACGGCGAAAAGATGATCAAGATCATGGAGCTGGCAATCGACACCGGCCGC

>RXA02364-upstream

GCGAAAGTATCTAAGGTCGTTTGATTGGTTTACTACCCCCGAAGTGGGGGTTATTGGCAG  
CATCGAGCACCAAATGAGCGTGATCCGGGATCAGGATCTG

>RXA02364

ATGGAGCCACTGTTCCAAAGTCTTGCGGAATCGGACAATATTTCTGTCATTGGTGGATTT  
ACCCAAGGCACCCGAAATCTGTACACCACTGATGCGCCGGTGAAAAGACCCGCTGACCTG  
GCTGGAAAGAAGATTCGCGTCCAGGAATCCGCCATGCACATCCGCATGATTGAACTCATG  
GGTGGCTCGGCAACCCCGTTGACTTACGGCGAGGTATATACCGCGATGCAGTCTGGTGTG

CTGGATGGCGCGGAAAATAACGAGATCAGTTACGTTACCCAAAACCACTTCGAGGTTGCT  
CGCTACAACAGCAACACCAATCACCTTGTCGGTTTGGATTACATGGTCATGCGACACGAT  
CTGCTTGACGCCATGAGCGAGCCAGACCGTGAATTGTTCTGGAAGAATGGGACGCCGCG  
ATGACTGAGCACACGGATCTGTGGAACACAGAACTGATGCCGTTATTGAAAAGGCGAAA  
GCTGGGGGAGCGGAGTTCGTTGAGGTGGATGCGCAAGCATTACCGATGCACTGGCTCCC  
ATCAAAGACGAATTCTTGACCTCAGAATTCAGCGTGAACCTACGAAGCAGTGC GCGCC  
GCTGATACTTCAGGAGGTGCGGCATCA

>RXA02364-downstream  
TGATGAATTTTAAGTCCATCGTG

>RXA02372  
GATGCGGTCAACAAGATGGATCGCACCGACTTCGTAGAAACCTTCGCACCGCTGTTCAAC  
AGCAAGACCTGGCCTTTGGAAACCGCATGGGAATCCCAGCCATTTCGCCAACGTCACGGAA  
CTGCGCGAAGCCATCCAAGTCGCTGTGCTCACCGCACCGTTGTCCGACCGCGAAGAGCTC  
ATCCACGACTACCCCGACATGGCACAGCTCATTTTGGCCACCGAAGAGGAAGCCGCCACC  
ATCTCTCAAGACCGTGGTTCGATCGGTCTTGATGATCTCGATGACGTGGATCAAGAAAAG  
CTCATCACCGTCACCGAGCAGTACCGCGAACGGTTCAACATGCCGTATGTTGCGTACTTC  
GACACCATGGATTCTGTGGATAACCGTCGTAGCCGCCGGCTTGCGCCGCCTCGACAACTCC  
GACGAGCAGGAGCACCGCCAAGCGCTATCGGAAATCATTGAGATTGCCAATGACCGCTTC  
GATATATTGCTTGCCGACGCTAACCCAGCCCGTTCAGCTTTCGATCGCAAGTTTACCGAG  
ACTGACTTCCTCGGC

>RXA02372-downstream  
TAAACACCAAAAACAAATTAAG

>RXA02377-upstream  
GACAATACTGATGGATAAATTTTCATATCGAGGACGAAGGGACAACCCCGAACGCCGTGAC  
AACATCAACCACAACCCGGGTGAAACATCCGGTAGACCAG

>RXA02377  
GTGCCACCCGCACCCAAACTTGCAGCCCTAGGGCTCCAACACGTTCTTGCTTTCTACGCA  
GGAGCCGTCATTGTTCCGCTGCTGATTGCACAGTCGCTGAACTTGGACACTGCGACCACC  
ATTCACCTGATTAACGCTGACTTGTGACATGTGGCATCGCCACGTTGATTCACTCTGTG  
GGCATTGGTCGCCACATTGGTGTGCGCCTACCGATCGTTCAAGGTGTCACCACTACTGCT  
GTTGCTCCCATCATCGCCATTGGTTTGGGCGTTACTGATGGTCAAGGTGGCGTTGCGTCG  
CTGCCTGCCATTTACGGTGCAGTCATTGTCTCCGGCATTTCACGTTCTTTGCAGCGCCG  
GTGTTTGC GCGTTTCTCAAGTTCTTCCCACCAAGTTGTACCCGGTACTGTGCTGTTGGT  
ATGGGTGCTTCCCTGCTGTCGGTATCTGCAAATGACTTTGTGAACTACGCCGATGGGGTG  
CCTGCTGCCCCGCGATCTTGCTTACGGTTTGGCACCTTGGCGGTGATCATTTTGGCGCAG  
CGCTTCTTCCGTGGATTTCATGGGCACCTTGGCTGTGTTGATCGGCCTGGTTGGTGGCACC  
GCAGTTGCTCTGATCTTGGGCGATGCCAACTTGGATGAGGTGGGAAATGCTGAAGCGTTC  
GACATCACCACTCCGTTTTATTTTGGTGTTCAGAAATTAACGCTGTTGCCATTTTCTCC  
ATGATTATCGTCATGATCATCACCATGGTGGAGACCACCGGTGATGTGTTTGCAACGGGG  
GAAATCGTCGGCAAGCGAACTCGCCGCGAGTGATGTCACCCGCGCACTGCGCGCTGACGGC  
CTGTCCACCCTGATGGGTGGCGTCATGAACTCCTTCCCGTACACGTGCTTCGCGCAAAAC  
GTTGGCCTGGTGC GCATCACGGGCGTGAAATCTCGCTGGGTGCGGCAGCTGCTGCCGGC  
TTCATGATCATCCTCGGTGTGCTGCCCAAGGCTGGCGCGATCGTCGCTTCCATCCCTTCC  
CCAGTCCTCGGTGGCGCATCCTTGGCACTGTTCGCCAACGTTGCATGGGTGGGCATCCAG  
ACCATCGCCAAGTCTGACCTCGCTGATAGCCGCAACTCCGTCATCGTGACCTCCGCACTT  
GGCCTAGCCATGCTGGTGTCTTCCGCCCCGATGTTGCTCAAGGCGTTCCC

>RXA02377-downstream  
TGAGTGGGCGCGTATCTTCGTCT

>RXA02397-upstream  
GTGTGAATAAACTTGTTCCTGGTCATTTCCCCTACTGAACTGCGCTTATGCCTATGCT  
TAGAAACCAGAGACAAGCTTAAGAAGGACAGGGGGCCGGCC

>RXA02397  
ATGAATGATTTCGAAACAACCATCGATCGGATCTCTAAAGAACAAGATCCCGCAGCCCGA

AGCCGCGTGGAACAGTTCATTGTGGAAACAGTACGTGCACTACCCAACTTGACCACCAAA  
CAAGGTGCATCGTTGGCTATCCAACCTTCTTGATGCGGTACAGCTCGCGGATGCGGCGGGA  
ACCAAGGGGGGTGCGTCGACAAGCAATGCTTCATCGCTGCCTGACACCTTTGACGCGCTG  
ACCAGCCTGATTGGCAAGCTCGATGTGCGCAGCGATTCTGAATGGCGCTCGTTTGGGTTC  
CAGCCTTCTGAAACTGCGCACCCGCTAATGATCGCTATCCCTGAGATTGAGATTTTTTAT  
CAGCACACCGATGTGGAGCCGGGAAGCGATGACGCCGTGGCGCCGGACTTTCAGGAAAAT  
CAGGATATGTGGCGCAGGCGTCTCGGATCTGTCACCGAACCAACCTTATATATAAAGAG  
TTTTCCGGACCCGGCAAAGCGCAGCGTGCCGTAGAAATGCTGGGCAATCTGTGGAAGATC  
GGCGTGGTGGTGAGTAGGAATACGGAAAGTCGCCTTGGGTAACTCGTGTGGAATACACC  
CCCACCCCTGGCGAAGTACCCGTGCCGTGATGTGCGAGAAGAACTGTTGGTACAGCATT  
CGGGTGTCTGAAACCATTGGTGAGAACCAGGTTCCGGAAATTGTGCGCTGCTTAGGCGAG  
ATTTTCTGTGGCTATCTTCCCCAGATGTGGCTCAAAGAACCAGTAAAGGCCGCAAGTTG  
CGAATCCAAGAATCGGAAGCAGCAGCGTATATCGCGATGGCGCGACTAGATCTTCCCCA  
CGCACCGGCAACACCACTTGGAACCAACAGCTATATTTCCACGCGTCCTCTCTCCCCCGCT  
TTTAGGTGGGACGTGGTGCTGGAGGCTTCCCACCAATTGGAGAACCCTGCTGCGTGGAGAC  
ACAGGGCCGGTCACTGCCACACAATCGGCAGCTGGT

>RXA02397-downstream  
TAACCAAAAGTTCACGTGGAGAT

>RXA02424  
ACCGGAGCAACTCACTACGCGCCTTTCCTTGAGGTGCCAGCTTTGCCCTCCGCTGTTGAT  
GTGGAAGTGCATCATGGTGATTCAATTGAATTTGAGGGTCATGTATTCCCTATCAGCATT  
CTGCGCGGCCACACCCAGGCGGTGACGACTCACCCTGAGATCGACGGTAAACTCAC  
CTTTTCGTGGGTGACAGCCTCTTCCCCGGCGGTTTGGGCAAAACCAGCAGCGAAGGCGAC  
TTCGTCCGACTGTTCAACGATGTCAAAGAGCGCATCTTTGACACCTACGACGATGACAGC  
ATCGTGTGGCCAGGTCACGGCAAGGAAACCACCCTTGGAGCCGAGCGTCCACAGCTGGAA  
ATCTGGTGGGAGCGTCGCTGG

>RXA02424-downstream  
TAAGCGCTTTTCTCAACCAGGCA

>RXA02426-upstream  
TGCAGCAGCATAATCAGGGAAAAATAGGAACTGTTTACTGAAAACTGACAAACCTGACA  
GACCTGACCCGAAGAGACCTTATTCATGACGATATTGTTT

>RXA02426  
ATGCTCATTACATTGCTGCTCGCCACCGTGATTGTGGTGGCCATCGGCGATAAAACCGGA  
CTCCCCTGGCCTGCTTTGATGACTATTGTCGCCGAGGTGGAGCGTTGTTGCCATTTTGG  
CCGGAATTTACTATCCCGGCCGATCTGATGTTGCCTATTTTCATTCCGCCGCTGCTGTGG  
GCGCTGGCGAGGAAGTCATCGTGCGGCGGTGATTAGGTGCGAGATGTCTACCATCATCACG  
ATGTCGGTGTGTTGGTGTTCGTGACCATCGCGGCACTCACGGGTGCATCCATGCTGTTG  
CTTCCTGGCATTGGTCTTGCTGGTGCGATCATGTTGGCTGCGGCTATTGCTCCACCGGAT  
CCTGTTGCTGTTGATGCAGTGGCGGAACCTGCGGGAATCCCGAAGCGCATCACCACCACT  
TTGCAGACGGAGGGTCTGTTTAAATGATGCAGCCAGCATCGTGCGGCTTCCATGTGGCTTTA  
GCTGCCCTGGTTCGCTGGTGAGGATTTGTCCTGGTCAACGGGTGTTTTGGAATTCTTGTTGG  
TCGTGTCTTGCTGCCGTTATTTTGGGCTTGGTTATTGGCCGGGCGGCTGCGTGGTTTACC  
GATCACGTGAGTTCGTTGAGGCTCGAAATGCGTTTACGTGGGTGCTGCCGTTTGCCATT  
TATGTGGTGGCGGAAGAAATCGGCGGATCGGGCGTTATCGCCATTGTGATCGCTGCAGTG  
GAGATGAATTCGAGGGCGTCGATTGGTGCGGAGGATCGTCTAACGGGTCTGCGTTCTGG  
GGAACCATTGAGGTGCTGTTTACTGGCGTTGCCTTTGGTTTGATCGGCCTGAATGTGCGC  
GCTGCGATTGATGAAGTTGGATCTGAGCTGTGGCATGCCGTGGTTCGTGGGCATTGTGCTC  
TCGGTGGTGGCGATCGTTGTCCGTGGTGTGTGGATGTTCCGCGCGTATAAGCGCAATCGT  
TTCAAGATCGATAAGAAGGGTGCAGACCAATAGTTTCATTGCGGGCGCCTCTTCGACTGCAG  
GAATCGTTGCTGATGACGTGGGCGGGCATGCGCGGTTTGGTGACGTTGGCGCTGGTGCTG  
TCTATTCCGGAGGATATTTTCCCGTATCACCACGAGTTGCAGGTCATTGCGCTGGTTCGT  
CTCTTAATCACCATTGGTGGGCCCTGGTTTGACGTTGCCGTGGCTGATGCGGAAGCTCAGC  
TTGGATAAGGGTCCCGATGCTGCGGGCGATGAGAGTATCGCCGCGCTGACAGAGAGGGCT  
CACAAGGCCGCAACAACGTATTTGGTGGATACCACGGAGTTGCCGATGGAGCAGATGGTG  
GCGATCAAGAATTGGTTCTCGCAAGAAATTGACGCTGATGAACTGCAGGAGAACGTCGAT  
AAGCTGCATCAGCGCGCGCATCATGCGCGTGTGGGGCAATTAAGGCGGCCAGGAGGAG

CTGTTGAAGGCGCGGCGGGAGCGCGGCGTTAATCCGGCCTATGTTGATGAGGTGTTGACC  
AACATTGACCGGATGCTTGTGCGGCTGAACGC

>RXA02426-downstream  
TAGATAAACAGCAGCAGGCTGAT

>RXA02487-upstream  
GGCGAGTGGTACCGCACCGCGACGTCGGAGTGATGAAGAAGCCGGGTTCATCCGCCTAGT  
TGCTCGCATCAAGAAAGTCATCATCACTGGCGGTTTCAAC

>RXA02487  
GTGTACCCAGCTGAGGTTGAAGAAGTCCTCGCAGAGCACCCAGACATTGAAGATTCCGCA  
GTCGTTGGTATCCCGCGTGAAGACGGCTCCGAAAACGTCGTTGCTGCCATCACTTTGGTG  
GAAGGTGCAGCGCTGGATCCGGATGGCCTGAAGGAATTCGCCCCGCAAGAACCTCACCCGC  
TACAAGGTTCCGCGCACTTTCTACCACTTTGAGGAGATGCCGCGGGATCAGATGGGCAAG  
ATTAGGCGTCGTGAAGTGCAGGCGGAGTTGTTGAAGAAGCTCGGCAAG

>RXA02487-downstream  
TAGACGCCGATTTAAGAGGTCGA

>RXA02490-upstream  
TCATAGCTACGCGCATGCCACATTCTAGATCGCCGAAGAAAGCAGCGGGACGTCTCTAT  
ATACTAAAGGGCACTAAAGCAACGCAGTTGAAGGGACACC

>RXA02490  
ATGTCAGCATACGAAACCAAAGAATGGCTCCAGCACTACCCAGAGTGGACGCCACACTCG  
CTGGAATATGGCGACACCACCCTGCTGGACGTTTACGACAACAACCTGGCCATTAACGCA  
GACAAGCCAGCCACCTACTTTTTCGGTTCGTTTACAAACCTACGGTGAACCTGGACAAAGAA  
GTCCGCAAAACTGCCGCTGGCCTGCGCGCACTAGGTGTCCGCCCCGGCGATCACGTAGCG  
ATTATCCTCCCCAACTGCCACAGCACATCGCAGCTTCTACGCAGTGCTGAAACTCGGC  
GCAGTAGTCATTGAGCACAACCCGCTCTACACCGCCACGAACCTGCTCGAACCCTTCAA  
GACCACGGTGCCCGCGTTGCCATCGTCTGGGACAAAGCCTCCCCACCGTCGAACAGCTA  
CGTGGACAGACCCAGTTGGAAACCATCGTGTTCGGTCAACATGATCAACGCGATGCCACCA  
CTCCAGCGCCTAGCACTTCGGCTCCCAATCCCTGCACTGCGCAAGAGCCGCGAATCCCTC  
TCCGGCGCAGCCCCAACACCGTTTCTTTTGAACCTTGACCAGCGCAGCAATGGGCGGC  
GACGGCGACGACGTAGTTTCAGAACCCACCGTGACCAAGAATCCGTCGCGCTGATCCTC  
TACACCTCCGGCACCAACCGGACGCCCCAAGGGTGCCAGCTCACCCACGGAAACCTGTTT  
TCCAATCTCCTCCAAGGAAAGCACTGGGTTCAGGTCTCGGAGACAAACCAGAACGCATG  
CTTGCAGCCCTACCAATGTTCCACGCATACGGT

>RXA02511-upstream  
CCATGCTTGCGCAAGCATGGGGCACCATTGATGGGGCACCAGGCACTGTCGACCCAACGC  
TGACTTCAGCGATCCGTACCGCAGCACCGAAGGAGCACTG

>RXA02511  
ATGCTGGGACTTCATGGACGTAAGCCTGCGCAGGTTATTGTTGAGCCTGTTGCCAAATTG  
ATGATCAAGTTGAAGGTGACGCCTAATCAGCTCACCTTAGTCAGCGCTGGCCTCACCGTT  
GGGGTGGCTTTGCTGCTGATTCTACGGGGCATTTGATTTGGGCGGCAGTTTTGACGGGC  
CTGTTTGCGGCTTTCGACATGATTGATGGCACGGTTGCTCGCATGCAAGGTGGTGGCACC  
AAATTTGGTGCCACCTTGGATGCCACGTGTGACCGCATCACTGATGGTGCCTATTGGT  
GCGATTACCTGGTGGCTGGTGTATTCCTACGATGCACCACAGGCATTGGTCGCTGCCTCC  
TTGGTTTGGTTGGTTGCCTCCCAGGTGATCTCTTACGTGAAAGCCAGGGGAGAGGCCTCC  
GGATTACCATGGACGGCGGTCTCGTGGAACGCCCTGAGCGTCTGATTGTCAGCCTTGTT  
GGTTTGGGGCTGACCGGAATGGGCGTTCCATATGCCATCGATGTGGCACTGTGGGCCCTT  
GCAGCTGGCAGTATTTACACTGTTGTGCAGCGCTTGGTCATGGCTGGAAAGTCCCCATTG  
GCTAAGGAATTTACCAAGGCACCAGCAGGTGCGAAGGCAGATTACAGCAACACCAA

>RXA02511-downstream  
TAAAAATTAGCCGAGGGAGCATC

>RXA02512-upstream



GCTGGAAAGTCCCCATTGGCTAAGGAATTTACCAAGGCACCAGCAGGTGCGAAGGCAGAT  
TACAGCAACACCAAATAAAAATTAGCCGAGGGAGCATCGC

>RXA02512

ATGAAGCCGAAGGATTTCTGCACAGCGGAAAATTGGGCGGAGAATTTAAGCGCACTGGGC  
TATCTAGCTGGTTGGCGTTTTGTCCGGATGCTCCCTTTGCCTATTGCTCGCCGGGTGTTT  
GACCTTGGGGCGGATCTGGCGTCGAAAAGCGGAAAAGGCATGGGGCAGCTACGCGCTAAT  
CTGGCGCGGGTGGTTCGGTGCAGGAAAACGTTACGCAGGCGCTGGTGAAGCAAGCAACGCGC  
AGCTATGCGCGGTATTGGCTGGAAGCGTTCCGGCTACCGGCGATCGCGCGAGATCCTGAG  
CTGCTTGCAGCGTTGCGTAAGGGAACGTTGGCCTAGATTTGTTGGATGAATCTTTGGCT  
GCCGGCAAGGGCGTAGTTTTGACGCTCCACACAGCGGCAACTGGGATATGGCTGGCGCT  
TTTCTGATTAGCCATCATGGGCAATTCACCACCGTTGCAGAAAGGGTCAAGCCGGAACGC  
TTGTTTGAAGCGTTCGTGGAGTTTCGAGAAAGCCTTGGAATTTGAGGTGCTGCCTCTCACC  
GGTGGCGAGCGTCCGCCGTTTGAAAAGCTGAAAGAGCGCCTGACATCTGGAGGTATCGTG  
TGCCTTCTTGGGGAGCGTGACCTGCGGCATTCCGGCGTGGAGACCACTTTTTTTGGTGAG  
AAGACCTCCATGCCAGCAGGACCTGCGCAGCTGGCCATTGAAACAGGTGCGGCGCTGCAC  
GTGGTGCATCCATGGTTCGATGACGACGGCTGGGGTCTCAGCGTATCCGATGCCGTGACC  
GTGGATAATTTATCCGACACGGTGCAGCGGATCGCACATCTTTTTATGGCAAATATTACG  
GCGCACCCCGCTGATTGGCATATGCTCCAACCCCTGTGGTTTGGTGATTGTTGGATCCGGAG  
CGTCTCAAGCGCTCTAGGGAGCAGACAAATGTTCAAAACCGGTGGCATTACAGGAG

>RXA02527-upstream

ATTGGAGCAATCTTTTAATCAAGTTGGGAATTCAGCGTTGATTGTGGTTGCCATGTGGT  
TTGCCCGCACCCCTGAAGCACTCACGGATCAAGCGTGGCGG

>RXA02527

ATGTTTGGCCTGTTTCATCGCGACGATTGTGGCGATTATTCTCAAGCCAATGCCAATGGGT  
GCCGTGACAATTATCGGCATGATCGCCGCGGTGTTGACTGGTTTGGTGCCGTTGACGGCG  
TCTTCTGATGATCCCGGCGCGGTGTATGGCCTTATTGGTTTCAGTAACGGCACCATTTGG  
CTGATTGTGATGGCGTTCCTGATTTTCGCGTGGATTTCATCAAGACGGGGCTTGGACGTCGA  
ATAGCGTTGTTCTTTGTGTCTAAAGTCGGCGGAAAATGCTGGGTGTGACCTATGGTTTG  
GCGCTCGCTGATTTGGTGTGGCTCCTGCGATTCCATCAGCAACTGCCCCGAGGTGGTGGC  
ATTATGGCTCCGATTATGAAGTCGGTGGCATTGACTTATGATTCCACTCCTGGCCCAACT  
CGTCGCAGGGCTGGCGCGTTCCTTGGCGCTGAATGTGGGACAGGTAAATGCGATTACGTGC  
GCGATGTTTCTAACTGCAATGGCAGGAAACCCCTTGATCGCCTCTTTGGCTTCGCAGATG  
GATGTCAATATCACGTGGACAACTGGGCTGTGGGTGCGATTGTGCCTGGTCTGGTGGCG  
CTTATTGTGGTGCCGTGGGTGGTATACAAGATCTATCCACCTGAGTTGAAGGACACCCCT  
GAGGTCAAGAAAATGGCTTCTGATGAGCTCAAGCAATTGGGTGGGTTTACTTATGGTGAG  
AAGGTGCTGGCGGGAACCTTTGTTGTGTTGCTGCTGCTCTGGACAGGTGGCGATTTGGTC  
TTGGGAATCTCGGCAACTACCACCGCTTTCGTTGGCGTCATCATCTTGCTAGTGGCTCAC  
GTGCTGACGTGGGAGGACATCATTCAAGAAAAGACTGCGTGGGACACCATGGTGTGGTTC  
GCGGTGCTATACATGATGGCAACAGCGTTATCGCAGTACGGATTCATCGCATGGATCTCT  
GAGGTAATTGCTTCCAGTTTGGGTGGCATGAACCTGGGTCGTTGCTTTGGTTGTGTTGGTG  
CTGATTTACTTCTTCACTACTATTTCTTTGCCTCGGCAACAGCGCATATTTCTGCGATG  
TACTTGGCCTTCTTGGGTGCTGCGATTGCGATTGGTGCACCCCGTTGATGGCGGCCCTG  
GTGTTGGCGTACACCTCCAATTTGTTCTCTTCACTCACTCAGTATTCTGGTGGTCTCTCG  
CCAACATTGTTTGGTTTGAACATACACGGTGGGTGAGTGGTGGCGGACCTCGGCAATT  
GCTGGCGCGGTATCGATTACAATCTGGTTGGTTATCGGTGGTTTGTGGATGAATGTCATC  
GGACTCTGG

>RXA02527-downstream

TAATCGAAAATTAAAGGTAAGGG

>RXA02547

GCTGCGCGGCTGACCGTGGATGAGTATCCGGCGGCGAGGGAAGCGCTTGAATCTGCAGGT  
CAGAGGAATGTAGAGGACCGAACCCGTGCGGTTGATGAGTTCAAAGCGGCGGATCAAGAG  
CTGTCTTCTTTGAGTAAAGGCAGCAGTAATATTGAGTACCGTTTGTGTCAGGTGCGGGAA  
AATTTGTGTCAGGATTTGGGCGTGAGCCCGCGGGATATGCCCTTTGCCGGTGAGCTGATT  
GATCCGAATAATGCGGAATGGGAACCCGTTGTGTCAGCGCATTTTGGGTGGTTTGTGCTGCG  
GAAATGTTGGTTCCTCATGGGTGTTGCCACGGGTTCGGGATTGGGTAAATGCCAAACAT  
TTGGCAGCGCTGCTGAAATTCAACGGCGTGGTGACAACGGGGGAGTACAAAACCTCGCGT

TTTCCGGCGGATTCCCTGATCCGAAAAGTTGATGTTGTGGAGTCGCCGTTTCGCGATTGG  
GTAAATCAAGAATTAGGCAAGCGTTTTAATATTTCGGTGCCTGCGCACTCCTGAGGAATTG  
TCGGCGCTGGGGCCACGCGATCAGGGCGTGACCATTTTGGGTGTGCGAAAATTTGCGCAG  
CAGACAGGCGATCCGACGACGCGTTGGGAAAAAGATGATCGCCGAAAGCTGGGGGATCGT  
TCCACATACCGTTTGGGTTCCACCAATGATGCCAAGGTGGAAACGCTTCGGGAAACCGTG  
AAAGCTGGCAAAGCAGTTGTGCAGGCAGCTGATAATCGCATTTGCTGCAAACCGCGCTGAG  
CTGCGGGAACCTTGAACGGCAGTATCAAGCTTCGCAAGAAATTTTGAAAGTGTCTGTTGGCT  
CAGATTGATGTGGAATCAGCCGACGCGGCGATTGCTGAGCTGGACCGATTGCTGGAAGAG  
CTGAACAACACTCCAGAGGCCACCGAGCTTTCCGCGCGGCATGAGGCGGCGAAGCAGACG  
CTCGCGAGGGTTTCTGACTTGCTTGTGCGCAGCTCAGAGTGAGGAAACCGTGGCGTCGATG  
AACCTGAAACGCGCCGAAACTGAATTGAAACGGCTCGAAAGCCTGCCGGTTGCGGAGGTT  
TCTGAAGAAATCGCGCGGGAAGTGGAGAACTATTTCTTGCCAACACCCGCCGGGTTTAC  
GCCGCCAACGTGGATGAGCAGACCATTCGCGTGCAGGAGGATCTGGACAAACAAATCGAT  
GCCAATGAGGCAGAACTTCGACGTTGTGAAAACCAAATTTGTTGGCATTTTGCGCAGCTAT  
ATTGAAACGTGGCCTGCGAACCGCGCTGACTTACAAGCCGAACCTGAGTTTGTGTTGGTGAG  
GCCATCAACCGCCTCGGCGAGCTTCGCGAGCGATCGTTTGGCAGAATTCACGGCCAAATTC  
CTAGGGCTCATGAACGAGATGTCCACCCGAAACCTCGGCCAAATCTCGCGGCGTCTACGT  
GATGCGCGCCGGGAAATCGAGGAGCGCATCGAGCCGATCAACGCCTCCTTGGCGCAGTCG  
GAATTCAACGAAGGTCGCTTCCCTGCACATCGACATCCGTGATCAAAGTGGTCCGATTGTG  
AGGGAATTCCAGCAGAACTTGATGCCGCTACCAGCGGTGACCTGGGAACCAGTACCGAG  
AAACAAGCCTTCGCCCCTTATGCGCTGATCGCTGAAATCATTTCCAAACCTCGCCTCCAC  
GACTCCGCGACGCCCCTGGCGCAACACCGTTCTAGACACCCGCCGCCACGTTTCGCTTC  
ATCGGCCTCGAGCGCGATTCCGACGGCGCAACCGTCAACACCTACGTGACTCCGCATCA  
CTTTCAGGCGGACAAGCCGAGCTGGTGTCTTTCTGCTCGCCGCTGCCTTGCCTAC  
CAGCTAGCCGAACCCGGCGCCCATTTATCCACCTACGCCACCGTCATTCTGGACGAAGCC  
TTCGACCGCGCCGACCCCGCTTACCCGCCAAACCATGAACGTCTTCCACAGCTTCGGC  
TTCCACATGGTGTGCTCGCGACCCCGCTGAACTTATCCAAACCTCGGCGATTATGTGGC  
TCCACCATCGTGGTTCAGCTACACCGAAAAACCAAACGCCCGAGGGCGCAATTCAGGGCAAT  
TCCAGTTTCTCTAGGATCGAGAAA

>RXA02547-downstream  
TAACATGCCATTGTTTATCGACG

>RXA02561-upstream  
ATCTGCTCAATAACCTAACCTAAAGTCCATGCACGCCTCGTCGCCCCAACCTCACCTCA  
GCGCACCCGTGTTCTCAGCGGCCTGATTTTCGCCCAAATC

>RXA02561  
ATGGTTGGTGCATCCAATGGCGTGACGCTATCGATGGGAAGTTTGCTGGCAGCACACTTG  
GCGGGAGCTTCGTGGGGAGGATCAGCCGCCACATTGACCACGATCGGCGCAGCTATCTTT  
TCGATTCCCCTTGCCCGCATGGTCTCCACATACGATCGCCGAACTTCACTCAGCACGGGC  
ATGTTGCTTGGTTGCGTGGGCGCACTACTGGCGATCCTCGGCGCACAATTCGGCTTGTTT  
CCAGTAGTACTTTTGGCATTTTTGTTCCTCGGATCCATGTGCGCGGTAAACCTCCAAGCA  
CGTTTCGCGCAACCGACGTGGCCAGTGAAGAAACCCGCGGCGCGACCTCTCGATCGTT  
GTGTGGTCCACCACCATCGGCGCAATCGCCGGACCAAATTTATTTGAACCAAGCGCCCGA  
TTCAGCGAAACCTGGGCCTCGAACAACATGCCGGCGCATACCTGCTGTGTTTATTTGGC  
CAGCTCATCGCCATCGCAGTCTGGCGATTACCCCTCCCCAAAGGCCTCAAACCCGAAGCC  
ACCCCAAATGCACCAACAGAAAAGAAGCGCCTCACCCCGAAAGCCCTCCAAGCCATCACA  
TCGGTTGCAACCGCACACTTCTCCATGGTTCGGTCTCATGTCCATGGCCGCCATCCACATG

>RXA02566  
ATCAGTTTGCACGTGCGCGGAATGTACGCACTCTCACCAGTGTTTCGGCCTGCTCACAGAC  
AAACTCGGCCGCAATGTCACCATCTATTCCGGCTTCGCCATGCTCGCCACATCCGCAGCA  
TTTCTTATCATTTGGCCCGAACCACAGTGGGCCATGATCACATCCATGATCCTGCTTGGG  
CTCGGCTGGAACCTGCCCCTCGTCGGTCTTCAACATTGCTTGTGACGCCACCCCATC  
CACCACCGCACCTACGCCAGGGGCGCAGCGACCTAACGATGAATCTTGCGGGAGCTTCA  
GGCGGGTTGATCGCCGACCGTTAATTGCCATGGGCGGAATGCCCTTGTGTTGGCAGGCGTC  
GTTCTTGCAAGTTGTGGCGCTTCAAACGGTGCTTAGTTTCAGAACCCGTTCAATTGAAAAG  
ACTCCTGCTTCATGTTTT

>RXA02566-downstream

TAGCCTAGGAATTCACGCACGAC

>RXA02571-upstream

TGGACAGGCCGGGGCCGCGTACGGTGTGGTTGAGGTGGTGGAGGGGCGCGTCGAAAAGC  
ATTGTCGCTGGTTGTTGCCGCTTTTGGCAGTCGGGATGGC

>RXA02571

GTGGTGGCTCTAACTCAAATCGTCGGACCGTCCGGCTCCGGGCTCACGCGGGAATTGGAA  
AAACGCTACCGGGAAACGCCCGGAGCGGTGATGCTGACCGCCGACCCGCGCGCATATC  
ACCTACCTGCGCGCGACAGTCGCCGAGGAGCTGGCCTTTGGGCTGGAACAACGCGGCATC  
GTACCCGCGCAGATGTGGGAGCGCGTCCGAAACATCGGGCTCGGCCTCGAGAATCTGCTA  
GACCGCGCACCCGCGCAACTTTCCGGCGGGCAAACACGGCGGCTGGCGATCGGCACCGTC  
GCCATCTTAGAGGCGCCAACGATGCTTCTCGACGACCCCTCTCCGGTCTTGATACCTCC  
TCGCGAGCCCAACTCATCACAATGTTGGAATCATATGAGGGCGATGTCATCGTCGCTGCG  
CACAAGCGGTGGCTCGACGCGCCGACTGTGTACTTAGGGGATTTGGAGGAGCTGTCCCTG  
CCTGCGCGGGTGGAAATTTCCGGTCCATCGCGAACGTTTTTCAGCGATTACAGGAACCCGC  
GGACAACAACGCCGACGCTGGTGGCAATTC AACGAATCCCAACCACAGTTTCAGATCGGC  
CCCCTGGATATTACTGTTTCTGCAAGTCAAGTGTGTGGTTGCAGGGTCCCAATGGTTCA  
GGGAAGTCCACACTCCTGCGTGGTCTTGCCAATGAACCCGGCACTGAATTGATGCTGCAA  
AACCCTAGCGATCAAGTCATTGACTCCACTGTTGCTAATTGGGTGCCAGGCAGTAACAGT  
GAAGAACATCCGCTGGATTTATCGCAACGCGAACTCCGCCTTGCCCAATGCGACGCAGCC  
CTGGGTAAATAACCCGGAAGTTTTGCTTGCTGATGAACCCGACGTCGGCCTTGATGTCGGC  
GGTCGAAACGCCATCCACCAGCGCTTTGCGGATTTCTTAGGGAAATGGGGGAGCGCTGATC  
CTGACCTGCCATGATGAAACCTTCGTGGCAGAGGTAGCTGAATACGCGATAGTGAAGGAA  
ATGGGGCTC

>RXA02571-downstream

TAGGTTTCTTTGGACCAAACCAC

>RXA02578-upstream

GGCAAAATGAGGAACAGCACGCCCGCAATAATGAGGACCGTTGCAGATCGCTTCATAAA  
AACAGCCACACCTTTCCGCTAAACTCGCATGTTGAAATA

>RXA02578

ATGTCTACCCAATCATATGCACCCATCCGCCATCGCGGATTCATCAGCTCACTCGAGGGA  
CTACGCGCAATCGCCTCCCTGGGAGTCTTGGCGACCCACGTTGCATTCCAAACCTCCGTC  
GACCCCGCCAGCAACATCGGTGCAGTACTCGCGCGTTTCGACTTTTTTCGTCGCCGTCTTC  
TTCGCCCTCTCCGCCTTCGTTCTTTGGCGACGCCGCGCCGGGCAACCAGTGGGACTGTAC  
TACCTCAAACGCCTAGCCCGCATCATGCCCGCATACTGGGCAACGGTCATTGCAGTCCTG  
CTGTTTATTCCCACCGGCCCTGGTTAGCCAACCTGACGATGACCCAAATCTACTGGCCA  
GACGGGCTCATGACAGGCCTCACCCACCTTTGGTCCCTGTGCGTGGAAGTGGCGTTTTAC  
CTGGTGATGCCGCTTCTCGCGTGGGTGTTGGATAGGTTTGGTTCGGCCGGTGCGCATCCTG  
TTGATTGTTGGTGGGGCAGTGTTGAGTCTGGCGTGGCCGTGGATTCCCCTTGTGGAGCAT  
GCGTTGGACGAGGGGTGGGCGAACATGCAGATCTGGCCACCCGCTTACGCTTGCTGGTTT  
GCAGTCGGCATGATCGCCGAGAAATTGAAGGAGTTCGATTCCCACGGGTTCGAGCTTT  
GTGTGGGTGGGTTTAGCTTTAGTGGTCTGCTTGGATCGCGGGCCAAGAATGGTTCCGACCA  
CTAGGTTTAGTGACCCCCAGCCCCTGGGAATTCAACTTAAGAGTCCTCGCGGGCACACTT  
TTCGCTGTATTTCTGGTGGTTCCCTACGCGCTGGGTACGCCCTCTCGGCTTCTTGATTCC  
AGTTGGATGAAAACGCTCGGCACCTGGTCTGATTCCATCTTCCTCTGGCACCTTCCCGTG  
CTGACGATTGTGTTCCCACTGCTCGGGTTGCCTTTATTTAGTGGAAATTTCTGTTGGTG  
TTCATCGTGACGGTCTTGTTGACGATCCCAAGTTGCCGCCATCAGCTACACCTTCATCGAA  
GAGCCCATCAGCGGTGGACCCGGCGCGCCATTAGGCTGGGGGTCGTTAGGATTCACCAT  
TTTTCTGGGGGTAGGTCTGGAAAA

>RXA02578-downstream

TGATGAATTGGCACCACGTCAAG

>RXA02581

GTCCCTGTGCCGCTTTATGATCCAAACGAGCCAGGACACGCAGACCACCTCAACGCTGTT  
TTCGACAGACGAGCCAGTTGTCGTTCTGACCAACTCCAAGTCCGCAGGTGCCGTGCGC  
AAGCACTTCTCCAGCCTTCCAGCTGCAGAACGCCACGCATCCTCTCTGTAGATTCTTG

CCTGATTCTCTCGCGGATTCTTACGAGAACCCAATGCTGACCGAAGCCGGCCGCGCCTG  
GCTGCTCTGCGCCAGTCCGCGCCCATTTGATCTGACCGCATTCTGTCAGTACACCTCCGGC  
TCCACCCGAACCCAGCTGGCGTTGTTCTGACCAACCGCTCCATCCTGACCAACGTCTTG  
CAGATCTTCAGCGCCGCACAGCTGAAAACCCCACTGCGCCTGGTTTCATGGCTGCCACTG  
CACCACGACATGGGCATTATCCTCGCGGCGTTTGTCACTATGCTTGGCCTGGACAACGAG  
TTCATGAACCCACGCGATTTTCGTGCAGCAGCCTTCCCGCTGGATTAAGCAGCTCAACCGT  
CGCGAAAGCGACGTGGACGTTAACGTCTACACCGTGGTTCCCTAACTTCGCCCTCGAGCTT  
GCAGCACGCTACGCAAAGCCAGCAGAGGGAGAGACCCTGGATCTTTCCGCATTGGATGCC  
ATCATTATCGGTTCCGAGCCAGTCACAGAAAACGCTCTGACCACCTTCCGTGAAGCTTTC  
GAGCCTTACGGCCTGCCTGTTTCAGACCCTGCGTCCTTCCTACGGTCTTGCAGAAGCATCC  
CTGCTGGTCAACACCCACAGACCGAAAACCGCCCACTGATCTCCTACTTCGACCGCGAG  
GCCTTGGCCGAAAACCGCGTTGAGCTTGTAGAAAAGGGCAATAACAAGGCTGTTGCTTTC  
GTCTCCAACGGCCAGGTTGCAGCCCCACAGCAGCTGGTCATCGTTGATTCCGAAACCGGA  
ACCGAGCTGGCAGACGGCCAGATCGGCGAAATCTGGACCCACGGCGAAAACACTGCTGCA  
GGTTACCTCGACCGCGAGGAAGACACCGCAGAAACCTTCCGCAACCGTCTGACCACCCGC  
CTGGAAGAAAACCTCCCGCGCAGAAGGTGCTGCCGACGACAATACTGGATGGCCACCGGT  
GACCTCGGCGTCATCGTAGACAACGAGCTCTACATCACCGGTGCTCTGAAGGACCTCATC  
GTTGTGCGCAGGCCGAAACCACTACCCACAGGACATCGAGTACACCGTCCAGGCTGCTTCC  
GCACACATCCGTGCAGATTCCGTGCGAGCATTGCGAGTCCAGGCGATGACATTGAAAAG  
CTCATCATCCTGGCAGAACGCGACACCACTGCAAACGAAGCCGACGATGCAGCTGCTGAA  
GAAGCAATCCGCTCCGCCGTTGGCACTGCACACGGTGTGTTCCAGAAGAGATCCGTATC  
CTCGCACCTGACGAGATCGCGCGTTCCTCCTCCGGAAAGATCGCACGCCGCGTCAACCAG  
CGCAACTACATTCAGGAACAAGCTAAC

>RXA02581-downstream  
TAGTTCTTTGCAGACACCGCAGG

>RXA02582-upstream  
TGGATGTCTATTCTCCTCAGCCTCGTTTTGGTTGAGGCGGATAGTTTTAATATTTTTTTTA  
AGTTTAAGTTGTAATCGAGCTGAAAGGCTGAGGCCTCAAT

>RXA02582  
ATGGAACAGAGCCAATCGTCGGATCAGAAGATGACCGTTGAACAGGTTTCGCACCTGGCTC  
CGTGATTGGGTTGTCCGCACCACGGGTATTCCGGTGGAGGAAGTTACGGATGACAAGGCA  
ATGGAGACCTTTGGCCTTTCTCTCGCGATGTTGTTGTGTTGTCTGGTGAGCTGGAAAAC  
CTGCTGGACACCTCCTTGGATGCCACCATCGCTTATGAGTACCCAACGATCCGTAGTTTG  
GCGCAGCGCCTTGTGAGGGCGAGCCTCGTCGTGCACATAACCCAGCGTGAATTGAATTTT  
TCCGCGGTGAGCGATTCCCCAGGTTCCACGATATTGCGGTTGTGCGTATGGCTGCGCGT  
TACCCAGGCGCTGAGAGCCTGGAGGATATGTGGAAGCTACTCGTCGAGGGCCGTTGACGGT  
ATCTCGGATCTACCGATTGGCCGTTGGTCTGAGTATGCAGGCGATGAGGTTATGTCTCGG  
AAGATGGAAGAGTTTTCTACCATCGGTGGCTACCTGTCAGATATCTCTAGCTTTGATGCG  
GAGTTCTTTGGTCTGTCTCCGCTCGAGGCCGCAACATGGATCCTCAGCAGCGTATTTTG  
CTGGAGCTAACGTGGGAGGCTTTGGAGTACGCTCGCATCGCACCAAAACACTTTGCGTGGC  
GAAGCCGTGGGCGTGTTTCATAGGTTCTCCAACAACGATTACGGCATGATGATCGCTGCC  
GATCCAGCAGAAGCACATCCTTATGCGCTGACTGGTACTTCTAGTGCGATTGTGCTAAC  
CGCATTAACCTACGCTTTTCGATTTCCGCGGTTCCTCCGTCAACGTGGATACCGCATGTTCT  
TCTTCTCTGGTAGCGGTTACACAGGCTGTCCGTGCGCTGCGTAATGGCGAAGCGGATCAC  
GCTATCGCTGGTGGAGTGAACATTTTGGCATCTCCATTTGTACAACTGCATTGCTGAG  
CTCGGTGTGATCAGCCCAACCGGCAAGATCCACGCATTCTCTGATGATGCCGATGGTTTC  
GTGCGTTCCGACGGCGCCGGAGTCGTTGTGCTGAAGCGCGTGGATGACGCAATCCGCGAC  
GGCGACAAGATCATCGGTGTGATCAAGGGTTCTGCAGTGAACCTCCGATGGTCACTCCAAC  
GGAATGACCGCTCCAAACCTGACGCACAGGTTGATGTGCTGCAGCGTGCATATGTTGAC  
GCTCAGGTTGATCCCACACCGTGGATTACGTTGAGGCTCACGGCACCGGCACCATCCTG  
GGTGACCCCATTTGAAGCAACTGCCCTGGGTGCTGTTTTGGGCTATGGCCGTGACGCATCC  
ACCCCAACTCTTCTGGGCTCTGCAAAGTCCAACCTTCGGCCACACTGAGTCAGCTGCGGGT  
ATTGCAGGTGTCATCAAGGTGCTGCTTTGCTTTGCAGAACAAGACTCTGCCACCAACCGTG  
AACTTTGCAGGTCCAACCGCTACATCGATTTTCGATGCTGAGCGTTTGGAAAGTTGTGGAA  
GATCCACGTGAATGGCCGGAATACAACGGTCACGCAGTAGCTGGTGTGCTGCGTTTCGGG  
TTCGGTGGAAACCAACGCGCACGTGGTGATCTCTGAGTACAACGCAGAAGACTACGAAACC  
CGTGCCCCGAAGGAGGCGTTGCTTCCCTGACCAGCAGGTTGCCCTGCCGGTGTCTGGTCAC  
CTGCCATCCAGGCGTCGACAAGCAGCTGCTGACTTGGCGGACTTCTTGGAGGGCCGCAA



GATTGCGACCTAACCCAGTAGCCCGCGCGCTGGCAGGCCGCAATCATGGCCGCTCCCGC  
GCAGTCGTGCTTGCAAGCACTATCGAGGAAGCCGTAAAGCGCCTGCGCCAGGTCGCAGAA  
GGCAAGGTCAGCGTCGGTATCTCCGCAGCTGATTCCCCAGCGGCCAACGGTCCTGTGTTT  
GTGTACTCCGGTTTCGGATCCCAGCACCGCCTCATGATCAAGGAATTGTGCTCAATTTTCG  
CCACAGTTCCGCGAGCGCATCGAAGAGCTCGATGAAATGGTTAAGTTCGAGTCCGGCTGG  
TCCATCATGAAACTTGTTTTGGATGATGAGCAAACCTTACGACACCGAGACCGCGCAGGTT  
GTGATCACCGCAATCCAGATCGCACTGACTGACCTGTTGGCAAGCTTCGGTGTAAGCCA  
GCTGCCGTCATGGGCATGTCGATGGGTGAGATCGCTGCCGCTTACGCTGCCGGTGGACTC  
AGCGACCGCGATAACCATGCTCATTGCCAGCCACCGTTCCCGCCTAATGGGCGAGGGCGAG  
AAGTCCCTGGCTGAGGATCAGCTGGGTGCCATGGCTGTGGTGGAATTTCGCCGCTGCGGAC  
CTGGATAAGTTTCATCGAAGAAAACCTGAGTACAAGGGCATTGAGCCTGCTGTTTATGCA  
GGCCCAGGCATGACTACCGTGGGTGGACCTCGCGACGCCGTGGTTTCAGTTCGTAGAGAAG  
CTGGAATCTGAAGACAAGTTTGCCCGCCTGCTCAACGTCAAGGGCGCTGGCCACACCTCT  
GCTGTGGAACCACTTCTTGGTGAGCTCGCTGGCGAAATCGCTGGCATCGAGCCACTTCCG  
CTGCAGATCCCGTTGTTTCAGCTCTGTGATCAGGGTGTACCTACCCAGTTGGAGCAGTG  
GTCCACGACGCCGATTACATGCTCCGCTGTACCCGCCAGTCCGTGTACTTCCAGGACTCC  
ACCGAAGCTGCATTCGCTGCAGGCCACAACACCTTGGTGGAATTTCCCCGAACCCAGTT  
GCACTCATGGGCATGATGAACACCGCGTTTACCGTGGGCAAGCCTGATGCACAGCTGCTG  
TTCAGCCTGAAGCGAAAAGTCCCAGAGGCAGAATCCCTCCGCGACCTTCTGGCGAAGCTG  
TACGTCAACGGCGCAAACGTTGATTTCTCCGCGCTGTACGGCGAAGGTGAAACCATCGAT  
CCGCCACACATCACCTGGAAGCACCAGCGCTTCTGGACTTCCGCACGCCCATCCTCTGGC  
GCATCCCTGGATCTGCCGGGCTTCCGCGTGAATCTGCCAAACAACACTGTGGCGTTTTCC  
ACCGCAGCCGAACCTGGCACCATCCGCAGTGGCAATCATGGAAGCAGCCGCCATGGCTGTC  
ACCCCAGGTTCCCTCCGTCGACGCAGTGGACGAGCGCGACATGCTGCCACCAAGCGGCGAA  
ATCACCAACCATCGTGACTCGCTCCTTGGGCGGTTTGAGCCTGTCCGTATACAAGATTGAG  
GGAACCACCAGCACTCTTGTGCGCGAAGGTTTCGCAGCCAACCCAGGATTCGCCGCAGCA  
TCTTCCTTTCGACGGTCCAGGCTACGACGGATTCAACACCGATTACAGCGACCAGCCAGAC  
CCTCGCTCCGACCTGCCTTTGGACATCGAAGCAGTCCGCTGGGACCCAGCGACCGAAACC  
GTCGAAGAGCGCATGCGCGCCATCGTCTCCGAAGCAATGGGCTACGACGTGGATGACCTC  
CCACGCGAACTCCCACTGATTGACCTCGGCCTCGACTCCCTCATGGGCATGCGCATCAA  
AACC GCATCGAAAATGACTTCCAGATCCCACCACTCCAGGTCCAAGCGCTCCGCGATGCA  
TCCGTCGCTGACGTGGTAATCATGGTGGAACATGGTTCGCTGGCCGCTCCTCTGAGACG  
CTTGTGCGACGCCACCCCGCAGGTGCCAGCTGAGGCAGCAGGGGAGGCTCAAGCTGCTGAG  
TCTTCTGCTTCGGGCGAGGACGTGCAGGGCGTTGGCGTTGCACCGCGAGATGCGTCCGAA  
CGCATGGTCTTTGGTACTTGGGCAGGCCTGACTGGCGCTGCGGCAGCTGGCGTGACCAGC  
AAGTTGCCACAGATCGATGTCGATACTGCAACCGCAATTGCCGAGCGCCTCACCGAGCGT  
TCCGGAATTGAAATCAGCACTGAACAGGTGTTGGCTGCAGAAACCTCGAACCCTGTCT  
GACCTGGTGCGTGAAGGCCTCGAAACTGAAGTTCAGGGCAACATTCGTGTGCTGCGTGGA  
CGTGCAAGAGGCTCCACCAAGCCTGCAGTGTTTCATGTTCCACCCAGCTGGCGGTTCTTCC  
GTGGTCTACCAACCACTAATGCGTCGTCTGCCTGAAGATGTCCCTGTCTATGGCGTTGAG  
CGTCTGGAAGGCGATCTCGCTGACCGCGCGGCAGCATATGTTGATGACATCAAGAAGTAC  
TCCGATGGCTTCCCAGTAGTTTTGGGTGGCTGGAGCTTCGGCGGTGCCGTTGCCTTCGAG  
GTTGCCACCAACTGGTTGGCTCCGATGTTGAGGTAGCTACCGTGGCGTTGCTGGATACT  
GTGCAGCCTTCAAACCCAGCACCAAGATACCGCTGAGGAACTCGTGCACGCTGGACTCGC  
TACGCGGACTTCGCCAAGAAGACCTACGGCCTTGATTTTCGAGGTACCTTTTGAAATCTTG  
GACACCATCGGTGAAGACGGAATGCTGTCCATGATGACCGACTTCCTGGCCAACACCGAC  
GCCTCCGAGCACGGATTGTCCGCAGGTGTGCTTGAACACCAGCGCGCTTCTTTTGTGGAC  
AACCGCATCCTGGCTAACTTAATTTTGCAGACTGGGCCAACGTTGAAGCCCCTGTCATC  
CTGTTCCGCGCGGAACGCATGCATGATGGAGCTATCGAACTTGAACCAAATATGCCAAG  
ATTGATCAAGATGGAGGATGGTCCGGAATTGTCAACGATTTGGAAATTGTTTCAGCTGAAT  
GGTGACCACCTGGCAGTTGTGATGAACCAGAAATCGGCACAGTCGGAGCTCATTTGAGT  
CGCCGCATTGATGAGATTTCTCGGAAGAAT

>RXA02582-downstream  
TAGTAACGGAGAGCTGACGGAAG

>RXA02583-upstream  
CAGTTGTCGATGAACCAGAAATCGGCACAGTCGGAGCTCATTTGAGTCGCCGCATTGATG  
AGATTTCTCGGAAGAATTAGTAACGGAGAGCTGACGGAAG

>RXA02583

TTGAGTAACACCACTACTGCAGAGAAGCTAGCGGATCTGCGCGCACGCCTGGAGATTGCC  
AAAGACCCAGGTAGTGAACGCGCACGTAAAAAGCGCGACGAGGAAGGCCGAACCAACCCCT  
CGTCAGCGTATTGATGCTCTGCTTGATGCCGGATCCTTTGTGGAGATCGGCGCACTAGGC  
CGTACCCCGGATGAACCCGATGCGCCTTACTCTGACGGTGTGGTGACTGGTTATGGTCGC  
ATCGATGGTCGCCCAGTGGCCATCTACGCCCATGACAAGACCGTTTACGGTGGTTCCGTG  
GGCATGACTTTCGGACGTAAAGTCAGCGAAGTCATGGACATGGCTATCCGCATTGGTTGC  
CCAGTTATCGGTATTCAGGATTCGGGCGGAGCCCGCATTTCAGGATGCGGTGACCTCCTTG  
GCGATGTACTCAGAGATCGCGCGTCGTCAGCTTCCGCTGTCTGGCCGCAGCCCTCAGATT  
TCCATCATGCTGGGTAAATCGGCAGGTGGCGCAGTGTATGCACCTGTGACCACTGACTTT  
GTTATCGGCGTGTGATGGTGAAACAGAAATGTATGTACCGGGCCAGCCGTGATCAAGGAA  
GTCACCGGCGAGCAGATCACTTCCGCAGACCTCGGTGGCGGTGCGCAGCAGATGCAAAAC  
GGCAACATTTCTATTTGGCGTCTCTGAAGAAGAGGCCCTGAATATGGTCAAGGATTTG  
CTCGACTTCCTGCCTTTGACCTGCAATGATCCAGCCCTGTGTTTGCAGCACCAACGGAT  
GAAGAGATCGCCTACGACGAAGCTCTGAACCTCGTTCATGCCTGACGACACTAACCAGGGC  
TACGACATGCATGACCTGCTGGACAAGCTTTTCGACGACGCCAACCTGCTGGAAATCCAA  
GAGGAGTACGCCCCAACCTGATCACTACCTTCGCCCCGCTTGATGGCAAGGCAGTCGGT  
GTGGTGGCCAACCAACCAATGGATAAGGCAGGCTGCATCGACGCTGACGCCGCCGACAAG  
GGCGCCCGCTTCATCCGTATCTGCGACGCCTACAACATCCCGATCATCTTCGTCGTGGAC  
ACCCCTGGCTACCTGCCTGGCGTGGACCAAGAGAAGGTCGGTTTGATTACCGTGGCGCA  
AAGCTAGCCTTCGCAGTGGTGGAAATCGACCGTCCCTAAGATTTCTTTGATCGTGCGCAAG  
GCCTACGGCGGAGCATATGCCGTGATGGGTTCGAAGAACCTCACCGGTGACCTCAACTTC  
GCATGGCCAACCGCACAGATCGCCGTGATGGGCGCAGCCGCAGCTGTCGTGATGATCCAG  
GGCAAGCAGCTCGAAGCCGCCACCTGAGCAGCGTGAATACATGAAGAACTGTTTCATG  
GACTTCTACGATGAGAACATGACCAGCCCATATGTGGCCGCCGAGCGTGGTTACATCGAC  
GCCATGATCGAACCTGCAGAGACCCGTTTGGTGCTTCGCCGAGCAGTCCGCCAGCTGGAA  
ACCAAGGCTGTGCGAGACCTCGACAAGAAGCACACGATCATGCCGATG

>RXA02583-downstream  
TAACGTCCAAAGAATTATCCAGA

>RXA02599-upstream  
GATCAAGCATCATACGATGTCGGAGATTGTGGCGGGCGTTGTTACAGGAGCAGTTGCAAC  
CGGCATTTGTTATGCACTCCTACTTGCGTAAAGGAGAATT

>RXA02599  
ATGGATCAGCTAATCCTCGACGCATTTATCGGCTTGAGAGTGACTTGGCTGAGTCCGGTG  
ATTATTTTGTTCACCCAGCTCACCGGGCCAACACTGATGTTTGTGTATGCGCTTGTGTGG  
GGCTTGTGCGCAAGAGCGCCACTGCCCCGATCGCGGTGGGGCTGGCTAATCTGATCAGT  
CATTTTCTCAAGAGGGCGTTTGAACGGCCTCGACCAAATACAGCAGAGCACTTGGTTGTA  
GAAACTAACTTTTCATTCCCTTCTGGTTCATGCTGTGGGCGCTGCAGCATGTGCCGTGGCA  
GTGGGGTACTCCGTGAACCGGTGGTGGAACTCACGCTGTGGGTAATCGCGCTGCTTGTG  
GGGCTGTCTCGGTTGTATGTGCGGTGTGATTGGCCAGCGATGTGCTTGCCGGCTGGGCC  
ATCGGTGCGTTGACTTCAGTGGTGGTGTACCAGCTGGAACCTCCTCCAGCGCCGC

>RXA02599-downstream  
TGAAACCACTGCTGAAAGTGGA

>RXA02618-upstream  
CGAAACCAGAAACACCCAGCGGCTCCTCGTCGAAAAGCGAATCTTTGAACTAGAAGCCCA  
GGCACGTTGGCTCGACCGAATTGAAGCATTGGAGCAGTAA

>RXA02618  
ATGACAAACACGCCTTTCCCCCTTGAACCTTCAAAACATCTCCTGCGCCTTCGGAGAAGGC  
CCACGCCACGTCTCCGCGCTCAACAACGTCTCGCTGGCAGTCAATCCCGGCGAACTCGTT  
GCCATCATGGGCCCCGTCCGGCTCAGGAAAATCCACCTTGCTCAACGTGCGCCGGCCTCCTG  
CAGCGCGCAACCTCTGGCCATGTGCTTATCGACGGTGCCAGCGCCTCAGACCTCAACGCC  
AAACGCGCAGCTGAAACCAGGCGTCGCCACATCGGAGTTATTTTCCAAAACCTACAACCTG  
GTCCCCACCTCACCGTCGGAGAAAACATCGGTCTGCCCTAGAACTCGACGGCAAAACC  
GACCGCCAGGCAGTAGCAATCGCACTCGCGGAAGTCGGCCTCAAGGGCTCTACGACCGCT  
TTTCCCGAGAGATCTCTG

>RXA02634-upstream

CAACGCGAAGGCTTAGTTGTTTATTACCGGCTCACCTACCCGGAGGTCGCAGACTTTCTT  
AAGGTGAGCCGCTCACTATTAAAGAGGATGGCTGGCGAAG

>RXA02634

ATGCGTGACCTTTTACCCTCTAGAGACGACTATCAGCTACTCCGCTTCTCCTGGAAGATG  
GACATTGCTGCTGGCGTCACCGTGGGCATTGTTGCCCTCCCCCTCGCTCTCGCCTTTGGT  
GTGAGTTCTGGAGTCGGAGCCGAGGCAGGATTAGTGAAGTGCATTATTGCTGGCCTGGTT  
GCAGCAATCTTCGGCGGTTCCAATGTGCAGGTTTCAGGACCAACAGGAGCGATGGTGGTT  
GTTCTCGCTCCAATCGTCGCCCAATATGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
GCTGGAGTTATCGTCCTTGTGCGCCGAGTGCTTCGATTAGGCCGAACGGTGAGTTTCATT  
CCGTGGCCGGTTCATCGAAGGATTTACGGCAGGCATCGGTGTGATTATTTTCCTGCAACAG  
GTGCCAGCTGCGTTTGGTTATTCGGGCCATTTGCCACCAATGCGCTCCTCGCTGCGATT  
CACACTGTTTCACACGCCACGAAGGACGCAATTCTACCTCTCTTAATTATTATCGTCACC  
GCTGCGATCATGATTGTGTTGGGAAAGATCGCCCCAAAGCTCCCTGCCAGCTTCATTGCC  
ATTTTGGTGGTGTCCATTGGCGTGGCTCTGCTCAAGCTTCCCGTTGAGTTGATCGGTGAG  
CTCCCCAATTCCCTTCCTGCCCCCTCACCTGCCTGATGTGAACCTGGAGATGTTACGAGT  
TTGCTGGGGCCAGCTTTTGTGTCGCGCGCTCGCTGCTATTGAGTCTCTCCTTTCCGCT  
CGTGTGGCAGCCTCCATGGCCGATACGGGTCTTATAATGCTGACCGCGAATTGGTCCGT  
CAGGGGTGGCGTCGATAAGCGCTGGCTTTTTTGGCGGCATGCCGGCAACTGGCGCAATC  
GCGCGTACGGCGGTCAATGTGCGCTCCGGCGGGCGTACCCGTATAGCGTCGATTATTCAC  
GCGCTTGTGCTGCTCGGCGTTGTGTATGTGGCGGCGAATATCGTTGCGGTTCATTCCGCTC  
GCCGCACTGTGCGGCGTGTGCTCATGGTCACCGCGAGCCGCATGGTGTCCATTGAAGTGATC  
TCGCGCGTTCATGCGCTCCACTCGCTCTGATGCGATCGTTTTTGTGTCATCACCGCGATCGTC  
ACCATCAGCGTCGACCTCGTCATTGCGGTTCGGCATCGGCATTGCCGTGCGGACGTTCTTC  
ATGCTGCGACGCATGAGCATGAACGCCGGCGTCTTCCGGGAAACCTTGCCCCGAACCGGCC  
ACGCTTAACGACGAAAAGATCGGCCTTTTCCGTATCGAGGGCGCATTTGTTCTTTGGCGCA  
GCTGAACGTCTTTTCGACGCAAAATCCTTGATTATGAGGACCTCGAAGTGGTGATCCTGCGC  
CTGTACACATCCAAATGATCGACGCCACCGGCGCCCCACAGCTCACCGAGCTTGTCAAT  
GCGCTGGAAAGAAAAAATGTCACTGTATTAATTAAGGGCGTCCGGAAAGAACACATTAC  
GTTCTCGGCGTCTCGGAGCGATCAGATCACTGCGGCATGAGAACCACCTCTTCGATGAC  
CTTGCCCCAGCGGTGAACATGCCCCGAAACACGTTAAGATCGACAACAGT

>RXA02634-downstream

TAAGGCTTCCGGGGCGATCTAAA

>RXA02638-upstream

ATGAAGA

>RXA02638

ATGGCGCGGAAGCGTCTTAACGCCGGCAGCCTCGTCGGTATCTTCCCTGAGGCGACGGTG  
TCACGGTCCCTTTGAAATCAAGGAACATAAACTGGCGCCGTCCGCATCGCCGACAGCGCT  
AACGTTCCGCTGCTGCCACTTATTATTTGGGGCGGCCAGCGCATCATCACCAAAGACATC  
GAGCGCGACTTCGGCCGCTCCCACATCCCCGTATTCATCAGCGTGGGTGAACCCGTCGAC  
GCCAGCGGCGATCCCGACGAAGCAACGGAACGCCTCTACGAGGCTATGAAAAAGCTTCTC  
GACGAAACCCGCACCGCCTACGAACAAAAGTATGGCCCATTCGAAGGTGGAGAATTGTGG  
CGCCCGAAATCCCTCGGCGGCGGCGCCCCAACGTTGGAGCAGGCGAAATGTTGGAAATC  
GCCGAACGGGAACGTGACAAGCAAAACGCGCGGCAAGGTGCGCAAGAAACGCACCACC  
TTTATAAGGAAAATCTTTAAAAAA

>RXA02638-downstream

TGATTGCACTGGGTTCAGCGCCC

>RXA02659

TTCGGCAACGACCCAGACCTCCTCATGCGCTGGTGGTACGCCGGCGACGTCTGGACCGAC  
TCCCGCATGCACTGGAAGGGCAGCGAATCCTACGACCAGGTACAAAACCTCCTGGAAGAA  
GGCATCCGCGCTACCGACAAGGCAGAACAGCAAGACATCTGGAACCGCACCTTCGATGTC  
ATCTCCGACAATGTTCCCTCTACCCGCTGTTCCACCGCAAGGTCCCAACCGCATGGAAC  
TCCAACGCCCTCGTCGACTTCAAGCCAATCTCACTACCGGCTTGAACCTCTCAGGTGTT  
GCAACTACTGAA

>RXA02659-downstream  
TAACAACCCCAGTGGCTTTCAA

>RXA02676-upstream  
AACCATTGGGTATTAAGAAATTTGTGGCTTAGATCTCAATTTCTGTATAGTTTGATCATA  
CTAATTCATCCACTTCCAAATTTTCACGAAGGATCACCCC

>RXA02676  
ATGGACACCTGGGAACAAACCCTTGGAACAGGGCCACTGCTAGGCATTGCAGCCGGCGCC  
ATTGCCCTCATCTTGGTTCTCGTCATCGTTTTTAAACTCCATGCTTTTCTCACCCTAATA  
CTGGTTTCAATTGTTACCGCACTTGCTGCCGGCATTCCCGTCACCGCAGTAGTGGACACT  
CTCCTTGACGGTTTTTGGTAAAACACTCGCCTCGGTCGCCCTATTGGTAGGCCTGGGTGCC  
ATGCTTGGTCGATTGGTTGAAACATCCGGTGGCGCAAAATCTCTAGCCGACACTATGGTG  
CGAATCTTCGGTGAAAACGAGCAGCTTTCGCACTCGGTGTGCGATCGCTGATCATGGGA  
TTCCCTATCTTCTTCGATGCTGGCCTCGTGGTCATGCTCCCAGTGATCTTCGCAGTAGCT  
CGACGCCTCAACGGCTCCGTCCTTACTTTTGGTATCCCTGCAGCTGGCGCCTTCTCTGTC  
ATGCACGTGTTTCGTCACCTCACCCAGGCCAATTGCAGCCTCTGAATTCTTCGGCGCA  
CAAGTTGGATACGTACTAATCGCTGGCATCATCGTTGCACTACCCACCTGGTATTTAACC  
GGTTACCTGCTAGGTAAGTTCTTAGGCCGAAAGTTCCCCCTTCCCGTACCCGATCTACTC  
AGTGGTGGAGCACAGGAAGATGATCAGCCTCAGAACCCAGCTAACGCAGTGTCGATCATT  
GTCATTTTGCTCATTCCTATGCTCCTTATTTTGGCAATACCGGAACATCAATGGCAGTT  
TCCGCCGGCCTCCTAGATGCAGAATCCACCATGGTGAAAATTCTAGGATTCCTCGGCGAA  
ACACCAGTGGCACTGCTCATTACCTTGATCATTGCCCTGTTCTTCCTAGGCAACCGACGT  
GGCATTAAATGGTTCTGCTCTAGAGAAAACCATCGAAGGCGCACTCGGCCCAATCTGTTCA  
GTCGTATTAATCACTGGCGCCGGTGGCATGTTCCGGTGGAGTGCTACGCACGTCTGGAATT  
GGAGGAGCGCTTGCAGACTCCATGGCAGATCTAGGACTTCCAGTTATCGCAGGTTGTTTC  
ATCGTGGCAGCCGTCCTTCGTGTCGCGCAGGGTTCTGCCACCGTTGCGCTAACCACCGCC  
GCAGCACTCATGGCACCTGCTGTTGCCGCTGCTGACTTTAACGAATTCCAGCTTGCTGCC  
ATCGTTATTTCCACTGCCGCTGGTTCTGTTATTGCCAGCCACGTCAACGACTCCGGATTC  
TGGCTCGTTGGTCGACTCATGAACGCCGACGTACCCACCACGCTAAAACTTGGACCGTA  
AACCAAACCTGCATTGCGATTGTGGGATTTGTGATGGCCTATGCAATGTTCCGATTGGCA  
TCGCTTGCA

>RXA02676-downstream  
TAGTCCGCTGACCCCATTGATTC

>RXA02677-upstream  
TTAGTGCAGTGTATTTATTTCCGTTACGCTGCGGGGCTGGTGGTTTGGAGGGATACTAG  
AGTCGATAGCAGGTATATAAAGGCCAGGAGAGATGGGTTC

>RXA02677  
ATGAAAGTCATCGCGCACCGAGGTTTATCGTCTCGCTTTCCCGAATTAACAGAGTCTGCG  
TTTCGGGCGGCTCTAGAGCTACCGATTTCATGGAATTGAAACTGATGTCCGGCTGACTAAA  
TGTGGCGAAGTGGTTAACGTCCATGACCCCATTTGTGGATCGCGTGTCGAATGGTCGCGGT  
CGGGTGTGCGGTTTGGACTTGGAATCCTTGCTGAGCTTGAACCTTGGAAACCAAGAAACC  
CCAGAAAAAGTGCTTACTTTAAACAATCTATTAGATATTTTGGAGGATTATCCAGATAAG  
CACCTTTATATAGAAACCAAGCACCCAATGCGCTACGCGGTTCATGCTGGAAGAAGAAATC  
ACAAAAATCTTAAATATCGTGGGCTGACGGAAGACCCACGCATCCACATCATTTCTTTT  
GCACTTCCCGCGATGTATCGCATGGCTCGCCTTGCTCCACAGCTTGATCGCATTCATCTG  
CGCAGGTCGTGGGAGCGTTGGGGTAATCCGCGCGATGTGCGCTGCGGTGTACCCACCGGT  
TTGGGGTTGTGCTGGAGCGGGCGAAGATGGATCCAAGGATGATTGGGGCGAAAGGGTTA  
CCCACCTATCTTTTACCGTCGATAAGCAAAAAGACATGCTGTGGGCGCGCGAACAGGGC  
GTCGACATGCTCGCCACCAATTATCCGGACCGTGCGGCGGAGCTTTTGAACGCACATCCC  
AAGCCCGCCATGTACGCTAATGCGCATGGCAAAGAAGAC

>RXA02677-downstream  
TAAGAAGAATGAACAGCTGCCGG

>RXA02691-upstream  
CTTAGGGCTTATCTGTTTTCCAGCCTTGCTTTTTACTAGGCGCTCCTGTCCCGCTTCAGT  
CACCAAACACACCCCTGGTTATGACCAGATCGGCTAAA



>RXA02691

ATGAACACCATGCCTGACCAACCGCTCAACCAGGACGGATTCCCTACCGCATCCAAAGGG  
GTGGAACCCGACAACCTCCCCGACCGCGTTCTCGTGGACGGCCTTAAACCAAAGCATCAG  
CAGCTTCGTGAAATTTTGGAGGAAATCTGCACCACCCAGCTTCAGCCTGGGGACATGCTG  
CCTGGTGAGCGCATCCTGGAAGAAAAGTATGGCGTCAGCCGAATTACGGTTCGTTCGGGCG  
ATTGGTGATCTGGTTCGCGTCCGGCAGGTTGAAGCGAGCTCGCGGCAAAGGTACCTTCGTG  
GCCCCACTCGCCGTTGATTTCCCGCCTGCATTTGGCCTCGTTTTCCGCAGAGATGGCCGCC  
CAGAAGCTATCGGCTACCAGCAGGATTTTGAGTTCTTCCCGCGGTCCCGCCCCAGATGAT  
ATTGCTGATTTCTTTGGTACCGATCGCGCGGCCAGCACATCACGTTGCGCCGCTGCGC  
TTTGGAATATGGTCGACCCCTATGCCATTGACAACGGTTGGTACAACCTCCGAATTCGCACCT  
GACCTGCTGGAATATGATGTGTACAACCTCCGTGTACTCCATCCTGGACCGCGTCTATGGC  
GTCCCCGTCACCCAGGCCGAGCAAACGGTCACCGCCGTAGCAGCCGACGAAGACACCGCA  
CGGCTTCTGGACGTCACCCCCGCGCCCCACTCCTTCGTATCCTTCGACAGTCACTTTCT  
GGCGATAAGCCCGTGGAATGGTGCGTTTCCTTGTACCGAACCGACCGATATTCTTTAAAA  
ACATTGGTTACACGCTCCGAAGATCTC

>RXA02691-downstream

TGACGTGAACCCATTTTGGTGGC

>RXA02718-upstream

TCCACCAAATTCAGCCCGCATCCCCCTATTCGATTGAAGGACGTCTCCTTGAGCAGTTT  
CGATGCCCATGACCTTGACCTCGACAAATTTCCGGAGGTC

>RXA02718

GTGCGAGATCGTTTGACGCAGTTCCTCGATGCTCAAGAGCTAACAATTGCTGATATCGGC  
GCTCCTGTACAGATGCTGTGGCCCATCTTCGCAGTTTCGTGCTCAATGGAGGAAAGCGA  
ATCCGTCCTCTTTATGCGTGGGCTGGTTTCCTGGCGGCGCAAGGCCATAAGAATTCTTCT  
GAAAAACTTGAGTCCGTCCTTGACGCCGAGCGAGTCTCGAATTCATCCAGGCTTGTGCC  
TTGATTCATGACGATATTATCGATTCTTCTGATACCCGGCGCGGAGCCCCACAGTTCAC  
CGGGCTGTGGAAGCTGATCACCGCGCCAATAATTTTGAAGGCGATCCCGAGCACTTTGGC  
GTTTCAGTCTCGATTTTGGCTGGCGATATGGCATTGGTGTGGGCAGAAGACATGCTGCAG  
GATTCCGGTTTGAGTGCAGAGGCATTGGCCCCGACGAGGGATGCTTGGCGTGGCATGCGT  
ACTGAGGTTATTGGCGGCCAGCTGCTTGATATTTATCTAGAGTCGCACGCCAACGAGTCG  
GTGGAGCTTGCGGATTCTGTCAACCGCTTCAAAACGGCCGCTTACACGATTGCGCGCCCA  
TTGCACCTGGGCGCCTCCATTGCTGGCGGTTTCGCCGAGCTTATCGACGCGCTCCTCCAC  
TACGGCCACGACATCGGCATTGCATTCCAGTTGAGGGATGATCTGCTTGGTGTGTTTGGG  
GATCCCGCTATCACCGGCAAACAGCTGGAGACGATATCCGTGAAGGCAAGCGCACTGTT  
CTTCTTGCGCTCGCTCTACAACGCGCTGATAAGCAATCTCCTGAAGCTGCAACGGCCATT  
CGCGCAGGTGTTGGAAGGTGACTTCACCAGAAGATATTGCTGTGATTACAGAGCATATT  
CGAGCTACTGGTGCTGAAGAAGAAGTTGAGCAGCGAATTTCCAGCTGACTGAATCCGGT  
TTGGCTCACCTCGATGATGTAGACATCCCCGATGAGGTGCGCGCACAGTTGCGGGCACTG  
GCTATCCGCTCAACCGAACGTTCGGATG

>RXA02718-downstream

TAGTAGACGCGTATGACACTTTT

>RXA02749-upstream

CAACCTAGACTTCGGTAAGAAGTAACTTTGCTTTAGTTGGTTCGGCGCATCACTTTCCCTA  
AGCGATGCGCCGATTACTTGTTTTTGCTACAAATTTAACT

>RXA02749

ATGTCACCCATCCTAAAAGTGCGGGACCTCGTCAAACGCTATGGCGACACCGTTGCGGTT  
GACGGTTTAAATTTTGATGTTTCACAAGGGGAAATTTTGCCTTTCTAGGGGAGAACGGC  
GCAGGAAAAACAACCACGATTTTCATGCCTGATTGGCATTGATCAAGCCACCTCTGGGGAG  
ATCGAACTGCAGGGTGGCCAAGTAGATTCTGAAAAACTTGAGTGGTGTTCACAATCC  
GTCTTAGACCCTTTGCTGAGTGCCAAAGAAAACCTTGGAACACGCGGACAGCTGTACCCA  
GGGGTGGGGAAGCAGCGGGTGCACAGCTCATTGAGCAAATCGGGATGGAAGGGTTTGCG  
GACCGCCGATACGGAGTGTGTCGGGCGGTGAAAACGTCGCACCGACATCGCACGAGCT  
TACTGCACAGCCCAGACATTCTTTTTCTTGATGAACCCACAGCAGGCCTCGACCCAGA  
TCACGACGCCAAGTTTGGGACACCATCAATTCCCTGCGTAACGATGTGGGCCTCACTGTC

TTTTTGACCACTCACTACATGGAAGAAACAGAACTGGCTGATTTCAGTTCTAATCATTGAC  
CGTGGCAAAGAGGTCGCATCAGGAACCCCGATGGAACTGCGCGCCCGTTACACCACAACA  
GAATTGACTCTTAGAACAAACGACCCTACTCATTCGGGTAAAGAGTTGGCCCACTTGAGC  
CCAGAAATCGACGGTGACCGACTGCGGATCAAGTTGGAAATGGGCTCGAAGCTGCGCGC  
CTGGCAACAGAACTAGATGGGGTTCTCGACGTAGAGATCCGCCACGGTTCCATGGACGAT  
GTATTTCTAGCAGTTACAGCTGAACGGAAACGATCA

>RXA02749-downstream  
TGATTACAGTTCTGACACGCAGA

>RXA02762-upstream  
TTCCCAGTCGGCGATCCTCTTCGCCCTACGTTATCTTGACTCTGGTTGTGGTCTTCGTG  
GGATCCATGCAGACCTTCCTCAACGGTAGCTACCTGGGTT

>RXA02762  
ATGCTCTCTGAGCTCTTCCCGCTGGCAATGCGCGGTTTCGCAATCGGTATCTCAGTGTTT  
TTCCTCTGGATCGCAAACGCGTTTCCTCGGATTGTTCTTCCCAACCATCATGGAAGCAGTA  
GGACTAACCAGAACCTTCTTCATGTTTCGCCGGAATCGGTGTGGTTGCCTTGATCTTCATC  
TACACCCAGGTTTCCTGAACTCGTGGACGTACCTTGGAGGAGATTGATGAGGATGTTACT  
TCCGGTGTCATTTTCAACAAGGACATCCGAAAAGGAAAGGTGCAC

>RXA02762-downstream  
TAAAAACCCAGACACTGCATAGA

>RXA02767-upstream  
GGGAAAACGTTTCCTCGCCGCCACAGAAATCATAAAAATTTTCTGAGGTTGTCATGGGTA  
CCAGTCTAAGCCCTGGCCTTACGCCAGTAAGGTGTTACCC

>RXA02767  
ATGCGCGAACTAGCACTCAACATGGCCGGCGTCACCGTGCGGCGCGGCGAGAAATTGCTT  
CTCGACGATATCTCCCTCTCAATTCCGCAAGGGTCGCACTGGGCCGTACTTGGTCCAAAT  
GGCGCCGGTAAAACCACCATGCTGAAGATCGCAGCCACCTTGCTGTACCCATCGGAAGGC  
ACCGTGACATCCTGGGGCATCGCTTTGGTTCGGGTGGATACTCGTGAGCTGCGGAAAACA  
ATCGGCCTGGTGGACCCGAAGCAAAGATTTACCAACCTGCCGGCCACGAAATTGTGCTG  
TCGGGGTTAACC GCCTCCAACGGGTTGTTGCCACGGTGGTTCGGCTTCGGCTTCGGAGTTG  
GAGCGGTGCGCTTTGATGTTGGAGTTGGTGGGCATGACAGCGCGTGCCGATCGTTACTGG  
GCCGATATGAGCCAGGGCGAAAAAGCCCGCACCTGATTGCTCGTGCGCTGATTATCTCA  
CCGACCCTACTGCTGCTTGATGAACCCACCAACCGGCCTTGACCTGCCCGGACGTGAACT  
TTGCTCAGTGTGATTGATGGTTTTCGAGCCGCTCTTCCTGGTCTGACGACAGTGATGATC  
ACCCACCACGTCGAAGAGATCGCCGCCTCCACGACAGATATCCTCATGATCAAGGACGCC  
CGCATACTGGCTTCGGGGACTGTTTCAGAAGTGATGACTCCTGAAAATTTGGGCGCGCTG  
TATGACATGTCGGTGTGCTTGAAACTGTGCGCAGCCGGTGGTTCGCGTTTCGATGCTCTG  
CAT

>RXA02767-downstream  
TAAAAGGGGCTAGTTTTACACAA

>RXA02792-upstream  
AGAACAAAGTGCTGCCATACTCATGAACTTTGCCGAACCCCCAACCCCGCTGGCCGTCG  
ATGGCCTAGAAAAAATCATCGACTTTGTGGAAACCCACCC

>RXA02792  
ATGATCGAGGCCACACACCTACGCCACAGTTTTGGCGACAACATCGTCATCGATGACGTC  
ACCTTCCATCTACCTGCACACGGCACCGTCAGCTTGGTCGGCCCCAACGGCAGTGGCAAA  
ACCACCCTGCTGCGTGCACTATACGGAGCACTGCAACCAAATGAAGGGCACATCCACGTA  
GATGGCGTTCCACTAATAAGCTTGACCCGCAAAGACATCGCAAAAACCATGGCCGTAGTC  
ATCCAAGAACATGACTCCGACCTCCCCATGACCGTCGCTGACCTGGTCTTACTAGGCAGA  
CTCCCCACCAAAGATGTTTGGCCGGCAACTCTCAAGCTGATCAGTTACTCGTTAAGGAA  
GCACTCACCCGAGTCGGCGCCATTACCTGGCCGACCGACAATTCGGCGCACTTTCAGGC  
GGTGAACGCCAACGCGTCCTCATCGCACGAGCACTCGTACAAAACGCCACACACATTCTG  
CTCGACGAACCCACCAACCACCTCGACATCCGCTACCAGCACGAAGTCCTTACCTCGTC

CGCGAACTCAGCTCAAGTTCCATCATCGTCCTCCACGACCTCAACCTCGCAGGTGCCTAC  
AGCGACCACATCATCCTCCTTGACCAAGGACGTGTGGTTACTCAAGGAACGCCCTCAGAG  
GTATTGACCCAGAGCATTGGAACCTGTGTATGGCGTTCGTGTTGAGCGCTTTGACCTA  
GGCGATGAAGTCCACCTTCGGTTCAAGCGTCAC

>RXA02792-downstream  
TAGGAGTTTTGTTGAGGAGGTGG

>RXA02794-upstream  
TGAAGTCAAGTGCAGTTGCGGTGCGGCCGCTGCCTTACTGTTGAGGAGTGGGCGCTGGAT  
TTGGCGATTACGCCCTCCAAGCAGCGCGTTTCTCGGCGCA

>RXA02794  
ATGGCAGCTTCCGGATTGATCTTCTTCGTGGCGCGCGCAGCGGGGCGCATCTCCTCGACC  
CGCTTGTTGATGTCCGGCGTAGCGATCGGATACATGCTCTCTGCGGCAACAAGCTTTCTC  
ATCTTCTCCTCCGACTCCGCCGAAGGCAGCCGCTCCGTGTTGTTCTGGCTGCTTGGATCC  
TTAGGACTTGCCGCATGGAATGGGCGCATGGCGATCATCTTCCTCATCGTGGGCATTGCC  
CTGGCGTTGCTCATGGTGTGGGTCCGCAATTGGATGCCTTAAACTCCGGCGATGAAACC  
GCACTTACCTTGGGAGTATCCCCTGATCGCCTCCGCATTCTCCTCCTGGTGATCACCTGC  
CTGCTGGTGGGATCCATGGTTGCCATGGCCGGCAGCATCGGATTCATCGGCCTTGTCATC  
CCCCACCTGGCCAGGCGTTTTGTTAGTGGAACACCGACTCATGCTGCCTGTATCCGCG  
TTGATGGGCGCAATTTTGCTCATCTGGGCTGATATCGCCGCCCGCACCTGCTTGCGCCC  
CAAGAGATTCCCATCGGCATCATCACCGCACTCATCGGAGCACCTTCCTCCTGATTCTG  
GTTCCGCCGATGCACACCTAC

>RXA02794-downstream  
TGATTTTAAAGGAATTATGCGTA

>RXA02809  
GCAGCACTAACCAACGCCCTTTCCTACCTCTCCGCAGAGTGGAACAACAAGGCTGCAGGC  
ATCGTCTCCTACGGCTCCGCAATGGGCGTTTCGCGCAGCTGAGCACCTCCGCGGCATCCTT  
TCCGAGCTTCAGATCGCACACGTTCAAAGACCGGCCTGCTGAGCATCTTCACCGACTTC  
GAATACCTAACTTCAAGCCTTCCGAGCAGGGCATCTCCTCTGTGGACGCTATGCTTGAG  
CAGCTTGTTGTCTGGACCAAGGCAATGTCCACC

>RXA02811-upstream  
CATAATCACTCTTTCCAGATAGCGGAATCCCTTTGATTGTAACCTGGCTCACCTCGATTA  
TGTGTTTATGACATCACACGCACCAGAATCGGGAGGACTT

>RXA02811  
GTGACAGAGTCAACTCTCGGAGCATCGAATAGCTCCCAAACAATTGAAAATAAAGGCCTC  
ACCATCTTGGGCATCAGCGGCCGACGCTTGGCTGCGGTGCTCATTGGCTGGTTTTTTGTC  
ATTTTCGACGGCTACGACCTCATTGTGTACGGCACCGTCCAATCGGCCCTGGCTAAGGAG  
TGGAAGTTAAGCTCTGCAACGCTGGGCACCATCGGCTCCACCGCGTTCTTTGGCATGGCG  
ATCGGCGCTGTGTTTCAATTGGTTCGACTGTCAGACCGCGTGGGCCGAAAAGCAGCGGTGATT  
GGATCCGTGCTGATTCTCTCTGTCTTACCATGCTGTGTGCATTTGCTCCAAACCATGG  
GTGTTCCGGCGCTTTCGGTTTCATC

>RXA02836-upstream  
CCATCACTCGGCTTCACCGTCTACGGTGCTGCCCCGAGGACAGAGCGCCCCCAAAGCTC  
GCTTCAGACGGGATCCACCCCTCGAGATGGACGTCACCG

>RXA02836  
ATGACAATCGATGAAGGCCGTCGCCAGTTCGAGGTCAATGTATTCGGCGCGATGGCCCTC  
ACCCGACTCGTCCTGCCCCACATGCAGAAACAAAAGTGGGGGACGATCGTGAACATCACA  
TCGATGGGCGGGAAGATCTACACGCCTCTCGGCGGCTGGTATCACGGCACCAAGTTCGCC  
CTCGAGGCCCTCTCGGACGCCCTCCGCCTGGAGGTGCGCCCATTCGGCATCGACGTTGTT  
GTCATCGAACCGGGCGGCATCGCCACCGAGTGGGGAGGAATCGCTGCCGACAATCTCGAC  
GCAGTG

>RXA02850

GAAGAGCTTGGCGGAGCAACCACCCACATGGTGACCGCTGGTAACTCCCACTACACCGCT  
GCGACCGATGAGGAAGCACTGGATTGGGTACAGGACCTGGTGTCTTCTCCCATCCAAC  
AATCGCTCCTACGCACCGATGGAAGACTTCGACGAGGAAGAAGGCGGCGTTGAAGAAAAC  
ATCACCGCTGACGATCTGAAGCTCGACGAGATCATCCCAGATTCCGCGACCGTTCCTTAC  
GACGTCCGCGATGTCATNGAATGCCTCACCGACGATGGCGAATACCTGGAAATCCAGGCA  
GNCCGCGCAGAAAACGTTGTTATTGCATTTCGGCCGCATCGAAGGCCAGTCCGTTGGCTTT  
GTTGCCAACCAGCCAACCCAGTTCGCTGGCTGCCTGGACATCGACTCCTCTGAGAAGGCA  
GCTCGCTTCGTCCGCACCTGCGACGCGTTCAACATCCCAATCGTCATGCTTGTGGACGTC  
CCCGGCTTCCTC

>RXA02851

CCTCGCCAGAAGGCCGACATCATGATCGGTTCCATCCAGGAAAACATCAACGATGTGGAT  
CTGGAATTGGACACCATCATCCCGGATTCCCCGAACCAGCCTTATGACATGAAGGAAGTT  
ATTTCCCGCATCGTNGACGACGCCGAGTTCTTCGAGATCCAGGAAGACTACGCAGAGAAC  
ATCCTGTGTGGCTTCGCTCGCGTTGAGGNCCGTTNTGTTGGCATCGTGGCTAACAGCCA  
ACCCAGTTCGCTGGCTGNTTGGATATTAAGGCATCTGAGAAGGCTGCCCCGTTTCATCCGC  
ACCTGCGATGCCTTCAACATCCCAATCCTTGAGTTCGTGGACGTTCCAGGCTTCCTGCCT  
GGCACCACAGGAATTCGACGGCATCATCCGCCGCGGCGCAAAGCTGCTTTACGCTTAC  
GCTGAAGCAACCGTCGGCAAGATCACCGTCATCACCCGCAAGTCCTACGGCGGAGCGTAC  
TGCGTGATGGGTTCGAAGGATATGGGCGCTGGCCTGGTA

>RXA02865-upstream

GAGCGGGGTTGCTATCGGCCGAAAGTTTAGGGTTTTGTTCAATCTGTTGGTTAGTATTGC  
TTGGGTAAACAAGTCATAACAATTTTCATTAAGGGTTCGTT

>RXA02865

TTGTCGCGCACAGGTGTTTCGAAAAAACCAAAGCTCACCGCTCCTGTTGTCATCATCGGC  
ACCCTCGTCTTGTTGATCATCGCCTTCACCGCTTCCCTCATGCTGGGTCCCGTGACGGTT  
CCATTGAATGAGCTTGCAACCAACCCCGTTGTCACCGATATCCGTGCACCACGCATTATC  
ATCGCAGCATTGGTGGGTGCGGCGCTGGCTGTCTCCGGTGCGATCATGCAGACGGTGTTT  
CACAACCCGTTGGCGGATCCCGGCATTGTGGGTGTGTCCTCCGGTGACGCTGTTGCAGCT  
GTCTTGGCGATTGTCACCGGTGCGAGTTTCTTTGGCCAATGGACCGTTCCTTTTGCGGCC  
TTCGTGGGCGCATTTGGTCACGGTGGCTGTGGTATATTTGATCGCTAGTTCCCGCGCGATG  
GATGGCCGTGGCGCAGATCCGGCCACGTTGGTACTGGTCGGCATGGCTATCACTGCCTTT  
TTGGGTGCTGTTATTTCCAGCGCCACTGCGAACGCACCACAAGATTCTGAGCTTCGATCC  
GTGACGTTTTGGCTCAACGGCGATCTGGTATCTCGGACGTGGGAACATGTGGGCGTTGCA  
ATAATCCCCATTATCGTTGGGTTGATTCTAGCTATCGGCGGTTCCCGCGATCTGAACTTG  
TTGCTGCTGGGTGATTCCACAGCGCAAACATCTGGACTCAACGTCAACCGCGCACGCATC  
ATTTTGCTAGCACTTGCGGCACTGCTCACCGCCACAGCTGTTGCGGTCTCCGGCACCATT  
ACGTTTGTGATTGGTAGTACCCACCTGGTGCGCATTGTTTTAGGTGCCGATCACCGA  
GCGTTACTCCCGGCCCGCGCATTTTGGGCGCCACGTTTGTATCGTTTCCGACACTGTT  
GCCCCGATGATCTTCTCCCCCATCGTCTTGCAAACAGGCGTGGTGGTGGCGTTTATTGGC  
TCACCAATTTTCCTTTATTTACTGCTCAGCATGCGCAAGCGACGCGGATTGGGGCTG

>RXA02865-downstream

TAAAACTCATGCCTCAATTAGT

>RXA02900-upstream

TATGTCCTTTGGCTCCGGTACCCTGGCAGGAGTACCTGGGCTGTTTTTCTAAAATGGCCT  
GACGTTTTCAAGATTGAATTTAAGGAAAGCATCGTAGTTC

>RXA02900

ATGAGTAACCCTGCCGCGAGCACACCTGCCAACAATTCGGACGATGTTGCGAAGGAGAAT  
TGGGACTCTTCTTTTACGCCGAAGACTGACATTGACTCTTCCCAGCCTGTCAATAACTCG  
ACTGGTGAAGCCGCTGCGCGCGCAGTGAACCTGTACAAGGCGTATGGCCAGGGTGATACC  
ACTGTCACCGCGTTGGATCACGTCAACGTGGAGTTTGAGAAGAACAAGTTCACTGCCATC  
ATGGGTCCTTCTGGCTCGGGTAAGTCCACGTTGATGCACTGCATGGCTGGTCTGGATGCT  
GCGACTGGTGGTTCGGCATTTCATTGGTGATAACGGATCTGTGCGGGTTGAAGGACAAAGAG  
ATGACCTCTTTGCGTCGTGATCGTTTGGGATTCATTTTCCAGTCGTTCAACTTGGTTCCT  
ACTCTGACGGCGTCGGAGAACATTACGCTGCCTACCGATATCGCGGGCCGCAAGATTGAT  
CAGTCGTGGTTTCGATGAGATTACCTCTCGTCTGGGTCTGACTGAGCGCCTTAAGCACCGT



CCTGCAGAGCTCTCTGGTGGTCAGCAGCAGCGTGTGGCGTGTGCTCGTGCGTTGGTGTCT  
CGTCCGGAGATCATTTTCGGCGACGAGCCAACCGGTAACCTGGATTTCGAACTCTTCTAGG  
GAAGTGCTGGATATCCTGCGCACCGCAGTTGATCAGGATGATCAGACCGTTGTGATCGTT  
ACCCACGATGCCAAGGCGGCGTCTATGCAGATCGTGTCAATTTCTTGGCGGACGGTCGT  
ATCGTGAACCAAGTTGTTTGATCCCACCATCGAGGAAATCTTGGCCACGATGAACGGAATT  
GAGGATATTGCC

>RXA02900-downstream  
TAATGAATTCCGGTCCACAATG

>RXN00024-upstream  
TTAAGACATCAACATATGGCTTGTGCTACTGAAAGATTTTCTTCTGAAATTCTGTAGAA  
ACGCTCCTATGCTCGGGGCAGTAAGTTGTGAGCATAGGAA

>RXN00024  
ATGGAGCACGGCGTGACCGTTATTAAAGGCACTGAATTTGATGTTTTCCCACTAAACCTC  
GGTGGAAATACCTTTGGCTGGACCTCGAATAGGGAACAGACCTTCGCGGTTTTGGATGCA  
TTCGTGGCAGCGGGAGGAACTTTGTTGACACCGCCGATTCTTATTCTGCATGGGTGAA  
GGCAATGAGGGTGGCGAGTCGGAGCGGGAGCTCGGCGCGTGGATTAAGGAACGTGGCGCA  
GACAAGCTGATCATTGCTACCAAGTCTGGTGCGTTGGAGCCTGTTGCTGGTCGTTCCCGT  
GAGGCAACTTTCAAGGCTGTGAGGGTTCCCTGGAGCGTTTGGGCGTGGAATCGATCGAT  
ATTTTTTACTACCACTACGACGATGAGGCAGTCAGCATTGATGAGCAGGTTGCTATCGCT  
AATGATCTGATTGCACAGGGCAAGATTAAGCACCTCGCATTGTCTAACTACAGCGCGGAG  
CGTTTAGCTGAGTTCTTTGAGAAGTCTGTAGGCACTCCAGCGCAGCCGGTTGCTCTGCAA  
CCGCACTACAACCTGGTGTGAGGAAGGATTATGAGGAGAACGTGCAGCCACTCGCCGAG  
AAGCATGGCGTTGCAGTCTTCCCTTATTTTCGCGCTTGCCGCGGGTCTTTTGACCGGAAAG  
TACACCTCCAAGGAGGATATTTTCGGGTAAAGCGCGTGCGGGGCAGTTGGATCGTTACGCC  
AGCGATGAGGCGTTTGCCGTGGTGACAGAGTTGCGTGCTGTTGCCGATGAGTTGGGTGTT  
GCGCCAACGACTGTGGCGCTTGCGTGGTTGGTTGCGCATGGTGTGACCGCACCGATTGCG  
TCCGTGTCCAAGGTAGAGCAGTTGAAGGATTTGATGGCTGTGAAGGATGTGGAGCTGAGC  
GCTGAGCAGCTTGCACGTTTGGATAAGGTTTCGGAGCCTTTCGCT

>RXN00024-downstream  
TAAGCTCTCCTCAAAGTAAGTG

>RXN00092-upstream  
CGAAACCAGAAACACCCAGCGGCTCCTCGTCGAAAAGCGAATCTTTGAACTAGAAGCCCA  
GGCACGTTGGCTCGACCGAATTGAAGCATTTGGAGCAGTAA

>RXN00092  
ATGACAAACACGCCTTTCCCCCTTGAACCTCAAACATCTCCTGCGCCTTCGGAGAAGGC  
CCACGCCACGTCTCCGCGCTCAACAACGTCTCGCTGGCAGTCAATCCCGGCGAACTCGTT  
GCCATCATGGGCCCCGTCCGGCTCAGGAAAATCCACCTTGCTCAACGTGCGCGCCTCCTG  
CAGCGCGCAACCTCTGGCCATGTGCTTATCGACGGTGCCAGCGCCTCAGACCTCAACGCC  
AAACGCGCAGCTGAAACCAGGCGTCGCCACATCGGAGTTATTTTCAAACCTACAACCTG  
GTCCCCACCCTCACCGTCGGAGAAAACGTCCGGTCTGCCCCTAGAACTCGACGGCAAAC  
GACCGCCAGGCAAGTAGCAATCGCACTCGCGGAAGTCGGCCTCGAAGGCTTCGACGACCGC  
TTCCCCGAAGAGATCTCCGGCGGCCAAGCCCAGCGCGTCGCCATCGCGAGAGCCCTCATC  
GGCCCCCGAAAAATCTTGCTTGCCGACGAACCCACCGGCGCCCTCGACACCTCCACCGGC  
GACGCAGTCCTCCGCGTCTCCGCCAAAGAATCGATTCCGGTGCCGACGGCCTCCTTGTC  
ACCCACGAACCCCGCTTCGCCGCGTGGGCAGACCGAACAATCATGCTTAGGGATGGTGAA  
ATCCAG

>RXN00092-downstream  
TGACCACACTTCTAGCAGCAACC

>RXN00099-upstream  
CTCTGGTGAAGAGGATGTTGACTCGGGAGATTCTTCCACTGATTCACTGATTAAGTGGA  
CCGCGCAAATAGGTAGTCGCTTGCTTATAGGGTCAGGGGC

>RXN00099

GTGAAGAATCCTCGCCTCATAGCACTGGCCGCTATCATCCTGACCTCGTTCAATCTGCGA  
ACAGCTATTACTGCTTTAGCTCCGCTGGTTTCTGAGATTCTGGGATGATTTAGGGGTTAGT  
GCTTCTCTTATTGGTGTGTTGGGCATGATCCCGACTGCTATGTTTCGCGGATGCTGCGTTT  
GCGCTTCCGTCGTTGAAGAGGAAGTTCACTACTTCCCAACTGTTGATGTTTGCCATGCTG  
TTGACTGCTGCCGGTCAGATTATTCGTGTCGCTGGACCTGCTTCGCTGTTGATGGTTCGGT  
ACTGTGTTTCGCGATGTTTTCGATCGGAGTTACCAATGTGTTGCTTCCGATTGCTGTTAGG  
GAGTATTTTCCGCGTCACGTCGGTGGGAATGTTCGACAACTTATCTGGTGTGCTTCCAGATT  
GTTTCAGGCACTTGCTCCGACGCTTGCCGTGCCGATTTCTCAGTGGGCTACACATGTGGGG  
TTGACCGGTTGGAGGGTGTGCTCGGTCGGTTCGTGGGCGCTGCTGGGGTTGGTTGCGGCGATT  
TCGTGGATTCCGCTGTTGAGTTTGCAGGGTGCCAGGGTTGTTGCGGCGCCGTCGAAGGTT  
TCTCTTCTGTGTGGAAGTCTTCGGTTGGTGTGGGGCTCGGGTTGATGTTTGGGTTTACT  
TCGTTTTCGACGTATATCCTCATGGGTTTTATGCCGCAGATGGTAGGTGATCCTCAGCTC  
GGTGCGGTGTTGTTAGGCTGGTGGTCAATTTTGGGATTGCCGCTGAACATTCTGGGACCG  
TGGTTGGTGACGCGTTTCACTAACTGCTTCCCGATGGTTGTTATCGCCAGTGTGATGTTT  
CTCATCGGTAATGGTGGGTTTTGTTTGGCTCCGATGTTGCGCCGTGGTTGTGGGCGACG  
TTGTCTGGTCTTGGTCCCCTTTCGCTTCCCGATGGCGTTGACGCTCATTAATATTCGTGCT  
GAAACTAGTGCTGGTGGTCTTCTGCGTTGAGTTCTTTCGGGCAGGGTTTGGGTTATACGATT  
GCGTGTTCGCTCCCTTGTGACTGGTTTCATTGTGCGATGCGACAGGCAGCTTCCGAACA  
ATCTTTGTGCTTTTTGCGGTTGCAACACTCTTCGTTATTAGAGGCGGTTACTTTGCGACA  
AGGCAGGTTTACGTGCAAAAGCTTTTAAATCGC

>RXN00099-downstream  
TAGGATGGCGCTATGCCGCAAAG

>RXN00113-upstream  
TCTGCGCATCCCCTCGAGGAGCTGGCAAACGGCCGACCATCGATGTTGAGGCACGCAC  
CGACTCCATCGAAGAGTCCGCATCCGGCCGTATCGTTACC

>RXN00113  
GTGCGCATCGTGCTCACCACCGAAGGCGAAGTAGCAGCCAAGCTGGTTACCCGCTTCGCA  
ATTCGTGGACGCATCACCACCAACGAAATGGCTGCACCAGCAGATTCTACGGCGCACGC  
GACGAAGTTGTGAGGCAACCCCTCGTTCTTTCATCCGCCAGGCAACTGTTTCTGCACCT  
GCAGACATGACCCCATTCGCCATGGTTTCTGGTGACTACAACCCAATTCACACCTCTGAC  
AACGCTGCAAAGCTTGTTGGCCTGGACGCAGCTCTTGTCCACGGCATGTGGCTGTCCGCT  
ACCGCACAGCACCTCGCTGGTCTTGGCTCTGAGGTCAATTGGTTGGACCTACTCCATGTAC  
GGCATGGTTCAACTCAACGACGTTGTTGACATCACCGTCGAGCGTGTGGCCGCGCAGGT  
CTGAAGCCTGCATACGAGGTCACCTGCCGCATTGATGGCAACGTTGTCTCCCGCGGACAG  
GCACTGCTCAAGGCTCCTTCCACCGCTTATGTTTACCCAAGCCAGGGCATCCAGGCTAAG  
GGCATGGGCCAAGGCGATCGCACCCGCAAGCGCAGAGGCTCGCGCTGTGTGGGAGCGTGCA  
GATGCACACACCCGCGCAAACCTGGGCTTCTCCATCCAGCAGGTCATTGATGAAAACCCA  
ACTGAGCTGAAGGTCGGGGACACCACCTTCGTGCACCCAGCTGGGGTTTTGAACCTCACC  
CAGTTCACGCAGGTCGCGCTCGCCGTGGTTGCCTACGCTCAGACCGAGCGCCTCAAGGCT  
GCAAACGCAATTGTGACGCGCTCCCTCTACGCAGGCCACTCCCTCGGCGAGTACACCGCA  
CTGGCATCCTTGGGCAACATCTTCGAACTCGAAGGCGTCATCGACGTTGTGTTCTCCCGC  
GGTTCCGCAATGCACTCCCTGGTTCCACGTGATGAGAAGGGCCGTTCCAACCTACGGTCTT  
GCCGCATTCCGTCCGAACATGATCAACGTTGCAGCCACCGAGGTGGAGAACTGGGTTGAC  
CGTGTGCTGAAGAATCCGGCGAATTCTTGCAGATCGTTAACTACAACGTTGATGGCCAG  
CAGTACGCAGTCGCAGGTACCTTGGCTGGCCTGAAGGCCCTCAAGGCTTCTGCATCTGCA  
AACCACGTGCTTACGTGAACATTCCAGGCATTGACGTGCCATTCCACTCCAGCGTCCTG  
CGCCCAGGCGTTCCCTGCTTTCGACAGAGAAGCTGGACGAGCTGCTGCCAGAGACCATCGAC  
ATTGATGCTCTTCGCGGCCGCTACATCCCGAACCTGGTTGCTCGTCTTTCGAGCTCACC  
CAGAGCTTCGTGGATGCCATCCTTGCTGTTGTTCCATCCGAGCGCCTCAAGGGCATCAAG  
GTGGAGGACACCGACGAGAACACCCTGGCACGTCTGCTCCTCATCGAGCTGCTGTCTTGG  
CAGTTCGCATCCCCTGTGCGTTGGATCGAAACCCAGGCTCTGATCATCGATACCGTCGAT  
CAGATCATCGAGGTCGGCTTGGCAGCATCGCCAACCCTGACCAACCTGGCACTGCGCACCC  
ATGGATGTCATTGGCAAGTCCCGCCAGTATTCAACGTGGAGCGCGACAGGACACCGTT  
ATGCTCAACGATGTTTCGCCAGGCACCTGTTGCTGAGGTTGAAGAAGAAGCAGTTGAGGAA  
GCACCTGCAGCAGCCGACGCTCCAGCAGCTGAGGCACAGTTGCTGCAGCTCCAGTAGCC  
GCAGCCGCACCTGCACCTGTTGGAAACGCACCTGAACTGAAGTTCAACGCTGCCAATGCC  
ATCATGGTTCTCTTCGCTGTCCAGAACAAGATCAACATTGATCAGATCACCGCAGCGGAT  
ACCTCTGAGACCCTGACCAACGGTGTGTCCTCACGCCGTAACCAGATGCTCATGGACATG

TCCACCGAGCTGTCCGTCCCAACCATCGACGGCGCAGCTGACGCTGACGTAGCTACCCTG  
CAGGGACGTGTTGTACCGCAGCTCCTGGCTACAAGCCTTTCGGACCAGTTCTTTCCGAG  
ACCGTTCGTGCACGTCTTCGCGCACTGACCGGTGCAGCAGGTCTGAAGACCTCCTACATC  
GGCGATCGCGTGACCGGCACCTGGGGACTTCCAGAAAGCTGGACCGCACACGTTGAGGTT  
GAATTGCTGCTGGGCACCCGCGAAGGCGAGTCCGTCCGCGGGCGGCAACCTGGGTAGCCTG  
CCTGCTAACGCATCCAGCAAGGGCGACGTCGATGCGCTTATCGACGCAGCCGTGCAGAAT  
GTTGCTGCAGCCAACGGCACCGAGCGTCTCCATGTCCTCCGGCGGTGCAGCTTCAGGTGGC  
GGAGTTGTTGATTCCGCGAGCACTTGATGCCTACGCATCCACCGTCACTGGTGAAGAAGGC  
GTCCTGGCAAACGTTGCTCGCGGCATCCTGTCTCAGCTTGGTCTCGACACCAAGGACGAG  
GTTGAAGGCGCAGAGATCGACACCGAACTCTACGACGCTGTGAAGCAGAACTGGGCACC  
GGCTGGCTGAAGCTTGTCACCCCAAGTGTCTCCGCTGATCGTGCGATCTTGTTCGACGAC  
CGTTGGGCATCTGCACGTGAAGATCTGGCACGCCTTGCCAACGGCGAGGATATTGCCGTC  
GAGCGCTTTGCTGGAACGGGGGAGACCGTCGTCAAGCAAGCTGCATGGTGGGCTGAGCAC  
GTTGAAGACACCGCTCTCGCTGCAACCCCTGAAGCAGGTTTCCGAGGTGGCTGCGAAGCCA  
GCCAACGAGCCACACATCGACGATGTTGCGCTGGTTACCGGTGCGGCTCCTGAGTCGATC  
GCCGGTGCAGTTGCGGCTCGCCTGCTGTCCCAGGGCGCGACCGTCATTCTCACCGCATCG  
AACGTCTCCAGGCGCGTAAGGAATACGCACGCAAGCTCTACGCTGCGAACGCAACCCCT  
AACGCAAAGCTGTGGATTGTTCTGCGAACATGTCTCCTACCGCGATGTTGATGCAGTC  
ATCGATTGGATCGGCAACGAGCAGCGGTACCGTCGGCAGCACCGTCACCGTGACCAAG  
CCAGCTCTGACCCCAACCCCTTGCGTACCCATTGCGAGCTCCATCCGTATCCGGTACCTTG  
GCGGATGCAGGCCCACAGGCTGAAAACCAGGCACGCCTGCTCCTCTGGTCCGTGGAGCGC  
ACCATCGCAGGACTTGAGATCTTGATCCCGCGGTGTCGATGGACGCGTCCACGTTGTA  
CTCCCAGGTTCCCCGAACCGCGGAATGTTCCGTGGCGACGGCGCTTACGGCGAAGTCAAG  
GCTGCTTTTCGACGCCATCCTTGCCAAGTGGGGCTCCGAGACCGGCTGGCCACAGTTTGTC  
TCCCTCGCACAGGCACGCATCGGCTGGGTGCGAGGCACCGGCCTCATGGGTGCGAACGAC  
GTGCTCATCCCTGCCGCTGAAAAGCTGGGCATCCACGTCTACACCCCTGAAGAGATCTCT  
TCCGAAGTGTGGGTCTTGATCCGCGAATCCCGCGAAAAGGCTCTGGAAGCACCGATC  
GATTACGACCTGACCGGTGGACTTTCCGGTGGCGTATCCATCGCAGCACTGGCAGCATCC  
CTCGAGTCCGACGCAGTAGAGACCACCTCTGCAGCAGAAGACACCATCAAGGCGCTTCCA  
TCACCTAAGCACCCAGAGCAGCCAGTGGGCACGCCAGTTGGAGAGGTCAAGACCGATCTC  
GAAGACATGGTTGTCATGGTTGGCGTTGGCGAAGTCTCCTCATGGGGCTCCGGACGTACC  
CGCTTCGAAGCTGAGTACGGCATCCAGCGCGACGGCTCCGTTGACCTCACCGCAGCAGGC  
GTCCTTGAGCTTGATGGATGATGGGTCTGATCTCCTGGAGCGAAGATCCAAAGCCAGCC  
TGGTACGACGCTGACGGCACCGAAGTGCCTGAAGAAGAGATCTACGAGCGCTTCCGCGAC  
GAAGTCATCGCACGATGCGGTGTTTCGTGAGCTTGTGACGACGCATTCTCTGTCGACGGC  
GGCTCCCTCGACGCAGCTGAAGTCTTCTCGACCGCGACATCTCCTTCTCCGTAACCTCT  
GCTGAAGAAGCACAGGCCTACGTCGATGCAGATGCTTCCGTGACCGTTGAAGAAGCAGAC  
GGCGAATGGATCGTGACCAAGAAGAAGGGCTCCACCTCCTTCGTGCCACGCAAGGCAACC  
CTGACCCGCTCCGTAGCAGGCCAGCTGCCAACCGACTTCGACCCCTGCCAAGTGGGGTATC  
CCAGCCTCCATGATCGATGCACTCGACAACATCGCAGCGTGGAACCTGGTCACTGCAGTC  
GACGCCTTCTGTCTCCGGCTTCAGCCCAGCAGAACTCCTGCAGTCCATCCACCCAGCT  
GACGTGTCCTCCACCCAGGGCACCGGTATCGGTGGCATGCAGTCCCTACGCAAGCTGTTC  
GTCAACCGCTTCTCTCGGCCAGGATCGTCCATCCGACATCCTCCAGGAGACCCTGCCAAAC  
GTTGTGGCTGCACACACCATGCAGTCTACGTCCGTGGCTACGGCCAGATGATCCACCCA  
GTGGCAGCATGTGCAACCGCAGCTGTCTCCGTGGAAGAAGGCGTGGACAAGATCCGCCTC  
AACAAGGCAGATTTTCGTTGTCGCCGGTGGTATCGATGACATCCAGGTTGAATCCCTGACC  
GGCTTCGGTGACATGAACGCCACCGCAGACACCCAGGCAATGCTGGACAAGGGCATCGAC  
CCACGCTTCATCTCCCGCGCAAACGATCGACGTCGCGCAGGCTTCTCTGAAGCAGCAGGT  
GGCGGTACCGTCTCTGGCACGTGCATCCGTTGCTGCTGAACTGGGACTGCCAGTTCTC  
GCAGTTGTTGCACACGCACAGTCTACGCCGATGGTGCTCACACCTCCATCCCAGCACCG  
GGACTTGGCGCACTGGGTGCAGCACGTGGTGGCAAGAAGTCCGTACTTGCTCGCGAACTG  
AACAAATTGGGTCTGACCCCAAGATGACGTTTCGCGTGGTCTCGAAGCACGACACCTCCACC  
AACGCCAACGATCCAAACGAGTCCGAGCTGCACAACCTGCTGTGGAAGACCATTTGGACGC  
GAAGCCGACAACCCGATGTTTCGTCTCTCCAGAAGTCCCTTACCGGACACTCAAAGGGC  
GGTGCAGCACTCTTCCAGATCGGTGGACTTGTCTCCATCCTGGAAACCGGCAAGCTGCCA  
CAGAACGCATCCCTTGACTGCGTTGACCCAGAGATGGAAGCAAAGGGCGAGAAGTTTCGTC  
TGGCTGCGCAAGCCACTGGATCTCGGCGCAGGCTCCATTAAGGCCGGCGTACTTACCTCA  
CTGGGCTTCGGCCACGTGGCTGCAGTCGTGCTGGCAACCAGCGGCATCTTCGAGCAG  
GCAATGCGCAACGCAGGCCTCGACGTCGAAGCATGGCGTGCACGCGCAACCCAGCGCCTG  
CGCACCGGTGCAAACCGCCTAGAAGCTGGCATGGTTGGCCGAGCACCATTTGTTTCGAGCAG  
GTCGACGGACGTCGCCTGCCAGAGCATGGCGCTACCAAGCAGAGATCAACTTGCTTATC

GACGCTGACGCTCGCCTCGGTGCTGACGGCATCTACCAGGGC

>RXN00113-downstream  
TAAACGTTAGATAGCTAAGAAAG

>RXN00164-upstream  
CTGCTTTGCGGGAGGTTATGAAATGAGTGGGGAGACGTCGAAAAGCATGCGCTTTCCGTT  
GGCCAGCCTGCCGCAAGTGCGGCGCGAGGTGGCCCGGCAG

>RXN00164  
GTGGGTCGTATTCGCGGGCGAAGTGGTGGTTTTAGGCGCGCTGGTGTGCTGAGTGCG  
GGCGCTTATGCGTCCGTGCTGGTGCCGCGAGGTGCTGGGGCGGATTGTGGATCTGGTGTCC  
GATGGCGCGCAGATGCGTGATTTTGTGAGCTCAGTGTGATTCTCATTGCGGTGGCAATT  
GCCGGCGCGGTGCTCAGTGCGTGCGGGTTCTATGTGGTGTGCGGGATTCTGAGAAGATT  
ATCGCCAATTTGAGGGAAGATATGGTGGGCACCGCGCTTGGGTTGCCACGACAGGTG  
GAAGATGCGGGCTCTGGCGATTTGGTGAGCCGCTCCACCGATGATGTCTCCGAGCTATCC  
GCAGCGGTGACAGAGACCGTCCCGATTTTAAGTTCCTCACTGTTTACCATTGCCGCGACG  
ATCATTGCGCTGTTTTCTTTGGACTGGCAATTTGTGCTCATTCTGTGCTGGTGGCGCCG  
GTGTACTACTTCGCGTCCAAGCACTATTTGAGCAAGGCGCCGGATCGGTATGCGGCAGAA  
CGCGCGGCGATGGCGGAGCGTGCGCGAAAGGTACTTGAGGCTATTCGCGGGCGTGCAACT  
GTGCGGGCGTATTCATGGAAGATGCCATGCATAATCAGATTGATCAGGCGTCGTGGTCT  
GTGGTGGTCAAGGGTATTCGTGCGCGCACCCCATGTTGATTTTGAACATGTGGATGCTG  
TTTGCGGAATTCCTCATGCTCGCGGTGCGGTTGGTGATCGGCTACAAGCTGGTCATTGAT  
AATGCGCTGACGATCGGCGCGGTTACCGGTGCCGTGCTGATGATTATTCGTCTGCGTGGC  
CCGATGAATATGTTTCATGCGCGTGCTCGACACCATTCATCCGGCTATGCGTCGCTGGCG  
CGCATCGTGGGAGTTGTTGCGGATCCGCCGATTCCTGTGCCCAGACAGCGGTGTGAAAGCA  
CCTCAGGGCAAAGTGGAATTGCGCAACGTCAGCTTTAGCTATGGCGATTCCTGGGCGGTG  
AAAGACATCGACATCACGATCAATTCGCGCGAAACTGTCGCGCTCGTGGGCGCATCTGGC  
GCAGGTAAGACGACGGTCCCGCCTTGCTGGCGGGCTTGCGGGTGCCAGATCAAGGGCAA  
GTGCTTGTGACGACTTCCCCGTCTCTCACCTCTCTGACCGCGAGCGTATCGCCCGCTTG  
GCCATGGTCAGCCAGGAGGTTTCATGTTTTCTCCGGCACGCTGCGCCAGGATCTCACCTTG  
GCTAAACCAGATGCCTCCGATGAGGAATTAGCGCATGCTCTTGGGCAAGTTAATGCCCTT  
GACTGGTTGGAGAGTCTTCCAGAAGGACTGGACACGGTCGTTGGTGCGCGAGGAATCCAG  
CTAGAACCAGTGGTGGCTCAGCAGTTGGCGTTGGCCCGGGTGTTGTTGCTCAATCCGGCG  
ATCGTCATCATGGATGAAGCCACGGCAGAAGCAGGATCGGCGGGTGCCAGCGCACTGGAA  
GAGGCTGCAGATGCAGTGAGCAAGAACCGTTCCGCATTGGTGGTGGCGCACCGGTTGGAT  
CAGGCATCGCGGGCTGATCAGATTCTGGTGATGGATAAGGGGGAGGTTGTGGAATCCGGT  
ACTCACCAGGAGTTATTGGATCACGGGGGTATTTATCAGCGTCTGTGGACTGCGTGGAGT  
GTCGGAAGA

>RXN00164-downstream  
TAGTTGACTGTTCAATGCGTTGA

>RXN00193  
AAAGCTTTCTNCCAACGCGAAGGTTTCATCTCAGCCTTCGGTTTTACCGTCCTCGTGGTC  
ATCGTCTCCGTGATCACAGTCAACATCTTCGCCTTCCTCTTGCGGTGGTTGCTGACCCGC  
AAACTCCGCGGTACCAACTTTTTCCGCACAGTCTTCTTTATGCCGAACCTTATCGGCGGC  
ATTGTGCTGGGTTATACCTGGCAGACCATGATCAACGCCGTGCTTTCGCACTATGCCACG  
ACTATTAGCGCGGACTGGAAATTCGGCTACGCCGGCCTCATCATGCTACTTAAGTGGCAG  
CTCATCGGCTACATGATGATCATTACATCGCCGGCCTGCAAAACGTCCCACAGAGCTC  
ATTGAGGCTGCCGAACCTCGACGGCGTCAACAAGTGGGAGATGCTGCGGCACGTCACTATT  
CCGATGGTCATGCCATCCATCACCATCTGCCTCTTTTTGACTTTGTGCAACTCCTTTAAG  
CTCTTCGACCAGAACCTGGCGCTGACCAACGGCGCTCCTGGCGGGCAAACCTGAGATGGTG  
GCGCTCAACATCATCAACACGCTGTTTAACCGTATGAATGTCGAGGGCGTCGGT

>RXN00201-upstream  
ACGTCGCGGACTTCAAGTAGTCGGCGATGAAAAAGTCCGTTTACTAAACCCCGATCTGTG  
TTACGCCATCGCGCGGCTCGGGCACACCGATACCTGGGCA

>RXN00201



GTGGCAGATTGCGGATTACCCATCCCAGAACACGTAGAGATCATCGATTTGGCACTCGTG  
TTTGGGATCCCCACCTTTGAACAAGTACTGAATGCTCTCAAGCCGGAAGTAGTTGTGGAA  
GGCGCGGTGATTGCCGAAGGGGCACCCCAACGTATCCGCGAAATGGTGGATACGGATGTG  
GAAGTATGTGCG

>RXN00243-upstream

CACTGCGCCAGATTTTGTGATGCCGACACTGTGGCAGGTGTGCGCGCTGAGTACGAAAAAT  
TTAACAAAGCAGCCCATGATGGAAATGAAGAGGAACAGAA

>RXN00243

GTGACCAGCGAACAAAGCTTTAGATCCTATCCACCCAGGTCAGTTCCGTCTTTCTCGGATT  
CAGTTGATCAACTGGGGAACCTTCCACGGAACGGTGGACATTCCTGTGACCAGGGAAGGA  
ATCTTAGTTACCGGTGGTTTCGGGATCAGGAAAATCCACGCTGATTGATGCGATCACGGCG  
GTATTGCTTCCGCAAGGAAAGCTGAGGTTTAACTCTGCCGCACAGGCTAATACTCCGCGG  
AATAAGGGACGCAGTTTGGTTACCTATATCCGTGGCGCTTGGCGTGCGCAGGAGGATCCG  
CTGCAGGATCAGATTGTCTCCACGTACCTACGTCCCCGCGCAACCTATTCGCTGGTTGGA  
TTGACTTATTCCAACGGTGAAGGCGTCGAGCACACCTTGGTGGCTATTTTCTATCTGAAA  
TCGGGACACAATTTAACCTCCGATATTTCTTCATATTATGGTGTGTTTCCCGTTGATCAA  
GACATCAATGCGCTGCTGGATTTCTGAAAGAGGGCATCGATAAACGCCAGATCAGAGCT  
GCTTTCAAGGAAGCCATCTTTAGCGAGCAGCATTCTGTATTCTCCGGCAGGTTTAGAAGC  
CGTTTGGGGATCTCCAGTGAGGAAGCTTTGCTGTTGTTGCACCGCGCGCAGTCGGCGAAA  
GATCTTCAAAGCTTGGATGATCTATTTCCGGGATTACATGCTGGTGGAAACCGGATACGTTT  
AGCATTGCCAAAACCTGCCGTGGAACAATTTCCAAGACCTTGAAGGTGCTTATGAGCAGGTC  
GAAGATATTAAACGGCAGATCCACACCCCTGGATCCTTTGGTGCAGCTGAAGAATCGGCGA  
GAGAAAGCGCAACAGTCCAAAGATCATGCCAATGCACTGAAGAAGGCGCTGCCGACTGTC  
GGGAATCGCATTAAGAAGGAAGAGCAAGAACCGCTGGTTCGACAATTTACTGTGAGCAA  
ACGCAGCGAAGTCGAAGGTGGAGTCCGCCAAAATTGAGACAGATCGTGCCCGCGAAA

>RXN00243-downstream

TGAAAACCCTCGCGCACGACAAC

>RXN00297-upstream

AACAAGGCACCGGAAAACAAGCAACGCACCTTGCAGAGGTGGTCTTAAGCATCTTGGAGC  
AAAACAACATGGCACAATAACGATCATGCAACAGGTGCTC

>RXN00297

ATGGGTTTTCACGGTGGTGTTCATCGTCATCGGAATAGGTTGGATTCTCGGTAGAAGAGAC  
ACCTTGGGCACACATGCCCAGAAACCTTTGAGCCTGTTTGTCTATTACGTGGCCACCCCA  
GCGTTGTTGTTTGTATCGGGTCACCAAGTCAGATACCTCGACGATTTTCTCTCTGAACTTC  
GTGGTCATTGCACTCTCTGCGTTGATCGTAGGTTTCCCTGTTTTTCTTACTCATGCGGTTT  
GTGATCAAAAGAACTGCCGCGATATCGGTGATCGGCATGCTAGCTGCGTCCTACGCCAAC  
GCCGGTAACCTGGGTATCCCTTTGGCAGCCTATATTTTGGATGATTTTACCCTGGTGATT  
CCCGTGATTTTGTTCAGGTGGCGTTCTACGCACCGATCACCATGACCATCATGGAGATG  
CTGACCAACAAGAAATCCACCAACTTGGTGCGCAACCTCCTGGTCACGCCACTAACCAAC  
ACCATGGTGCTCGCAGCGATTGCCGGTATTGCTGTGTCTTTGACTTCGATGAGCGTGCCC  
GTGGTGATTGCTCAGCCAGTGGAATGTTGGCGAATGCTTCAGTGCCACTGGCTTTGGTG  
GTGTTTCGACTGTCCTTGTCCAAGAGCAAGATCCTGGAAAAGGGGCAGGTATCCAGGCGC  
GATGTGTTTACGGCGGCACTGTTCAAGAATGTTCTGCACCCAATTGTTGCGGGACTTTTA  
GCCTTAGCCTTTGGTATGGAAGGTACTGCCTTGTGTGCGCGGTGATTCTCGGTGCACTG  
CCAACAGCGCAGAATGTCTACACCTACGCGTTGCGATTTAGAACAGCTGAATCGATGGCG  
AGAGACACAGGGGTGGTCACCACACTCATTTCCCTTCCCCGTATTGGTGGCGGTCTCCATT  
ATCTTTGGATCT

>RXN00297-downstream

TAGGGTTAGCATTAGTGGTCATG

>RXN00298-upstream

TTTAGACAAGTTCTGGTTAAAATTCTTCATGAAGGTGAGAATCTGGGAATTTCTCGGTAC  
TCTTTCAGATTCGTAGTTATCCACTGATTGGAAGAATGAG

>RXN00298

ATGAGCTCAAATATAGCTATCACGACCGAGCCTGAAGGGAAAAATAAAAAGGGTCTCAAA  
TCAGACCCGTTCAATTTTTTCCATTTCTGTGCGGTTTTATCGTGGTGTGTTGTCATCGCCACA  
ATTGCGCTAGGCGAGAAAGCTCGAACAACCTTTTCCGCGATTGCCGGCTGGCTCTTAGAA  
AATTTAGGGTGGATGTATATCGGGGGTGTCTCCTTGGTTTTTCATTTTCCTCATGGGTATC  
TTTGCGTCCCGGTATGGCCGGGTAAACTTGGTGATGACGATGATGACCCCGAGCACACC  
CTAATCGTGTGGTTCTGTATGCTTTTTGCTGGCGGTGTCGGTGCAGTCTTAATGTTTTGG  
GGTGTGCGCAACCGATTAAACCACGCGTTCAACGTGCCAATGGCTAATGAAGAATCCATG  
AGTGAAGCCGCAATTGTGCAGGCTTTTGCTTATACTTTCTATCACTTCGGTATTCACATG  
TGGGTAATCATGGCACTCCCAGGATTATCATTGGGATACTTTATTTACAAACGTAAGCTA  
CCTCCCCGTCTATCCTCTGTGTTTTCTCCGATCTTGGGTAAGCACATTTATTCCACACCC  
GGCAAGCTCATCGATGTACTGGCCATCGTAGGCACCACGTTTGGTATTGCTGTGTCAGTA  
GGTCTTGGTGTGCTGCAAATCAATGCAGGTATGAACAACTATGGAGCACCCCGCAAGTA  
TCGTGGGTTTCAGCTTTTGATCATCTTGATCATCACCGCGGTGTCATGTATTTCCGTTGCT  
TCCGGTTTGGATAAGGGCATTAAGTTACTGTCCAACATTAATATTGCAATGGCCGTTGCG  
TTGATGTTCTTCATCTTGTTCACTGGTCCAACCCTCACATTGCTGCGCTTTCTCGTAGAA  
TCCTTCGGAATCTATGCATCCTGGATGCCTAATCTGATGTTTTGGACTGACTCTTTCCAA  
GATAACCCAGGCTGGCAGGGCAAATGGACGGTGTTCTATTGGGCATGGACTATTTGTTGG  
TCGCCATATGTCGGCATGTTTCGTGGCGCGTATTTTCGCGTGGACGTACCGTCCGTGAATTT  
ATCGGTGGGGTTCTAGCTCTGCCAGCGATCTTTGGCGTAGTTTGGTTCTCTATCTTTGGT  
CGTGCAGGCATCGAAGTGGAAGTGAAGTAAACCCAGGTTTCTTGACCCAGCCAACTGTTGTT  
GAAGGTGACGTGCCAGCAGCGCTTTTTAATGTGCTGCAAGAGTATCCGCTGACTGGAATT  
GTCTCCGCGTTTGCACTTGTAATTATTGTGATTTTCTTTATCACCTCCATCGATTCCGCA  
GCGCTAGTTAACGATATGTTTCGCTACCGGTGCAGAAAATCAAACACCGACTAGTTACCGC  
GTGATGTGGGCCTGCACCATTTGGGGCGGTGCGAGGTTCTTGCTGATCATTTCCCCATCC  
TCTGGTATTGCCACGCTGCAAGAAGTGGTTATCATCGTGGCTTTCCCATTTCTTCCTCGTG  
CAATTTGTCATGATGTTTTCTTTGCTTAAAGGCATGAGTGAAGATGCTGCTGCGGTTTCGT  
CGTGTGCAGACTCGTCAGTGGGAAAAGACTGATACACCAGAAAACTTGAAGAGCATTCG  
TCCCAACCAGCCCCGGGCTATGATGACGAGGGCAACCCCTTGCCAATGCCTGCCCTCGAA  
CATGATGAGGACGGTAACATTGTTATCCCAGGCAACGTAGTCATTGAAGGTGATCTTGGG  
GTAGTTGGTGTGTTGCTGACGATCCTGAGGAAGCCCAAGAGATGGGGTCTCGTTTTAAG  
ATCGTCGAGCAAACCTCGGCCCCAGTCCAGGGACGAATACGATATT

>RXN00298-downstream

TAAACGATTGCTTTTCGACGCAC

>RXN00349-upstream

TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT  
GTGATTGGACTCTTTTTCTTGCAAAATGTTTTCCAGCGG

>RXN00349

ATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCA  
CCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTG  
ATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGAC  
ACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGAT  
ATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTC  
AACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGAC  
CGTTTGATCCGTTCCATTACAGGCTGGTGGACCCCGCCTGAGGTTGCCGAGAAAATCCTG  
GACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCA  
ATGATGGGTGGTGTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCT  
TTTATTACCGCGTTACGATCATTGCCACGACGTCAATTTTGGGAAAGAAGGGTTTGCCT  
ACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTAT  
TCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATT  
GTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCT  
CCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCT  
GGCGTGGGTTTGGGCATTACGCTTTCTGAAATCTTGATGTGATGTTGCCTGCCATGGAG  
TCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCCGATTATCGCTGGTGGCGTCACC  
GCAGCGGCCTTCGCAAGTGGGTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTT  
ACTGCGCTGATGGGTCTGCGTTTTATTACCTCTTCGTTGTTTATTAGGCCCCGTCTCT

GCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTC  
 TTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCA  
 ATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACATT  
 GCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATT  
 GCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCAATTTACCAAGGCGAAT  
 GAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAG  
 ACTAATCAGAGATTTCGGTAATAAAAGG

>RXN00349-downstream  
 TAAAAATCAACCTGCTTAGGCGT

>RXN00368-upstream  
 TTCTTCCAAAACGCAATGAAGTAGTTTTCCTATGCAGTTATCTCCTTCAAATACGTGAC  
 GCAGCGCTTTCACATCTCTGCGTTGACGTCTTTGTCTTTC

>RXN00368  
 ATGCGTCTGGGTGTGTGGCTGATTGTGCGGGGGTTGTTTATCACTCCGTTGGCGCTGGTG  
 GTGGGCTTGGCGTTGGGAGGCAATCAGTTTTCCTGCTCTGTGGGATTCCGGATTGGGCAA  
 GCCCTATGGAATTCGCCTATACAACAGTGCTTTCTGCGGTGGGCGCGACCATTATCGGC  
 ACGATCATGGCTCTCACGCTGGACCGAAGTATGTTTTCGGGCGCACCGCGTTGCGGTTA  
 TTTTTGTTATCCCCGCTGTTGATCCCTCCGTTTATTGGGGCTATTGCGTGGTTGCAGCTG  
 TTCGGGAAGAACCAGGGCATCAACCGGTTTTTCGGGCACGGAAGTGTGGGATATTTACGGC  
 GCTGATGGTGTGACATTTTTGTTGATTGTGCACTCCTATCCCACTGTGTACATCATTGTT  
 TCGGCAGCTCTGAGGCAACTTCCTAGTGATTTGGAGCAAGCTGCACGGATCGCGGGGGCG  
 GATACTTTTACGGTGTGCGCACCATCACACTCCCACTGCTCAAACCTGCATTGTTGTGCG  
 GCGTTTACTCTTACCACAGTGGCGAACCCTCGCCGACTTTGGCATTCCAGCTCTGTTGGGA  
 TCGCCAGCGCGTTTTGAAACCTTAGCCACCATGATTTATCGCTTCATGGAATCCGGCACC  
 GTGAGCAATCCATTGCAGGTGGTATCCACCATTTGGCATCGTGTGTTGTTTCTGGGAATC  
 GCAGCAGTAACCGCGGATTATCTGGTGTCTTTGTACGCGGCATCAAAGTTGCAAGACGCA  
 GGAACACCGCATCGCTTTACTCTCAACAAATCACGAATCCCAAGTCAGCGTGATCACGTGG  
 ATCATCGCGTTGATCATCACCGCCGCCCCGCTGCTGGGTCTGGCATAACAGAGCATTACTG  
 CCTGCCCCAGGTGTGCCGTTCAACCTAGACAACATCACGCTCAACAACCTTTGAAGCAGCA  
 CTGAGCAATCCACGAGTAATCGAAGGATTCAGCAACTCCCTCATGTTATCCCTGGGTGCA  
 GCCCTAATCTGTGGGGTGTGTTGGGATGGCTGATCGGAGTGCTCATCACCCGAACCCAGCAT  
 TTCGCCAACGTACCGTTGACACTCACTGTGCTGCTTCCCACCGCACTGCCGGGCATGATC  
 ATCGGCGTCGGCTGGCTCATTTTGGGCAGATACACCGGAATTTACAACACACCTTGGGTG  
 ATTTTGGGTGCATATGTGTGTGCTTTTACCGCGCTGGTTGTCCAAGCTGTACGCGGACCA  
 CTCAGTCAAGCACCCGAAGCAATCGAAGAAGCCGCACGAATCAGCGGCGCAGGCAGATTA  
 CGATCCATCATGGACACCACCGGAGCGATGGCAATTCCCGCAGCTTTCGCCGGCGCAGTG  
 CTGGTTGCGGTAACCTGCGGTTTCGAGAGTTAACCGTGTCCATTTTGCTCATCGCGCCGGGC  
 ACCACCACCCTGGGTGTGAGGTGTTCAATTTGCAGCAGGCGGGAAATTACAATCAGGCA  
 TCGGCGTTGTGCTGATGTTTGCATTATCGGTATCGTGGCGCTCGCGTTGACGGTGCGC  
 AGCCAGAAGGAGTTT

>RXN00368-downstream  
 TAGGTGTCATCGATCAAATTGCG

>RXN00378-upstream  
 ACCGTGAGCCTTATACTGTGAGGACATTAAAAGTGACACCTCTTTTTCTATCTTTTACAA  
 CCCAAGAAGGTTTATCGTGAGCACACCGGATTCTTCCTCG

>RXN00378  
 GTGGACAAGGCCGTAAACACTGCTATCTCTGACGCCAAAACAGCGGCGCTCAAGGCAGGT  
 GTTGGATTGAACCGAGCCACCGCCTCAGAAGAAGAGGAAGATTTAAGCTCAAGCATTAAAG  
 GTTCTTTGGCCTTTGAGCTCGAGGGGTAAAGCAATGCACCATCGTTGATGGTGGTGGAA  
 AAAGCCCTAGAGAAGATCCCCGGTGTATCCGCGGATCTGATTTACCCTTCACAACTGCA  
 TGGATTACAGCAACTGATCGGGTACATCCCGAAACCTCATTGAGGTGTTTGAGCAGTTC  
 GGCATCAAAGCACACCTTTCTAATTCATCGCTGCTGCGCAGGCATCAACAGCTCAGCGCG  
 GAAGTAAATAGGGAAGCACGCCTTGATCGTTACCGCTCCCGAATGGATGCCAAGCGAATC  
 TCGCCTCGTGTGCGAAGGCATAACCGACAAGAAATGGTACATGCGGTACGCGCTCGTGAA  
 AGTGGTTGGATTAAACGCAGGAATCACACCACCTCGCAGCATGAAGACCCAATGTCGGGC

GATGTGCTGTTACCGCCCCGCGCACTGATTACACCTAAGCGTTTGTGGGTGTCGTTGCCG  
TTTGCGCTCATCGTATTGGCGTTATCGTTGAATCCTTCGTGGCAGTTTGATTATTGGCAG  
TGGTTGTCCGCTGTGTTGGCTATTCCTGTGGTGGTGTGGGGTGCCTGGCCGTTTCACCGC  
GCTGCAGCAGGCGGTATTCGTGAGGAATTTCCGCTCTTGATGCGACCAGCTCAATCGCT  
ATTGCTGCTGCATACGCGTGGTCTATCGCCATGCTGTTGTTTGAACCCCAGGAGGTAAA  
TCCTGGCGGTCATATCCGTCCCTGGTTCGCTTTTGACCACGGCACGTTGACCCAAAACGAG  
ATTTATTTTGATGTGGCCTGCGGAATCACCGTGTGCTTCTTGCCGGACGGCTGCTGACA  
AGGCGTCGAAGCCAATCCAGTTTGTAGCGGAACCTGGTTCGCCTCCAAATCGATCCACAG  
CGCATTTGTCACTGTGGTGGCTAAACACCGATTGAAGCGCGTAGTCCAGGAACCTGAACATT  
CCAGTGCAGGAAGTCCGTGTCAATGACGATGTGAAAGTTCCACCTAATACCACGATCCCT  
GTGGATGGCACTGTATCGGTGGCGGTTTCGCGGATCGCAGCTAGCATCATCATGGGACAA  
GACCAGCGTGATGTAAAAGTAAATGACAAAGTTTTCGCCGGCAGCCTCAACCTCGAATCC  
GAAATCAAGGTTTCGTGTTATTTCGCACTGGTTCACCGCACCCGCATCGCCGCGGTACATAGG  
TGGGTTAAAGAAGCGACGTTGAAGGAAAACCGCCACAATAGGGCAGCGATCCGTTTCGGCC  
GGTAACCTTGTGCCCATCACGTTTCACCTTGCTGTGGTGGACTTCTGTCTGTGGGCACTG  
ATCTCTGGAAACATCAACGCTGCATTTACCACTACCTTGGCTGTCCTTGCGTGCGTGGCT  
CCGGTGGCCTTAGCGTTGTCTGCTCCACTTGCCACGAGGAATTCCATCGAAGCTGCAGCA  
CGACACGGTATTTTGGTCCGCTCTGGTGAAATTTTCCGAGTTCTCGATGATGTGGATACT  
GCCGTATTTAATCGTGTGGGCACACTAACCGATGGCGAAATGACAGTGGAAACCGTCACA  
GCAGACAAAGGCGAGGACCCAGAACTAGTGCTGCGTGTGCGCGGGGCGTTGGCCATGGAA  
TCCCACCACGCGATTTCCAAAGCACTGGTGAAAGCATCCCGTGAAGCTCGTGATACCGGC  
GCCGGTGGTGAAGATGTCCACACTGGATTGAAGTAGGCAACGTGGAAATCACCGAAGCC  
GGCTCATTTCAAGCAACCATCGAGCTGCCACTGATCAAACCATCTGGCGAAAAAATCATG  
CGCACACAGAAGCACTCCTGTGGCGACCACGATCCATGACAGAAGTCCGTGAGCACTTA  
AGCCCCCGACTAGTGGCAGCAGCAACCTCAGGTGGCGCACCACTGATCGTGCGATGGAAA  
GGCAAAGACCGCGGAGTTATCACTCTAAGTGACCACGTGAGATCAGATTCCTCCGATGCG  
ATTATTGCGATTGAAGAACAAGGCATCGAGACCATGATGCTTTCACGTGATACTTACCCG  
GTGGCACGTCGATACGCAGACAGCTTAGGCATCACCCACGTCTTGCCGGGCATCGCGCCG  
GGCAAGAAAGCCAGGTTCGTCCGTGCAGTCCACACCCGCGGATCCACTGTCGCGATGATC  
GGCGATGAATCAGTAATGGACTGTTTGAAAGTCGCTGACGTGGGTGTACTGATGGGCGTC  
GATCGTCCCTCAGATCTGCGTGATGATTCCGATGACCCGGCAGCTGACGTTGTGGTCATG  
CGCGAAGAGGTGATGAGCGTGCCGACGCTGTTTAAACTGGCTCGACGCTACGCCAAGTTG  
GTCAATGGCAATATTGCTCTGGCCTGGATCTATAACGGTGTGTCATGGTGCTTGCAGTG  
TCTGGCTTGCTGCATCCAATGGCTGCGACCGTGGCTATGCTGGCGTCTTCGCTGCTTATT  
GAATGGCGCTCGGGCAGGGCGCGCAAGTAC

>RXN00378-downstream  
TAACCAGCAATTCCCAAGCCCAA

>RXN00410-upstream  
GTGTTGATGCGTTAGTCCACCCACGCAGCTACGCCCCAAAGGAATAATCTTGAACCCTGC  
CACAGATAACGCTCCGCCGGTCTTTTCAGCCCAAGATCTC

>RXN00410  
ATGATGATCTATGGAAAAGGATCAACAGAAGTTCGGGCTCTCGATGGCATTTCTGTACAG  
ATTCAGTCCGACAAATGGACCTCCATCATGGGGCAATCAGGCTCTGGCAAAACAACTCTG  
TTGCAGTGCCTTTCCGGATTGGCGCAGCCAACCTCAGGCAGAGTGACACTGAACAAAAAC  
AACATCACGTTGAGCTCCCTGTCAGAAAATAAGCGTGCCAAGCTGCGTCGCACGCACATC  
AGCATGGTGTTCAGGATTTCAACTTGGTGCCTATTTTGTGCGGTGAAGGACAATATTTTG  
CTGCCGTTGCGTCTTGCGCATCGCAGGGTGGATAAGCAGTGGTTTGAACACATCACCAGT  
GTGTTGAAGATTGATAATCGTATGCGCCATTTGCCTGGGGAGCTGTCTGGCGGTCAGCAA  
CAACGCGCCGCGATTGCCCGGGCGTTGATGTCTAGGCCCGATATTGTCATTGCGGATGAG  
CCAACAGGAAGTTTGGATTCCGTACACAGCGATGCAGTGTTGAATTTGTTCCGCAGCATT  
GTTGATGATTTTGGGCAGTCACTTGTGTTTGTACCCACGATAAAGATGCTGCTCACCGT  
GGTGACGTGTTGATCACAATGCGTGATGGCAAGATCATCGATACGGCAGATTTGCGGGTG  
GGGCGT

>RXN00410-downstream  
TAATGTTTCAGGCTTGCTTTCGCT



>RXN00411-upstream

CATTTGGCAAATGACTGTTGCGACTCACCGGCAACACCGCTGCGATTGAAGAGTTCTATC  
AAACCTTGACCAAGACCACGACCATCAAGGAGATCACCCG

>RXN00411

ATGAACGAGATGATCCTCGCAGCTGACTGGAACCGGCTAGGACCCACCTTCCAAACAGCC  
ATCATTGACACCCTGTTGATGGTCATCATCACCATGGTGGTGGCTGGCTTACTGGGTCTT  
GTCGTCGGCCTGCTGCTTTACACCACCCGCGCTGGTGAATCTTGAAGAACAAGGTCATC  
TACACCATTTTGAATGTGCTGGTGAACCTTGTTCGACCCATCCCATTATTATTTTGATC  
GCCGCCATCAAGCCACTAACGGTCGCCGTCATGGGCACCTCCATCGGCCGAGATGCCGGC  
ATCTTCGTCATGGTTGTGCGCAGCGATTTTCTCTGTGGCTCGAATCGTGGAGCAAACTTG  
GTCTCCATTGATCCTGGTGTGTCATCGAGGCAGCTCGCTCCATGGGTGCGTCCCCGATGCGC  
ATCATCGCCACCGTGATCATTCCAGAAGCACTTGGACCATTGGTTCTGGGTACACCTTC  
CTGTTTCATCGCGATCGTCGATATGTCCGCAATGGTCGGCTACATCGGTGGCGGTGGTCTT  
GGTGAATTCGCCATTGTTTACGGCTACCGCGCCTTCGACAACGAAGTTATGTACGTTGCC  
GTCCTGGTTATCGTCATCATCGTGCAGGCAGCCAGCTTCTGGGCAATTGGCTGTCCAAG  
AAGATCATGCGCCG

>RXN00411-downstream

TAAACCTCTTGCATAGAAAAACC

>RXN00412-upstream

CTTTTGACGAACACCACGTCGCGTACGCTTCCTCGGGGCGTTAAACTATTTGTCTTCCAG  
CTTTTGTCCCCGACTTTTGTACGAATCGAGGACACCGTC

>RXN00412

GTGTCACACACCGCGTCCACACCGACGCCAGAGGAATACTCCGCGCAGCAACCCAGCACC  
CAGGGCACTCGCGTTGAGTTCCGCGGCATAACCAAAGTCTTTAGCAACAATAAATCTGCT  
AAAACCACCGCGCTTGATAATGTCACTCTCACCGTAGAACCCGGTGAGGTAATCGGCATC  
ATCGGTTACTCTGGCGCCGGCAAGTCCACTCTGTCCGCTCATCAATGGCCTTGACTCC  
CCCACGAGCGGTTTCGTTGCTGCTCAACGGCACCGACATCGTCGGAATGCCCGAGTCTAAG  
CTGCGTAAACTGCGCAGTAATATCGGCATGATTTTCCAGCAGTTCAACCTGTTCCAGTCG  
CGTACTGCGGCTGGAAATGTGGAGTACCCGCTGGAAGTTGCCAAGATGGACAAGGCAGCT  
CGTAAAGCTCGCGTGCAAGAAATGCTCGAGTTCGTCCGCTGGGCGACAAAGGCAAAAAC  
TACCCCGAGCAGCTGTCGGGCGGCCAGAAGCAGCGCGTCGGCATTGCCCGTGCACTGGCC  
ACCAATCCAACGCTTTTGCTTGCCGACGAAGCCACCTCCGCTTTGGACCCAGAAACCACC  
CATGAAGTTCTGGAGCTGCTGCGCAAGGTAAACCGCGAACTGGGCATCACCATCGTTGTG  
ATCACCCACGAAATGGAAGTTGTGCGTTCATCGCAGACAAGGTTGCTGTGATGGAATCC  
GGCAAAGTTGTGGAATACGGCAGCGTCTACGAGGTGTTCTCCAATCCACAAACACAGGTT  
GCTCAAAAGTTTCGTGGCCACCGCGCTGCGTAACACCCAGACCAAGTGGAATCGGAAGAT  
CTGCTTAGCCATGAGGGACGTCTGTTTACCATTGATCTGACTGAAACGTCCGGCTTCTTT  
GCAGCAACCGCTCGTGCTGCCGAACAAGGTGCTTTTGTCAACATCGTTTACGGTGGCGTG  
ACCACCTTGCAACGCCAATCATTTGGCAAATGACTGTTTCGACTCACCGGCAACACCGCT  
GCGATTGAAGAGTTCTATCAAACCTTGACCAAGACCACGACCATCAAGGAGATCACCCGA

>RXN00412-downstream

TGAACGAGATGATCCTCGCAGCT

>RXN00419-upstream

GCTGGTTGAAGACTCGAAATGAGATCGACCCAACCGGAGTCTTTGCATCTGACATGTCCC  
GCCGACTTGAGCTTTCTTAAGAAAGGGCTTGAATAAACA

>RXN00419

ATGCTTAACGCAGTGGGCAAAGCCCAAACATTTCTCCTTCTTGGTGGAACTCTGAGATC  
GGTATTTCCATTGTCTCCCGCTTCCCTCAAGCAGGGTCCATCCCATGTGACCTTGGCAGCG  
CGTAAAGATTCCCCACGCGTGGACGCAGCAGTCGCAGAGATCAAAGCAGCTGGCGCTGCT  
TCCGTTGCTGTTGTTGATTTTCGATGCGCTCGACACCGAATCCCACCCTGCAGCCATCGAC  
GCAGCCTTTGAAAACGGCGACGTTGACGTAGCAATCGTGGCTTTCGGCATCCTCGGCGAC  
AACGAAGCACAGTGGCGCGACCAAGCACTAGCAGTGGAAGCAACCACCGTGAATAACAC

GCCGGCGTTTCCGTAGGTGTACTGCTGGGCCAGAAATTTGAGCAGCAGGGCCACGGCACC  
ATCGTGGCATTGTCTCTGTGGCAGGCCAGCGAGTCCGCCGCTCCAACCTTTGTCTACGGC  
TCCGCCAAGGCAGGTTTCGACGGTTTCTACACCCAGCTCGGCCAAGCCCTGCGTGGATCC  
GGTGCCAACGTATTGGTGGTTTCGCCAGGCCAGGTACGCACCAAGATGTCCGCAGATGGT  
GGCGAAGCCCCACTGACCGTCAACCGCGAAGACGTGGCAGATGCTGTTTATGATGCAGTG  
GTGAACAAGAAGGACATCATCTTTGTCCACCCACTGTTCCAGTACGTCTCTTTTGCGTTT  
CAATTCATTCCGCGAGCAATCTTCCGCAAGCTGCCGTTC

>RXN00419-downstream  
TAACGGAAGTTACGGAAGTTACG

>RXN00432-upstream  
AGCTAATCTGCCTTGCTTTACACCTCCGGGCTATAACAATCCAGTGCCAGTGGCTAGGGA  
TTTACTAAAAATCGGGTAACACGCGCGTAGTATTTTTTCGC

>RXN00432  
ATGGAATTATTGGAGACCTTCATCACTGATGTCATTAATGACAATTTGTGGATGATCTTG  
CCCTTCTTGCTCGTTGCTGCTGGCCTCTATTTTCGGTGGGCGTACGTTGCTGGTTCAGATT  
CGGATGATTCCGGAGATGTTCAAAGCGGTCTGCGAGAAGCCTGCGAAGGATGGGGAGTTC  
GCGGACAAGCAGGACATTTTCGGCTTTTAAGGCGTTCACGATTTCTGCGGCGTCGCGAGTT  
GGTACGGCGAATGTTGCGGGTGTGCGCTGGCGATCACTCTGGGTGGACCGGGTGCAGTG  
TTCTGGATGTGGATCATTGCGCTGGTTGGCGGTGCGACATCGTTTATTGAGTCGACTCTT  
GGACAGTTGTGGAAGGTGAAGGACGGCGACAGCTATCGCGGTGGCCCTGCGTACTACATG  
ACGCTTGGTTTGAATGCTCGGTGGCTTGCGGTTGTTTTTCGGTGTGCGCATCACGTTGACC  
TTTGGTTTTGTGTACAACGCTTTGCAGTCCAACGCGGTTGTTGAGGCGATTACGGTATCA  
CTCGGCACCCCTTCTACCACTGCAAAGGCTTTTGTGGCTTGGGCATGGCTGGATTGTCT  
GCGCTGGTTATTTTTGGCGGCGTGCAGCGTATCGCAAACGTGACGCAGTGGATGGTTCCG  
TTCATGGCGGGTGGGTACATCATTGTGGGTGTGGTGGTGATTGTGATTAACATTCAGCAG  
GTTCCGACCATGATCAACGACATCATTGCTGGTGCTTTTGGTTTTCCGTCCGGTTGCTACT  
GCGTCCGTGTGGGGCGCGTTCTGGTTGGCGTTTATGAACGGTATGCGCCGTGGACTGTTT  
TCCAATGAGGCTGGTGAGGGTTCTGTCCCGAACGCTGCTGCTACCGCGACTGTGTCTCAC  
CCTGTGAAGCAGGGTTTGGTTTCAAGTCTGGGCGTATATTTTCGACACCCTGCTCGTTTGT  
AGCATTACCGCTTTTGTTCATCCTGCTGTCTGGAGTGGAGTACGCGACCGGCGATATTCAG  
TCTTCTTCTTTGACTCAGTCCGCGCTGGCTAGCGTTGTTGGTGGTTGGGGAACCCACTTC  
ATTACCGTAGTGATGTTCTTCCCTGGCGTTTTCTTCCGTGCTGGGTAACCTACTACTTGGCA  
CAGGCGAATATTCAGTACTTTCACCGATTTCGAAGACTGTCATGACTGTTTTCCGACTCTTG  
GTGCTGCTCAGCGTGTTCTCTGGCGCGGTTGCTTCGGTGCCGTTGATCTGGGCTTTGGGT  
GATACTTTTCGCTGGCATCATGGTGCTCATTAACTGGCGGCGATCATTCCGCTGGGTGGC  
GTTGCAGTGAAGTTGCTTAAGAATTACACCATTCAGAAGAAGGCTGGTCTGGATCCTGTG  
TTCCACCGCGACATGATGCCAGAGGTTTCGTAATATTGCGTGCTGGAACGGCAAAGATGCA  
GCTACATCCAATATCACGAAGCGATGGAAGTGATCAAGAAGAGC

>RXN00432-downstream  
TAGTCATCGAAGGAACAGTGGTA

>RXN00443-upstream  
TAAACAAGGAGCGTTTAATTTCCACCCAATCCCACTGAAAGTTTCCCACCCACAGTTAT  
GCTGATTAAGTACTGAACTTACCGTAGGAAAGGCACTCAG

>RXN00443  
GTGAACAAAAGTATCCGTGAGCTCTCTACAGTTTCATCACTATTTTCGGCGGGTATCTCA  
CTCGTAGCGTGCTCTTCTTCAGACACCGCAAGCACTACCACCCAGAATGCCTCTGCTACC  
GAAGCAGCTGGGGTTTCCGGAACCGCTAGCGTTTTTCGCTGCGGCGTCTTTGACCAACGTT  
GCTGAGGATCTCGCGGCTGCGTTCAACGAAGACAATCCTGATGCAAAGTTGGAGTTTAAC  
TTTCGCTGGTTCTTCCGCGCTGGTTTCGCCAGATCAGCGAAGGCGCACCATCTGATCTGTTC  
ATTTCTGCGGACATCGCCAACATGGACGATGCGCTGGCACTTCCAGAATTTGCCGGCGCA  
ACCTCGAAGGTCATCGCTACCAACAAGCTGGTGCTGGTACCGCAGACGGCAACCCCGGC  
GAAATTTTCAGAGCTTGCCGACGTCAAGGACTCCCTCGTTGCTATCTGCGCCCCCTGAAGTT  
CCATGTGGAACCATCACCCACGAGGCTTTGGACTACGCAGACATCGAGTTGAACACCAGC  
TCTGAGGAAGCCAATGTTGCTGATGTCGCCACGAAGATTTCCACCGGTGCAGTTGATGCG  
GGCTTTGTTTACCAAACCGACGCTCAGTCTTTGGCTAAACTCAGGACAACACTGTCATT

GAAGTCGAAGGTATCGACGCCAACGAATACCCAATGGCATTGACCACCACCGGTGAAGAC  
AACGAGGTAGCGAAGGCTTTCGCAGAGTTCCTCAGCAGCGATCGTGCCAAGGAGATCCTT  
GCCAGCTATGGTTTTGGCACAAAC

>RXN00443-downstream  
TAAAAAGGCTCGTCTGAAGCGAGA

>RXN00444-upstream  
TACCCAATGGCATTGACCACCACCGGTGAAGACAACGAGGTAGCGAAGGCTTTCGCAGAG  
TTCCTCAGCAGCGATCGTGCCAAGGAGATCCTTGCCAGCT

>RXN00444  
ATGGTTTTGGCACAACTAAAAAGGCTCGTCTGAAGCGAGAATCATATCCTCCCAGGGTGG  
TTGCTCATCCCAGCCACCCTGGCCATGCTGCTGATCATTGGACCTATTTTTGCTTTGCTG  
TTGCAGATCCCCTGGGATCGGTCTTGGGAGTTGCTTACCGCGCCGGAATCTTTAGGAACC  
GCACGGTTATCTATCGGAACTGCTCTGTTTTCTACCGCGCTATGCGCAATTGTGGGTTC  
CCGCTAGCGTTGGCGCTGCATTTATATGAGCGTTCGCACCCCAGGGTGACATCAGTTTTG  
ACGGTGCTGGTTTTATGCGCCTTTGGTGTGTCGCCGGTGGTGTCTGGTTTGGCGCTGACT  
TTTCTGTGGGGCAGGCGTGGTTTTTTAGGTTCTTGGCTTGATCAGGTTGGATTGCCGATT  
GCATTTACCACCACGGCTGTGGTGTGTTGCCAGGTGTTTGTAGCGTTGCCATTTTTTCATT  
TCCACTGTGACTACTGCACTGCGTGGCATTCCAAAACAGTTTGAGGAAATCGCAGCTACT  
GAAGGCGCAACCCGCTGGGAGATCATGCACAAGATGATCATTCCGCTGGCGATGCCTGGA  
ATTTTCACCGGTATGATTTTGGGATTTCGCCAGGGCCTTGGGCGAGTATGGTGCGACACTG  
ACTTTTGCTGGAAATATTGCAGGTGTTACCGCGACCATTCGTTGCATATTGAGCTTGGT  
TTGAGTTCCAATGACATGGATAAAGCCTTGGGAGCGGTGATTATGCTTTTGGCTGTCTAT  
GTCCTCATCATTGGAGCCATCGGAGCGTTACGATTGTTTTCCAAGGTGAGAAAGGTT

>RXN00444-downstream  
TAATTGATGTCTCGTTCGCCGGA

>RXN00449-upstream  
TCGTTGGCTTACATGGTCATTGATGACCGGGCTGAATATGTGAGAAAATCCATCCCTTCT  
TTAAGCAAGGGAGTGAATTACAGAAAAGGATTGTTTCAGCA

>RXN00449  
ATGAGCACACCTGACATTAAAGAAGGCTCGGCAGAATCACCGGGCGAAGTAATGGTCGTT  
GGAGACAGGCGAGAGTGGCGTCGACAAGCAACCGGCATCATTGCCGGCCTCGTCTTAGCC  
GCCCTGGTCTATCTTCTCTTCCCCTCGAACTCCGTGGAAACCGTCATGCAATCCAGTGGC  
GTCGATCCAGAACTGAATACACCAACAACGCGATGCGTCTTACTGCTGCAGTCACAATC  
TTGATGGCAGTGTGGTGGATGACAGAAGCAATCCCACTAGCAGCAACCGCACTTATCCCG  
TTGGTTGCATTCCCTGCTTTCCAGGTTGTGGACTTTGGGAAGGCAACAGCTCCGTATGCC  
AACCTACGAGCTTCCCTCTTCTTGGGCGGCTTTCTTATGGCACTTGGCCTGCAGAAATGG  
AACCTACACCGACGTATGGCTCTAGCGGTGCTGCTAGCTGTTGGTACTAAGCCAAAGCAA  
TTGGTCTTGGGTTTTATGGTGGCAACTGGATTTTTGTCCATGTGGGTGTCTAACACTGCA  
ACGGCCGTGGTTATGTTACCGATCGGTATGTCGGTACTGGCACTGACCGCTGAGACTGTG  
GGCGGAATGAAAAACCAAAAGAAATTCGCCACTGGACTCATGCTGTCCATTGCTTATTCT  
GCTTCCATCGGTTCACTCGGCACCTTAATTGGCAGGCCACCCAATGCCTTGCTTGCTGCG  
TATATGTCTGAATCGCATGATATCCACATCGGATTTGGTCAGTGGATGATTCTTGGTGTA  
CCAATTGCTGTGCTCTTACCATCATCGCGTGGCTTGTGTTGACCACCGTGTTCAAGCCA  
GAAATGAAAGAAATCCCTGGCGGACGTGAACTGATCAAACGTGAAATCGCTGAAATGGGG  
CCGTGGACTGCACCTCAGGTCACAGTGGGTGTTATTTTTGCGGCAGCTGCACTGGCTTGG  
GTCTTCATTCCATTAACCTCTAGATTGGACCGGTTCAGCTCTCTATCAATGACTCCCTC  
ATTGGCATCGCTGCCGGCCTGCTGATGTTTATCGTTCCCGCTAACTTTAAAACCGGCGAA  
CGCATTCTTGATTGGCGTACTGCAGGCGAACTTCATGGGATGTTCTCTTGCTTTTTGGT  
GGCGGGCTTTCACTTTCTGCGATGTTTACCAGCACGGGACTTTCCCTATGGATCGGTGAA  
CTAGCTAAGGGACTTGATGCCCTTCCAATCTTCATTCTCATCTTCGCCATTGCTGTCTTG  
GTGTTGTTCTTGACCGAGTTCACCTCCAACACCGCAACAGCGGCAACCTTCCTGCCAATC  
ATGGGTGGCGTCGCCGTAGGTATCGGACTGACCGCAGGTGGCGAGCAGAATGTTCTGCTG  
CTGACCATCCCAGTCGCACTGTCCGCAACCTGTGCGTTCATGCTTCCAGTGGCAACGCCT  
CCAAACGCGATTGCATTTCGGCTCCGGCTACATTAAGATCGGCGAAATGGTCAAGGGTGGT  
CTGTGGCTGAACATCATCGCAGTCATCCTCATTACGATTTTCACCTACTTCGTAGCGATC

CCACTCTTTGGCATCATGCTT

>RXN00449-downstream  
TAAAAGTTAACAGGCCCGCAGTC

>RXN00456-upstream  
CTCACCAACCCGGAGATCGTCACAGCGGTGCTAACGGATCATGCCTAGCTTATGGCGTGC  
TCGTGCGAGACTTTTGCTCATTGCCCTAGGTGTACTTGGT

>RXN00456  
GTGCTGCAGGCACTGCTGGCGATCATGGTGTCTGTTGAGCGTAGCCGCCATACTTGAGGGA  
AACCGAGCACTTGTGGATTGCTGCTTGCTACCACGTTGGGTTTGGGGGTGGCGCAGTGG  
ATTCAAAAAGTAGTGGCAGAAGATCTAGGCCAGCATTATGTGCATGAGGTGCGTCGTGAA  
TTGGTGGGTGCTGCGCTGGTGCCTGGAAATACGGCCTCGTTGGGCGTGACTGTCACCCGA  
GCCAGCAATGATCTCACCGCGGTGCGCAATTGGGTGGCTTTGGGCATTGTTCCGATGGTC  
ACCGGGCTGCCGTTGATTGCGATTGTGCTGGTGGCGTTGTTTATCCAAGATCTCCGCACA  
GGCGTGGCTGTTACTGTGCCACTGCTCATGTGTGTAGCCGTGCTGCCGGTGGTGGCGCGG  
TGGACTTTGAAAAGAGCACGTGAACTACGCAAAAACGTGGACGCATGGCTGCGCGGATC  
GCAGATTCTGTGCATGGCTGGAGAATTACTGCACGCAACAGGAGCAATAGACCGTGAGCTC  
AATGCAGTCACCCGAGATTCCGACCGAGTGGTGATAGCTGCTGTAAGACGTTCCCTGGGCC  
ACCGGTTTTAGCCGCGCATTGATGGCCATGGCAGCCTCGCTTGGCACTGTCAGCATTGTG  
ATTTCTGGCCACCTGGAAGTAAGTGAGGTTGCGGGAATAATGATGCTTCTTGGCGTTCTT  
GCCACTCCAGTTGCAGAACTTGGCCGCGTGGTGGAAATATCGCCAAAATTATAAAGCCGCG  
ACACGCATCCTGATTCCACTTCTGCAACGAGGCTCAGAATTTAAACACTCCCAACAAAAA  
CTACCCGGGTGCAAGCAACAGAAGGAATCCCCGGTGTCTATGTCAAAGGTATTTCCGCC  
CTTCCTGGAGAACGGATCTACCTCCACGGCTCTGCAGATGCGACGAGAAAATGGGTCAAC  
TCGTTGTCTGCAATGGAGGAAGGCACAGATGTAATAGTCAACGGTCAAAGGCTTTCGCAG  
CTTCCTTTGAAACAACGACGCGCCCTCATCGGAATCGCCTCAGCACACCACCACTTAAGC  
CGTGGTTCAGTATCGCGCCTGGTTGGTTTGCAGTGGCGGATGCCACCGTGGAAGAAATT  
GAGCAAGCACTGGAACAAGTTGGTCTGAACAACACCGGGAAACAACGCTTGAAAAACGGC  
GGACACCCCTGGAGTACTTCGCAGATCAACAACTGAAAATTGCCAGCGCCACCCTTCGA  
ACCCACCGCTTTTGGTACTTGAAGGCATACCCCTGAAAACCTCCTCAACTATCCCGGA  
GTGATCATCTCCACCGTTCAGGAGAACCCATCCGAAACATGGCGGCAAGTGAACATC

>RXN00456-downstream  
TAATCTAGAAACATGGCAGGACG

>RXN00466-upstream  
TTTAAAAGCGCACTAAGAGCTCGTCAATTCTTTAAAACAAGCTGAGAATGTGAATAATAG  
GATAGGTAAACCTGATTGATTAGAAAACGGAGATTTGTC

>RXN00466  
GTGCAATCCCGCCTGTCCAAAATCCTGCGCAGTAGCGTCGTAGGCGTTGCTGTCCTAGCC  
CTGTTAGCTGGGTGTTCTAACAATGCAGATGACACCGACGCTGATTCAACATCCACGGGA  
AACTCCGCTTTTCCTGTTTCGATTGAACACGAGTTCGGAACCACCACAATCGATGATGTA  
CCCGAAAGAGTTGTCACCCTTGGCGTTACCGACGCGGATATTGTCCTCGCATTGGGGACC  
GTCCCAAGTAGGCAACACCGGATACAAATTCTTCGAAAACGGATTGGGACCGTGGACTGAT  
GAGTTAGTGGAAGGCAAAGAATTAACACTGCTTGACTCTGATTCCACACCAGATCTTGAA  
CAAGTAGCAGCCCTGGAGCCAGACCTGATTATTGGAGTCTCTGCGGGGTTTGACGACGTT  
GTATACGAGCAACTATCTGATATCGCACCGGTGGTGGCCCGTCCAGCGGGAACAGCTGCA  
TACGCAGTAGCTCGCGAGGAAGCTACCAACCTTGTGGCCCGTGGCGATGGGGCAATCAGAA  
AAAGGACAAGAGCTCAATGAGGAAACAGATGCTCTGATCCAAGCTGCGCGTGATGAAAAT  
CCTTCTTTTGACGGTAAAACAGGAACCGTCATCTTGCCATACCAGGGTAAATACGGTGCC  
TACCTGCCAGGCGATGCACGGGGACAATTCCTCGATTCACTTGGCATTTCGCTGCCGGAA  
GCAGTTCTTTGCGGAGACACCGGCGACAGCTTCTTTGTGCGATGTCCCCGCTGAAAGCGTC  
AAAGACGTAGACGGTGATGTTCTCCTCGTGCTTTCCAACGACGAAAATCTGGATATCACA  
GCAGAGAATCCACTGTTTGAAACACTCAACGTTGTGCAAAAAGACGCAGTAATTGTGGCA  
ACAACCGAAGAACGCGGGGCGATTACCTACAACCTCAGTGCTGTCTGTTCTTTTGGCGTTG  
GAACATCTCGCACCACGTATTGCTGAGGCTTTGAAG

>RXN00466-downstream



TAAAACTCAACTACTCGAGCACA

>RXN00477-upstream

TGCGGGAGCGAATCAGAGTTCCACTTCATATCAAACCTCTCTACACTCGCTAGAGCCACGA  
TGAAAGGTCTATCTATGAGCATCTACAGAAAGAATTTCGTG

>RXN00477

ATGAAGGTCTCGACTAAAACCTCCACGCTCCTCAGGTACCGCCGTAGTCATAGGCGCAGGT  
GTTGCTGGTTTAGCCACTTCTGCACTTTTAGCACGTGATGGCTGGCAAGTAACTGTTTTG  
GAAAAAATACTGATGTCGGTGGCCGAGCTGGATCGCTTGAAATATCAGGCTTTCCTGGC  
TTTCGATGGGATACCGGACCTTCTTGGTACCTCATGCCCAGAGCCTTTGACCATTCTTC  
GCACTTTTTTGGTGCATGTACTTCTGATTATCTCGATTGTTGGTAGAATTAACGCCTGGTTAT  
CGAGTTTTTTCTGGCACACATGACGCTGTCGATGTCCCCACTGGGCGTGAAGAAGCAATT  
GCGCTATTCTGAATCCATCGAACCCGGCGCGGGTGCAAACTAGGAAATTATCTTGATAGC  
GCGGCAGACGCCTATGACATTGCCATTGATAGATTCCCTTTATAATAATTTCTCCACGTTA  
GGCCCGCTGCTTCACCGGGATGTACTGACCCGAGCTGGCCGACTGTTTTCTCTACTGACC  
CGTTCTTTTACAAAAGTACGTAAATAGTCAATTCAGTAGCCCGGTGTTGCGCCAGATCCTA  
ACCTATCCAGCAGTCTTCCTGTCTTCCCGACCCACTACTACCCCATCGATGTACCACTTG  
ATGAGTCATACCGATTTGGTGCAGGGAGTGAAATACCCTATAGGTGGTTTTACTGCAGTG  
GTTAACGCTCTGCATCAGTTAGCGCTGGAAAACGGGGTTGAGTTTCAACTCGATTCTGAG  
GTCATTTCCATCAACACTGCTTCATCGAGGGGGCAACACAAGCGCCACAGGTGTGAGCTTG  
CTTCACAACAGAAAAGTGCAAAATCTAGATGCGGATCTTGTGGTTTCAGCAGGCGACCTA  
CACCATACAGAAAATAATCTGCTTCCCCGGGAACCTTCGAACCTATCCCGAACGATATTGG  
TCCAATCGCAATCCTGGAATTGGAGCGGTATTAATCCTCCTGGGCGTAAAAGGAGAGTTA  
CCCCAGCTCGACCATCACAACTTTTCTTCAGTGAAGATTGGACAGATGATTTTGCTGTA  
GTTTTCGACGGGCCTCAACTTACCCGCCCCCACAATGCATCAAATTCCATTTATGTCTCC  
AAGCCTTCAACGTCCGAAGACGGCGTTGCACCTGCTGGATACGAAAACCTTTTTGTTTTA  
ATTCCGACCAAGGCCTCTAGCAGCATCGGCCACGGTGATGCGTATATGCAGTCGGCTTCA  
GCATCCGTGGAAACAATCGCGTCACATGCAATCAATCAAATTGCTACGCAAGCCGGCATC  
CCTGACCTCACTGACCGAATTGTGGTCAAACGCACCATTTGGCCCTGCGGATTTTGAGCAC  
CGCTACCATTCATGGGTAGGCAGTGCGCTGGGTCCAGCACATAACCTCAGACAGTCCGCT  
TTCTTAAGAGGGCGCAATAGCTCCCGCAAGGTCAATAACCTCTTCTATTCCGGTGCCACC  
ACCGTCCCGGGTGTAGGAATACCCATGTGTTTAATTTCTGCCGAGAATATTATTAAGCGT  
TTACATGCCGATACCAAGTGCAGGACCACTGCCCGAACCATTGCCGCCTAAAACGACACCA  
TCTCAAAGACCTCATACGATCAT

>RXN00477-downstream

TAAATTTTGATCCCTATCATCGA

>RXN00523-upstream

TGGTGACTCGTCCGAGTGAAATTGCCGTGGGCATCATCATGCCGATCATTGGTGCGCCAC  
TGTTTATTTGGATTATTCGTCGTCAGAAAGTCAAAGAGCT

>RXN00523

ATGAGCCTTAGCCATCAACTCAAGCGCCAGCGCGCATCGCGCAACTCCCGCAGGTGGCTG  
ATTGTTGCGGCATTGGGCGTTCGTCACGCTTGGTATTTTTGCTTTTTCTTTGATGTGGGGC  
GAGGTGTTTTATGGCCCTGCTCAGGTGCTGAAAGTGTTGTCTGGACAGCAGGTTCCTGGC  
GCGAGTTATTCCGTTGGCGTGTGCGTTTGCCGCGCGCGGTGATGGGTGTTGACTGCGGGT  
TTGGCGTTTGGCGCGGCGGGCGTGATTTTTTTCAGACGGTGTGCGTAATCAGTTGGCGTCG  
CCGGATATTATCGGCATTTCTTCTGGCGCGTCGGCGGCGGGCGTAATTTGCATTGTGTTT  
TTCGGGATGTCGCAGTCTGCAGTGTGCGCGATTTCTTTGTGTGCGTCCTTGGCTGTGGCG  
TTGTTGATTTATCTGGTGGCGTATCGCGGTGGTTTTTCGGCCACGCGTCTGATTCTTACC  
GGCATTGGTATTGCTGCGATGCTGAATTCATTAGTGTGCTATTGCTGTCCAAGGCTGAT  
TCTTGGGATCTGCCGACCGCGACGCGCTGGCTTACCGGCTCGCTCAATGGTGCGACGTGG  
GATCGTGCGATGCCGCTGATTGTCACCACTGTGGTACTCATTCCGCTGCTGGTGGCTAAT  
GCGCGCAATGTGGATCTTATGCGTTTGGGCAATGATTCCGCGGTGGGTGTTGGGCGTTGCT  
ACTAATCGCACGCGCGTCATTGCGATTATTGCCGCTGTTGCGCTCATCGCCGTTGCTACC  
GCTGCATGCGGCCCCGATCGCATTCGTGGCGTTTGTGTCTGGCCCCATTGCCGCGCGCATT  
TTAGGCTCCGGCGGATCGCTCATCATCCCTCCGCACTCATCGGCGGGTTGATCGTGCTC  
ATCGCCGACCTAATTGGCCAATACTTCTCGGCACCCGCTACCCCGTCGGAGTTGTCACC

GGCGCATTCGGCGCCCCATTCCTTATCTATTTACTCATTCGTTCCAACCGCGCGGGAGTA  
ACCCTG

>RXN00523-downstream  
TGACCACCAACCATCAACTATCC

>RXN00525-upstream  
CCATCGTGTTTATTACTCACAACCCTGAGCTTGCTGATGAATCTGATCGGGTGGTCACCA  
TGGTTGACGGGCGCATCATTGGGTCTGAGGTGAAACACTC

>RXN00525  
ATGAGCCTTGCAGAATCAATTCTTTTGGCGCTCACCAGCCTGAGAAGCAACAAGATGCGT  
GCATTGTTGACGCTGTTAGGAGTCATCATTGGTATCGCATCAGTCATCGGAATTTTGACC  
ATTGGTAAAGCCCTGCAGGATCAAACCTTTGAATAGTTTGGAAAGCTTGGGCGCGAATGAT  
CTGTGCGGCGCAGGTGGAGGAACGCCCCGACGAAGATTCCCCCGAACCCGATATGTTGCT  
TTTTCTGGGGCTGCAAACCTCTAGTGGCAATCTGATTCCGGAAGAAACAGTTGATACGCTG  
CGCGATCGTTTTCGAGGCAGCATCACGGGAATCAGCGTTGGCGGAATGGGTACGCAAGGC  
ACTCTCATCGGCGACACCGCAGATCTTAAATCCGATCTCCTCGGCGTCAACGAGGATTAT  
ATGTGGATGAATGGCGTCGAAATGAACTACGGCCGCGCCATCACGCAAGACGATGTTGCC  
GCTCAGCGCCCCGTTGCGGTCATCGCCCCAGACACCTTTAATACGCTTTTCGACGCAAAC  
CCCAACCTCGCTCTGGGGTCCGAAGTAGCTTTTGAACCTAACGGTCAAGAGACATTTTGT  
CGGGTTATCGGTGTGTATAAAGAAGCCGCGAGGTTGGACTTGTGGGAAGCAATCCAACC  
GTCCACACCTACACCCCATATACGGTGGCCAATGACATCACCCACACGGAAGATGGATTG  
AACACGTTAAGTATCCGTGCAGCTCAGGGCGTAGACCAGGATTCACCTAAGGGTTCACCTG  
CAAACCTACTTCGACGCGCTGTACGCCAACAATGACTCGCACCACGTTGCCATGTTGGAC  
TTCCGTAAACAGATCGAAGAGTTCAACACCATTCTCGGCGCAATGAGTTTGGGTATCTCA  
GCCATCGGCGGAATTTCTTGTCTGCGTGGCATCGGAGTGATGAACATTATGTTGGTG  
TCTGTACCCGAGCGAACCCGCGAAATCGGTGTCCGAAAAGCCCTCGGCGCTCGTCGACGT  
GACATTCGCCTGCAATTCGTGCTTGAAGCCATGATCATTGTTTCATCGGTGGCATCCTC  
GGCGTGCTTTTGGGCGGCATTTTGGGATTGATCATGTCCAGCGCTATTGGCTACATTTCC  
TTGCCACCACTGAGTGGAATCGTGATCGCCTTGGTATTTTCCATGGCTATCGGCCTGTTT  
TTCGGCTACTACCCCGCCAACAAGGCAGCAAAGCTCGATCCAATTGACGCCTTGCCTTAT  
GAG

>RXN00525-downstream  
TAAAAGCCTCGTTTTTAAGGTAG

>RXN00559-upstream  
CCCTTCAATCCAGTCTTTGACGGCCAATACGGCTTGCCGGGTTTCCAGCGGATCAATCCT  
CATGAAGCATCAGCCTAGTACGAACCGTTAAAGTGTCCAT

>RXN00559  
ATGTCTGATAATCCGCATGAGAATCCCCGTGAGAATCCACACCGCTCCCCAGAAGTCGTC  
CTTCGTTTTCATGGCTGCCCTACTGACGTTTTTGATGGCTGGTAGCCATGGCGTTGGCGGT  
GGCCGAGTCCTGGAATGGATCGATAAGGCTGCTTATGCTTGTGCTACCCAGTGGTCTGGA  
ACCTACTGTGTCACTGCTTATGTTGGTCACATTCACTTCACCTCGCCCTATTCCCTCTGGC  
CACATGGTTCGAGGTGCGTTCCCGCATTTGCGATGACTGGCCGTTCCCTCCATGCACATCGTG  
AATGAGGTGCTTTCTGCGGATCCTCGCGATGGCAACTACACCCGTGCGTGTGACTGCTTG  
GTTATTTTTCGTGGCGAAGGACACCGCAACTGGTCGCGCTACCCAGTTCTTTCATTTACC  
CCTAAGAATGAAGAAGAGCAGCGCGTGTGGAAGCTGCTAACTCCCGCATCGGGCTGCGC  
AAGGCTATTGAAGCGGAGATGGAAAAGCAGACGTACAACGGACCTTCTGAGGCCCTCGT  
TTGATTACCCGCTTCTTGGCTAAGCCAACAGATATCAACTGGGGTGGCAAGGTCCACGGT  
GGCACTGCCATGGAATGGATCGATGAGGCGGGTGTGCGTGCACCATGGAGTGGTCTGGT  
AACCACACCGTTGCGGTTTATGCTGGTGGTATCCGCTTCTACCAGCCCATTGAGATCGGT  
GACCTCATTGAGGTGGACGCCCGCATGATGCGTACCGATAAGCGTTCCATGCAGATGTCC  
ATCCACGTCCGTGCCGGTGATGCTCACCGTGGCCGTGCTGAGCTAGAAACCGCTATTCAC  
GCAACGGTGACCTACTTAGGAATTGATGTCGACGGAGAGCCTTTGCCTGCACCACAGTTT  
GTGCCTCGTACCCCTGAGGATATCCAGTTGGCTGAGCATGCAAACATCCTGAGGGATCTG  
CGTGCTGATTACACCCCAATGCCGCTGTTCCAGCGCAGGGTTCCACTGCAGATCGAC

>RXN00559-downstream  
TAGTTAGACCCGAAAAAGCCCCC

>RXN00563  
TTCTACAAGGATCTCTACGCACGTTCCGCACGCGGCACGGCAGCACTGTGGATCGTGGCG  
GCTAACTTGAGCTCCTACTCAGACATCGACGCCATCATCAACTGGGTCCGATCCGAGCAG  
ACCACCACCGTCAACGGCGCATCCAAGCTGGTCAAGCCAGCTTTGGTCCCTACCTTGCTG  
TTCCCATTCGCGGCACCTCGCGTGTCCGGATCCATGGCAGATGCAGGCCACAGGCAGAA  
TCCCAGATGCGACTTCTGCTCTGGTCTGTTGAGCGCCTCATCGCAGGTCTTGCGCCATTG  
GGCTCCTCCATCAACGTGGGTACCGCCTGCACGTGGTTCATCCCAGGTTACCAAACCGT  
GGACGCTTCGGTGGCGATGGTGCATACGGTGAATCCAAGGCAGCTCTCGACGCCGTGGTT  
ACCCGTTGGAACGCAGAGCAAGCTGCATGGGGAGCACACACCTCCCTCGTGCACGCTCAC  
ATCGGTTGGGTTCGCGGCACCGCCTCATGGGCGGCAACGATCCTTTGGTCAAGGCAGCT  
GAAGAAGCAGGCGTGGAACCTACTCCACCCAAGAAATTGCAGAGAACTGCTGTCCCAG  
GCAACTTCCACTGTTTCGCGAGCAGGCAGCATCCGCGCCAATCACCGTCGACTTCACTGGC  
GGACTTGGTGAATCTGATCTGAACCTGGCGGAAATGGCACGTGCAGAAGCAGCTAAGGCA  
GCTAACGCACCAGTGGTTGAGGCTCCACGCACAGTGGCAGCACTGCCAACTCCTTACCGA  
CCAGTGGTTCAAACCACCCCTGATTTTCGCAGGTCAAGTCACCCAAAACCTTGACGAGATG  
GTCGTCATCGTTGGCGCCGGCGAGCTCGGCCCACTGGGTCTGCACGTACGCGTTTCGAC  
GCCGAACCTAACGGTTCCCTCTCCGCGCGGGTGTTCATCGAACTTGCATGGACGATGGGA  
CTTATCCACTGGGATGAAGATCCAAAGCCAGGCTGGTACGACGACTCCGACGACGCAGTG  
GCCGAAGAAGACATCTTCGACCGCTACCACGACGAAGTCATGGCACGCGTTGGTGTCCGC  
AAGTACAATGACATGCCTGAGTACGGCATGATCGACAACCTTTGCACCAGAGCTGACCACC  
GTCTACCTCGACCAGGACCTCACCTTCAACGTGGGATCCCGCGAAGAGGCACCTGACCTAC  
GTCGACTCCGAGCCAGAACTCACCTTTGCTTCTTTCGACGAAGCAGCAGGGGAGTGGAAG  
GTCACTCGCAAGGCAGGCTCCGCAATCCGCGTACCTCGCCGCATGGCGATGACCCGCTTC  
GTTGGTGGACAGGTTCCCTAAGGACTTCGACCCAGCTGTGTGGGGCATTCCAGCTGACATG  
GTGGACAACCTGGACACCGTTCGCGCTGTGGAACATTGTCTGTACTGTCGACGCCTTCCTG  
TCCGCTGGATTACCCCCAGCAGAGCTGCTTGCTTCCGTTTACCCAGCACGCGTGTCTCT  
ACCCAAGGCACCGGCATGGGCGGCATGGAATCCCTCCGTGGCATCTACGTGACCGCATT  
CTGGCAGAGCCACGCGCCAACGACGTTCTGCAGGAAGCACTGCCCAACGTTGTTGCAGCT  
CACGTCATGCAGTCCTACGTCCGTGGCTACGGACAGATGATCCACCCAGTCGCAGCTTGT  
GCAACCGCAGCTGTTTCTGTGGAAGAAGCACTGGACAAGATCCGCATCGGCAAGTCCGAC  
TTCGTTGTGCGCAGGTGGCTTCGATGCCCTGTCCGTTGAAGGCATCACCGGCTTCGGCGAC  
ATGGCAGCAACCGCCGACTCCGCAGAGATGGAAGGCAAGGGAATTGAGCACCGCTTCTTC  
TCCCGCGCCAACGACCGGCGCGCGGTGGATTTCATCGAATCCGAAGGTGGCGGAACCGTC  
CTTCTGGCACGCGGATCACTCGCAGCTGACCTGGGCCTTCCAGTACTCGGTGTCATCGGA  
TTCGCAGAGTCCTTTGCAGATGGTGCCACACCTCCATCCCAGCCCCAGGCCTCGGTGCC  
CTTGGTGTGCTCGCGATGGTGTGGAATCTCGCCTTGCACTAGCACTGCGTTCCGTCCGT  
GTCTCTGCTGATGAGATCTCCATTATCTCCAAGCACGACACCTCCACCAACGCGAATGAT  
CCAAACGAGTCCGACCTGCACGAGCGCATCGCATCCGCTATCGGTGCTGCAGACGGCAAC  
CCGATGTACGTGATTTCCCAGAAGTCACTCACCGGACACGCCAAGGGTGGTGCAGCAGCA  
TTCCAGATGATCGGTCTCACCCAGGTCTCCGATCCGGACTGGTGCCAGCCAACCGCGCA  
CTCGACTGCGTTGACCCAGTACTGTCCAAGCATTTCCACCTCGTCTGGCTGCGCAAGCCA  
CTAGACCTTCGTGCGAAGGCACCAAGGCAGGTCTTGTTACCTCCCTTGGCTTCGGACAC  
GTCTCCGCTCTGGTTGCGATTGTTACCCAGACGCCTTCTATGAGGCAGTTCGTGTGGCA  
CGTGGTGTGAGGCAGCTGACGTATGGCGCGCATCCGCGATCGCTCGCGAAGAAGCAGGC  
CTTCGTACCATCGTCGCCGGTATGCACGGTGGCGTACTGTACGAACGCCAGTTCGAGCGC  
AACCTCGGTGTCCACGGAGACGCAGCTAAGGAAGTTGAAGCTGCAGTCCTCCTGGATTCC  
CGCGCCCGCCTAGTTGACGGTGTCTCCGCGCCGAAGGC

>RXN00563-downstream  
TAGTTGGTTATTGCGTTGAGCCC

>RXN00570  
ACGAGACCTCGGCCCCAAGAAATTGGCAACGGGCTTGTCGCACTGATTTTCTCCGCATCC  
GGACCCATCGCAGTGATCCTGGCTGCTGCTGCAGCGGGAAACCTTTGCGCTGATCAAACA  
TCTTCATGGATCTTCGGAGCATTTTTAGGCAACGGACTGCTCACGCTGTGGCTTACCTAT  
ATGTACCGCAGCCCGCAGGCATACTTCTGGACGATTTCCCGGAACCGTCATCGTGGGCGAC  
TCACTTACCCACTTAAGTTTCGCTGAAGTTATCGGCGCATACCTTGTTACCGGCGTTGTG  
GTGTTTGCCTCGGATGGACCGGTCTCATCGGACGGATCATGGCGGTACTGCCACCAACC

ATCGTGATGGCCATGGTTCGCAGGCATTTTCCTCCGCTTCGGACTCGACCTCATCGACGCC  
AGCGTGACCGACCCGCTCATTGCACTTCCCATGGTCATAGTTTTTGTGGCATTGAGCATG  
AGTCCCCGCTTGGCAAGCATCGCCCCACCCGTTGCAGTAGCCGCAGTAGTGGGAACCATC  
GTTGCCATCGCATCCGGCAAACCTAGCGTCCGGAATTCTAGACAACGGAATTATCTCCCGC  
CCCGTCTTTACCGCCCCAGAATTTTCCTTCGCCGCCATCATGGAACCTCGTTGTTCCCTTG  
GCGATCACCGTAGTCATTGTCCAAAACGGCCAAGGCGTCGCAGTGCTTAAAGCAGCAGGT  
CACCGCCCCGGAGTAAACCTTGCCGCCGCGGCCTCCGGACTGTGGTCCCTACCCATGGCG  
TTGATCGGCAACATCACACCTGCCTCACCGGCCCCACCAACGCGCTGATCGTCGCCGGA  
GCAAAATCACAC

>RXN00571

ACACTTGTTCACAGGTTTACGAAATAGTGATCTACGGCGCTGTGCTGTCAGCTGTACAT  
GAAGATCCAACCCAGATCGGTGCGCTCAGCCCAGCAGTCGCCGGCACCCCTTGGTTCCTAC  
GCCATGATCGGCGTGATGATCGGTGCTCTATCTGCAGGTGCCGTTGGTGACCGCCTTGGT  
CGTCGCAAAGTTATGCTCACCGCAATCGTCTGGTTCTCTGTGGGCATGGCGCTGACCGCG  
TTCGCGTCCCTCGATTGCGCTGTTCCGTTTCTTGCGCTTCCTCACCGGACTTGGCGTGGGC  
ATGATCGTTGCAACCGGCGGCGCAATCATCGCGGAGTTCGCTCCAGCGAATAGGCGCAAC  
TTGTTCAACGCAATCGTGTACTCCGGTGTCCAGCCGGTGGCGTGCTGGCTTCTATCCTT  
GCACTGCTCTTTGAAGATGTCATCGGCTGGCGCGGACTCTTCCTCATCGGTGGATCCCCA  
CTACTGTTCCCTCCTGCCACTTGCATACTTCTTCCTCCAGAGTCCCCGCGCTGGCTCACC  
TCCCGCGGCCGTGCTGCGGACGCCAAAGCCCTCTGCGCACGCTATGGGCTGCCGACGGAG  
GAATTTGTCGTCGAAAAGCAGCAGGAAACAAAGGGCACCGGATTCGCTGGAATTTTCTCC  
TCCAAGTACCTCATGGGCACCATTTCTCATCGGCGCAATGAGCTTCATCGGGCTGCTTTCG  
ACCTACGGCCTGAACACCTGGTTGCCAAAGATCATGGAATCCAACGGCGCAACCTCACAT  
GATTCCTGTACTCCCTGCTGTTCTCAACGGCGGCGCAGTGTTCCGGTGGCCTCATCGCA  
TCCTGGTTTCGCTGACCGCATCGGCGCGAAGACCGTGATCACCTCCACCTTCGCTCTCGCC  
GCGATCTGCCCTCGGAGTCTGCCAAACATCTCCTCCTGGCCAATGATGTACACCGCAATC  
GCATTCGCAGGCGTCGGCGTCTGGGCACCCAGGTTCTCACCTACGGCCTGACCTCGAAC  
TTCTTCGGAACCGAATGCCGCGCAGCGGGAGTTGCATGGTGTGCAGGATTCGGCCGACTC  
GGCGGAATCGTCGGACCAGCAATCGGTGGCCTGATCATCGGCGCAGGATTCGGACCAAGC  
TCCGCATTCCTCATCTTCGCAGCAGCTGCCGCAATCGGCGCGGTCTGCACCTTGCTGATC  
CCGCGCTCCCCAGCAGAAGTAGAGGTCAAGGTCGCGCAGGAACCACTTGACAGTGTC

>RXN00571-downstream

TAACCCCAATTAATTCGAAACAA

>RXN00590-upstream

TCTAAACTCACTCTCAACTCACCAAGATTGTTCAACAATCTGCGATTGGTGTGCAATCTA  
CCCCAATCATTTTGAAAGCCCCCACGAAAGGAGCGCGACA

>RXN00590

ATGGCCGACAACAAAATGCCGATGACAGCCAGCTAGTCTCAGCCAGCACTGGAACCCCT  
GGGCTGGCGACATTGCAAAAGCCAATGCGCCATCCCTCAAGCAAGCTGCAGTAACCGCC  
TCTGGCCGAAGCGCTCTGATGGGTGCCATCTTCTCATGGCAACTTCTGCCATCGGCCCA  
GGGTTCTCACCCAAACCGCTGTCTTACCAACCAGCTCGGCGCAGCTTTCGCATTTGCG  
ATCCTGGTGTGATCCTCATTGACATCGCGGTGCAGCTGAATGTGTGGCGCATCATCGGC  
GTCTCTGAAATGCGCGCCCAAGAACTCGGCAACACGGTTATCCCAGGTTTTGGTTGGGTG  
CTGGCCGTACTGGTCTGTATTGGCGGCGTAGTATTCAACATCGGCAACATCGCCGGTGGT  
GGCCTTGGGCTTAACGCGCTGCTTGGCTGGGACGTCAAAGTTGGTGGCGTGATCACCGCG  
GCCATCGCGATTGCGATCTTCTTGTTCAGCGACTTGGTGCTGCTCTGGACAAATTCCTC  
GTGGTCTCGGCGTCGTGATGATCCTGCTCACCGTCTACGTGGCTTTCGTCTCCCAACCT  
CCAGTTGGCTCGGCGCTGAAGAATGCAGTACTTCTGACACCATCGACTGGCTTGTCATC  
ACCACACTTGTGGGTGGAACCGTCGGTGGATACATCACTTACGCTGGCGCACACCGCATG  
CTGGACTCCGGACGAACCGGCCCAACAACGTCAAAGCTGTTTCCAATTCCTCTATCACC  
GGCATCCTGATCACTGGCCTCATGCGCGTGGTGCTCTTCCTCGCGGTTCTCGGTGTTGTC  
GCAGGTGGCGTCACCCTATCCACCACGGGCAACCCAGCCGCGGAAGCATTCAGCACGCT  
GCAGGCGATATCGGACTACGCATCTTCGGCGCCGTGCTGTGGGCAGCGTCCATTTCTCA  
GTCATCGGCGCCAGCTACACCTCTGCAACCTTCCTGGTGGAAAACAAGCCAGAGAAGAAG  
CGTCTGCAAACTGGGTGACCATCATCTTCATCCTGATTTCTTGCTCCGTGTTTCATCATG  
CTCGGCACGGCACCAAGCAATCCTTGGTCTTCGCCGGAGCATTCACGGTTTGGTCTCTC  
CCCGTAGGCTTTACCCTGATGATCTACGTAGCGATCTTCCGCCAAAAA



>RXN00661-upstream

CGGATGCAAGAGAACCGTGGTTTCGCTGATTTTTGGCGAACCCGGAATTAAGGCCCGAG  
GATTACATGCTTTTAAATCCTTTGAAAAGGGGACAAGATC

>RXN00661

ATGAATCCTATAACCGAATTATTAGACGCAACACTATGGATCGGCGGAGTTCCGATTCTG  
TGGCGCGAAATCATCGGCAACGTTTTTCGGATTATTTAGCGCGTGGGCAGGAATGCGACGC  
ATCGTGTGGGCATGGCCCATCGGCATCATAGGCAACGCGCTGCTGTTACAGTATTTATG  
GGCGGCCTTTTCCACACTCCACAAAACCTCGATCTCTACGGCCAAGCGGGTCGCCAGATC  
ATGTTTCATCATCGTCAGTGGTTATGGCTGGTACCAATGGTTCGGCCGCAAAACGTCGCGCA  
CTCACCCAGAAAATGCAGTAGCAGTGGTTTCCTCGCTGGGCAAGCACCAGAAAGAACGCGCC  
GGCATTGTGATTGCGGCGGTTGTGGGAACACTCAGCTTTGCCTGGATTTTCCAAGCACTC  
GGCTCCTGGGGGCCATGGGCGGACGCGTGGATTTTCGTCGGCTCAATCCTGGCTACCTAC  
GGAATGGCTCGCGGATGGACAGAGTTCTGGCTGATCTGGATCGCCGTCGACATAGTTGGC  
GTTCTCTACTTTTGAAGTGGCTACTACCCATCCGCGGTGCTTTACCTGGTGTACGGT  
GCGTTTGTGAGCTGGGGATTTGTGCTGTGGCTGCGGGTGCAAAAAGCAGACAAGGCTCGT  
GCGCTGGAAGCTCAGGAGTCTGTGACAGTC

>RXN00661-downstream

TGAAAAGCGTTTACTAAATAGAA

>RXN00733-upstream

ACGGCGAGGTTGTCGGTATTGGAACGCACACGAATTTGCTGAACACGTGCGGTACCTACC  
GTGAAATTGTTGAATCCCAAGAGACTGCGCAGGCGCAATC

>RXN00733

ATGAGTAATACTGCAGGCCCCCGCGGGCGTTCCCATCAGGCAGACGCGCGCCGAATCAA  
AAGGCACAGAATTTTCGGACCATCTGCCAAAAGGCTTTTCGGAAATTTAGGCCATGACCGT  
AACACCTTAATTTTTGTTATCTTCCTAGCCGTCCTGAGCGTTGGACTTACCGTCTTGGGC  
CCATGGTTGCTGGGTAAAGCCACCAACGTGGTGTGTTGAAGGATTCCTATCTAAGCGCATG  
CCGGCTGGTGCCTCAAAGGAAGATATCATCGCGCAGTTGCAGGCTGCAGGTAAACATAAT  
CAGGCTTCCATGATGGAAGACATGAACCTTGTTCAGGCTCAGGCATTGATTTTGAAAAA  
TTAGCCATGATCCTCGGACTGGTGATCGGTGCTTATCTCATCGGTAGCCTGTTGTGCTTG  
TTCCAGGCGCGGATGCTCAACCGCATCGTGCAAAGTGCCATGCACCGGCTGCGCATGGAG  
GTGGAGGAAAAAATCCACCGCCTACCGCTGAGCTATTTTCGATTCCATCAAACGTGGTGAT  
CTGCTTAGCCGTGTGACCAACGATGTGGATAATATCGGTCAATCCCTGCAACAAACCTTG  
TCACAGGCGATCACTTCCCTACTGACCGTCATCGGTGTGTTGGTGATGATGTTTATCATC  
TCCCCACTGCTCGCACTCGTGGCGCTGGTATCCATTCCGGTCACCATCGTGGTCACTGTG  
GTGGTTGCGAGCCGTTCCAGAACTCTTTGCGGAACAGTGGAAGCAGACCGGTATTTTG  
AATGCGCGCCTGGAGGAAACCTACTCTGGCCACGCGGTGGTTAAGGTTTTCGGACACCAA  
AAGGATGTTCAAGAAGCATTCGAGGAAGAAAATCAAGCTTGTGTA

>RXN00733-downstream

TAAGGCCAGCTTTGGTGCCCCAGT

>RXN00784-upstream

GTCACATCAGTTATCGCGCGGAATAGTTAGCGGGCGCATGTGGTTGGGATATATGAATAA  
ATCTATTCCAACACTACGCGTAAAACGAGGACGTTTAAAGCT

>RXN00784

ATGTCTATTGAATTCTCCGCACCAGCAAAAATGAAAATCGAAGTGTGGAGCGACATCATG  
TGCCCCCTTCTGCTACATCGGCAAAAAGCGCCTCGACGACGCCCTAAGTACCTTTGACCAG  
GCCGGACGCATCGAAGTGGAATACAAGAGCTTCGAACATCATGCCAGGCCTAGAAACCCAC  
CCACTGCGTTCCGACGTTGAATACCTCGCCGACGCCAAGGGCATGAGCCTCGAGCAGGCC  
CGCCAAATGAACGGCCAAGTCCAAGCAATGGCACAAGCCACCGGACTTGAAATGAATCCT  
GACGAAACCATCGCGGCCAACACCATCAACGCGCACCGCCTTACCCACTTCGCGAAAGCC  
CACGGCAAGCAACAAGAAGTGGCGCAGGAACCTTCAAGGCTCACTTCGTAGACGGCAAG  
AACGTTGATGACCTCGATGTGCTGGTCTCCATTGCTGCAGAGGTTGGTCTCGATGCCAGT  
GCAGCCCGCGAAGCTCTCGAATCCGACGTGTACACCAACGAAGTCCAACAAGACGTCCAC  
GAAGCCCGCCAACCTCGGCGTCCAAGGTGTGCCCTTCTTTGTATTTCGACCGCAAATACGCC

ATCAACGGCGCCCAACAAGAAGAAGTATTCACCGGCACCGTAGAAAAAGCCTTCGAAGAG  
TGGGCAGCCGAAAACCCAGTCAGCCCATTGAGGTCATTGACGGCCAAAGCTGCTCCGTC  
GACGGCACCTGCAAC

>RXN00784-downstream  
TAACTTTTGGGACCTATGTGCGT

>RXN00792-upstream  
CACCTTTGGTGCTGAGCCAGGCCACCCAGGCCTTTGAGGTTGGCGCAGATGCCTTAAACG  
GCGGCCACGTGGCTGCCCAATACACGATCGGATCCTTGTC

>RXN00792  
ATGAGCCAAGAAATTTTGAGCCATTTTGCACCCGCATTAGAGCGCATTTCGAAGCGGCGCC  
GTCGAGCGCGAACAGCAGCGCGCCTTGCCAGTGGAAAGAGATTAAAGAGCTGGTAGAGCTA  
GGTTTTACTGGGCTTCGAGTGCCCGAAGAAGTGGCGGTGCGGGCGCTTCCCTGGAAAGC  
GTAGTTGAGTTACTGATCGAGATCGCGGGCGCCGATTCCAATATCGCCCAAGCCCTGCGC  
GGACATTTTGCCTTCGTGGAAGTACTCCTGGAAGCGCCGGAGAGCGAATTCCGCACCCAT  
TGGCTGCGCGAAGTCGCCACCGGAAGACTTGTGGGCAACGCCGAAAGTGAGAAACGCGGC  
GTTTACGGCGATCCGCAGACCTTCATCGATGAGGTGGAGACTGAAAACGGACCGATTTC  
GTGCTCAACGGCACTAAGTTTTATACCACCGGCACCTATTTTGCGGACTACACCTGGACC  
ACCGCGCTGCTGCGCAACCTTAACGGCCAAGAACTTTGGTCAGTTTGCCGGTCGATCTG  
CACGCGCCGGGCGTGGATGTTGCTGATGATTGGAGCGGGTTTGGGCAAAGCTCACCGCC  
TCTGGAACGACCACGTTTAAAGACCTGGAGGTGGATCCGCGGTGGATCATTCCACGCACT  
GATGCGCCACGCTGGTGTGGACGTATCTGCAGCTGAGCCTGCTGACCGTGCTGGTTGGC  
AGTGCCGCAGCAGCTGTCGATGAGGTGGTTGCCCGCGCCCAATCCTCCACCAGAAATGCG  
TGGAACCCTGGCGTCGAGCGCCGAGCGATCCGGCCGCAACCATAGCGATCGGCGACGCA  
CGCAGCCGAGTCACCGTTATTCGTGGAGCGCTTCTCGACGCCACCCGCCACGTTTCCAAC  
GCCGCCACGATCGTAACCCCCGAAGCCTTCAACGAGGCGGACGCTATTGTTGCAGCGCTC  
TGGCCCATCGTCTCCGGACAAGCTTTGGTGGTGACATCCAACGTTTTCGATGCGGTGGGT  
GCATCTGCAGTGCTTGGTGAGCATTCCATTGATCGCCACTGGCGCAATGTGCGTACCGTG  
TCCTCAAACAACCCGGTGTTCTGGCCAAGAATGCAGTGGGGGAGTATGCCCTCAACGGC  
ACTCCTGTGGGTACCAACATTGGTAAAGCACTGAGCCGTCCGGTGAGCCTAAGCAGC

>RXN00792-downstream  
TAGACGTGTGATTTTCGCTGGTTT

>RXN00819-upstream  
GATGAGGTTTCGTCCGGGAATCCTCAAAGACAATGCGGTGAAGGTACTTGGCCTAGCCGCT  
AGCACTGAGCGCGGATCTCAAGCAGAAAAGGTTCGTGCAAC

>RXN00819  
ATGCGTGATCCCATTTCAAGGTGCTGTTATTCCTTCTGATCTTTTTGGTTTCGCAGAAGTT  
CTCACCGAAGCCGAACGCGCAGTTCTTCTGGAAACCCGCAGGGTGCTTGAGGAAGAGGTG  
AAGCCTTATATTAATGAGGCCTGGGATAAGGCAGTCTTCCCGATGAGATCGTGCAGCCC  
CTCCAAGATCTGCAATTGCTTGATCCGCCTGCACTTCGGGAAGCAGGGGAGTCGGTTCGA  
GACATTTTCACTGGTTTCCGCAATTTTGAAGTTCGCGCGCTGTGACATCAATGTTGGTACC  
TATTACAACGCATCTGCTGGTCTCTTCCGAACGGCCTGCATGGTTGGTGGCTCCCCGGAG  
CAGGCGCAGCGATTGGATGCGCAGATCAAATCTGGTGAGGTCAAGGGCGTTTTTGCAGTG  
ACGGAACCTGATCATGGCTCTGATATCGCAGGTGGTCTGGCAACCACGGCCACTAAGGAC  
GCAGACACCGGCGAGTGGATTATCAATGGTGAAAAACGGTGGATCGGTGGTGGCTTCCACT  
GCTGATTTGATCGCTACCTTCGCCAGGGATACAGCCGATAACCAGGTGAAATGCTTCCTC  
GTGGCACCTCAGGCAGAGGGCGTGTCATGGAGATTATTGATCGCAAAGCCTCACTGCGC  
ATCATGCAAAATGCACACATTACCTATAACAATGTCCGGGTGTCTGGGGATGCGCGGCTG  
CACAACATCAATTCTTTCAAGGATGTTTCGGAATGCCTGCGCCGTATGCGTTCCGATGTG  
GCGTGGATGGCGGTTCGGTGCGCAGGCAGGTGCCTATGAAGCAGCCGTGAAGTATGTGCGC  
AGCAGGGAACAGTTTGGCCGTCCGATCGCGGGGTTCAGTTGATTCAGGAAAAGCTCGCG  
CTCATGCTGGGCAATCTCACGGCGTCGCTGGGCATGATGGTCAAACCTACCGATCAGCAG  
CAGGCGGGGAATTTTCAAAGAGGAAAACCTCCGCGCTGGCGAAAATGTTTACCTCGCTCAA  
CTTCGGGAGACCGCTAGTTGGGCGCGGGAAATCTGCGGAGGCAACGGCATCATTTTGGAC  
AACGATGTTGCCCGGTTCATGCCGATGCAGAAGCCGTCTATTCATATGAAGGCACCCAC  
GAAATCAATGCACTCATCGTTGGNCGNNCCATTCTGGGNCNTCTNTTCTTTTATATTAT

NACNCTTTTGAGGAGGATCTTCATGACTACTTCCACCACCCCAAACCATCGTTTCTTTTCG  
AAGACGCACCAACCCTCACCGGCCAGGACCTGGGCTTTTCGCAGTGGCGCACTGTCACCC  
AGGAGATGG

>RXN00819-downstream  
TGAACACCTTGGCGGACGCAACT

>RXN00832-upstream  
GAGATTGTGCTAGGTTCTGATGAGGCTTCGGGACGACCCGAAGAAATCTATGACAGCCTG  
GGAACGGCCCAGAGTTCTTAAGAAAGTTTGGACTAGAGAAC

>RXN00832  
ATGCCGTTTTCTTGGCTAAAACCAATTGATTATGCCCGCATCTTTGTCTGGCTGGGCATCG  
ATTTTTATCATCCCCCTCATCACACTGCCATCAATTATTGAGTTGGCGCTGATCGTGGCA  
GTCATCCTATTCTGCGCATTTGGCGTGGTGAAGATGGCGGAGCGTTTGGCTCATATTTTG  
GGTGATCCTTTTGGATCGTTGATCCTTACCTTGTCTGATCGTGATCATTGAAGTGATTTTG  
ATCTGTGCGGTGATGCTGGGGCCTGCTGATTCAACCACTGCTGGTCTGGGATTCCGTGATG  
GCAGTGTCCATGATCATCATGGGTTTGGTCTGGGATTGTGCCTACTCATTGGTGGTTTA  
AGGCATGGAAGCATGCCACACAATGGGGTGGGAACCTCCGACCTACTTGGTGCTGATCGCA  
ACTTTTTCCGTAATCGCCTTTGCGGTTCAGCTTTCAGGGGAGAATACTCCACTGGGCAG  
GCACTTGTATTATTTCAACACTGACAGCAGTGGTGTACGGGTCTTCTCTGTTTCGCCAAATG  
GGTGCCCAAGCTGGTGAATTTCAAGAGGTCGAGGTCGCAGAAAAGGCAGACGACGCAGCA  
AAATGGGAGGTCCCATTTAGAGGCTTAATCTTGATTATCACTGTGCTCCCCATCGTGTTG  
CTGTCCCATGACATGGCCACGGTGATGGATGAAGTCCTGGCAAGCCTTGGTGCACCCGTA  
GCAATGGCTGGATTAATTATTGCCACCATTTGTCTTCTTGCCAGAGACCATCACCTCCTTG  
AAAGCTGCGTGGACAGGAGAGATTTCAGCGAGTAAGCAACCTCGCGCATGGAGCCCAAGTA  
TCAACGGTGGGGCTGACAATCCCAGCTGTTCTAGTGATCGGCGTGATCACAGGTCAAGAT  
GTAGTTTTGGGGGAGACCCCGATCAACTTGTGCTGCTGGGAACCACCATTTGCGGTGACA  
GCCATTGCGTTTAGCTCCAAGAAAGTCAGTGCTGTGCATGGCTCGGTGCTGCTCATGCTT  
TTCGGTGTTTACATGATGAGCATGTTTCGCC

>RXN00832-downstream  
TGATTTAGGTAGCCTGGTGGGAA

>RXN00842-upstream  
CCTTGTCGCGGAGGTAAGCGAGGGTATTTCTGGATGTGGAACAACGCGGATTATGGAAAA  
TCGTGACTTTCATAACGTTGAGCCTACTAAGGTTTGTTC

>RXN00842  
ATGATTATTCAAATCCTAAGAGTGGCATTTCGCTTCGTCGGCATCATTGTTGGCGCCGGT  
TTCGCATCAGGGCAAGAGGTCATGCAATATTTTGTGGCCTTCGGCATAGACGGAATTTGG  
GGAGTCATTGTTTCTGCAGTGATCATGTCTGGTGATGGCGTTGATCATTTTGCAGCTCGGA  
AGCTATTTCAATGCAGGTGAACACGGTGAAGTGTTCCGCCGAGTAAGTCACCCCGTTTTTC  
TCCAAAATTTTGGACATCGGCGTTGTGGTGACGTTGTTCTCCACCGGTTTCGTGATGTTT  
GCAGGCGCGGGATCAAATCTGAATCAGCAGTGGGGGCTTCCGCTCTGGATCGGTTCTGTG  
ATCATGGTTCTTCTGGTGCTGGCTGCGGGCATGTTGGACGTGGATAAAGTAACCACAGTC  
ATTGGTGCAATTACTCCGTTTCATCATCATTTTTCATCACTGCCGCCTCGATCTACACGCTG  
GTAGGTAATTTAGCTCAGTGGAGCAGCTTGATTCTGCTGCTTTAGAAGTCGGCACGACG  
TTGCCTCACTGGGCTGTTGCAGCGGTGAACATATGTGGGATTCAACCTGATGGTTGCGGTG  
TCCATGGCTGTGGTCATTGGTGGATCAATGTTTAAACCCGCGGGTCGCAGGTCGGGGCGGT  
TTGCTGGGCGGATTGATCCTGGGATTCTTGATCATCATCAGTGCGCTAACACTGTTTCGCC  
ACCGTGGAAGAAGTTGGCCAAGATGATATGCCTATGCTGACGATCATCAACAATTTGAAC  
CCGCTGGCTGGCCAAGTAATGGCAGTGGTTATCTACGGAATGATCTTCAACACGGCACTG  
GGTATGTTCTACGCATTGGGCCGTCGTCTCACTGCGAAAAACCCACAGCGATTCCGTCCG  
GTTTATGTGGTCACAGTGCTGATTGGTTTTGTGTTGAGCTTTGTGGGATTCAAGAACTTG  
GTGGGCTATGTGTACCCAGTCTTGGGATACATTGGCCTGCTGCTGATTGCAGTGATGATG  
GTGGCGTGGGTGAGGGGACGCGTACGCATCTACAAGGAATCCGAACGCCGCATGCGGATC  
GCAGACTTGTGTCAGATCGGCCATGACGGAGCGTTGAGTGGAGCAGAGCTGGCGGTGCTC  
AACCAGGAAATCCAAGATTCAAACCTGGATGAGGAACAAATTAAAGCAGCGGTTAGGAAG

>RXN00842-downstream

TAGTTACTCTGCAGGGACGAGCT

>RXN00931-upstream

CCGTAACCTAATCGTTGAAACATCACCTTATTGCTGGGCTTTGCACGCTACTCTTTGTGA  
GTAACCTCACCGAAGTGCATAAATTAATTGGGAGTGATCA

>RXN00931

GTGAAAACTATTGAAGATATTTTGACCTTGGAAGAAATCGACCGCGATATTTACCGTGGT  
CCCGTTATCGAATCTTATTTAGCCAGGACTTTCGGTGGCCAGGTCGCTGCCCCAAGCTTTA  
GTAGCAGCAACGCATACTGTTGATAAAGCCTTTACTGTGCATTCTTTGCATGGCTACTTT  
ATAGCTCCTGGTGATCCAACAGCACCCGCAATTTATTTAGTGGATCGAGTTCGCGACGGA  
AAAAGCTACGTCACCCGCTCGGTGCGTGGCATCCAAGACGGCGAAGTAATCTTCAGCATG  
CAGGCCAGCTTTCATCGTGGGGATGAAGGCATTGAGCACATGGACAAGATGCGTAAAGTT  
CCAGCTCCTGATGAGATCAAGGGAACAGTAGAACGTATGCCGATCTCAAGTAGGCGAGTG  
CTTGATGAATGGGCGGAATGGGATATCCGCGTTATTCCGCAGGATCAATTAGAACTCAGC  
GATTTACACCGCTACTGAGCAAGCTGTGTGGATTCCGGTGCACCGCTGATCTTCCGGATAAT  
CCCACCTTCCACCAGTGCTCACTGACTTATCTGTCCGATATGACTTTGCTGCATAGTGCC  
CTGGTGCCACACCCAGGTGAGAAAATGCAGATGGCCTCACTTGATCACGCTGTGTGGTTC  
CTGCGTCCCTTCCGCGTCGATGAATGGTTGCTTTATGATCAGCGCTCTCCATCGGCCTCA  
AGTGGGCGAGCCTTGACTCACGGGCGGCTTTTCAACCAGCAGGGAGATTTGGTCGCTATT  
GTCAATCAAGAGGGAATGACCCGCACACTCCACGAGGGTGCGCAATCAATTCCGATGCGC  
AAAGAC

>RXN00931-downstream

TAAAATGCAGCGAACTTGAAGAT

>RXN00934-upstream

CCAACCCCTGTGGTTTGGTGATTTGGATCCGGAGCGTCTCAAGCGCTCTAGGGAGCAGAC  
AAATGTTCAAAACCGGTGGCATTACAGGAGGACAATTAG

>RXN00934

GTGCGAATTGGAATGGTCTGCCCCGTACTCCTTCGATGAGCCGGGCGGTGTTCAAGCGCAT  
ATCCTTGACTTAGCGCGAACCTTCATTGCCCAAGGCCATGAGGTTTCAGGTGCTTGGTCCG  
TGTAAGTGCAGGATACGCAGGTGCCCGATTTTCGTGGTGCAGCGGTGGTGGCAGCATCCCGATT  
CCGTACAATGGCTCGGTTGCCCGCTTGAGCTTTGGGCCGAAAATGTTCAAGGCCGTGCGC  
ACGTTCCCTCCGCGAAGGCAACTTCGATGTGCTGCATATCCATGAACCGAATTCACCAAGT  
TTTTCCATGGCGGCGCTACGCTTTGCGGAAGGCCCATCGTTGCTACTTACCACGCCTCC  
AGTAGCGGATCGAAGCTGCTCAAGGCTTTCTTACCAGTGCTTTCCGCCATGCTGGAGAAA  
GTGCGCGCAGGCATCGCCGTGTCTGAAATGGCTCGGCGCTGGCAGGTGGAGCAAGTCGGC  
GGCGATCCCGTGCTGATCCCCAACGGGGTAGAGACCTCCATGTTCAAAGCCGCGCGCCAA  
ATCGAACCGAATGATCCTGTAGAGATCGTCTTTTGGGTGCGCTCGATGAGTCCCGCAAA  
GGCCTCGACATCCTCCTGCGCGCTCTGACCAGGCTGGATCGCCCGTTTACCTGCACCGTC  
ATTGGCGGCGGCACCCCGCGAGAAGTCGCCGGCATCAACTTTGTGGGCGCGCTCAGCGAT  
GAGGAAAAGGCAGCAATCTTAGGTGCGCGAGACATCTATGTGCGACCCAAACACCGGCGGC  
GAAAGCTTCGGCATCGTGCTAGTTGAAGCGATGGCCGCGGGATGCGCTGTGCTCGCCAGC  
GACCTAGAAGCGTTCTCCCTGGTCACCGATTCTGAAGCCGCACAGCCAGCGGGCGTGCTA  
TTTAAACCGGCTCAGACGCCGACCTAGCCAAAAAATTTCAAGCGCTTATCGACGACCCC  
TCCTCCCGTTCCACGCTTATCGCCGCGGGGCTAAAGCGCGCAAACGCCTACGACTGGTCG  
ACAGTATCCACCCAGGTCATGGCAGTCTATGAAACCATTGCGATCGACAAAGTGAGGCTT  
GGA

>RXN00934-downstream

TGACCCTTGTTTACCTCCTCATC

>RXN00960

ATGGCTCGGCATTGTTGCAGCAATCGCTACGCGTCCACCGTCTTCTCCGGTCTGATCGCC  
TACGGAGCATCCCAAGCGCTCTACCCATGGCTGCTGAAAGACCACCAAGCGTCACCGAA  
ATCGACCTTGATGCAGGTGCCCTCCAGCCCTACTTCAACATCGAGATGCCACCACCATTT  
GAAGTGATGACCGCACTGCTGCTGGCATTCTGCCTCGGCCTGGGCATGGCTGTAATTAAA  
TCAGACACCCTGTTCAAGGTAACCCGCGAACTCGAGCGCGTAGTCATGAAGACCATCACC



GCCTTTGTCATCCCCTGCTGCCACTCTTCATCTTCGGCATCTTCCTCGGCATGGGCATG  
AACGGTGGCCTCCTGGAGATCATGTCCGCCTTTGGCAAGGTACTGATTCTCGCCGTCGTG  
GGAACCCTGCTCTTCCTAGCCATCCAGTTCATTATCGCTGGTGCAGTATCCAAGAAGAAC  
CCATGGAAACTGTTCAAAAACATGCTCCCTGCATACTTCACTGCACTGGGCACTTCCTCT  
TCAGCGGCAACCATCCCAGTGACCTACCAGCAGACCCTGAAAAACGATGTTGATGTCAAC  
GTCGCAGGCTTTGTTGTCCCCTGCTGCGCCACCATCCACCTAGCTGGATCGATGATGAAG  
ATCGGCCTCTTCACCTTCGCTGTTGTCTTCATGTACGACATGGAAGTAGGCGTCGGCCTC  
TCCATCGGATTCTCCTCATGCTGGGCATCACCATGATCGCCGCACCAGGCGTTCCCGGC  
GGAGCCATCATGGCAGCAACCGGCATGCTGGCCTCCATGCTCGGATTCAACACCGAACAA  
GTCGCCCTCATGATCGCCGCTTACATCGCGATTGACTCCTTCGGCACCGCAGCAAACGTC  
ACCGGCGACGGCGCAATCGCAGTCATCGTGAACAAATTCGCCAAGGGCCAGCTGCACACC  
ACTTCCCCAGATGAAATCGAAGAAGACGACCGCGTTGCCTTCGACATCACTCCATCGGAT  
GTGGAACATCACAAG

>RXN00960-downstream  
TAGAAACCCGCATTTTCTGTAGT

>RXN00980-upstream  
AGAGAGAAAGGGAGAAATCATGAAAACGTGGAAGACCTGGGGGGTCGTCGGAGCTTCAGG  
CCTCTTGATTATTTTGTCTGTTGAGTTCATCGAGCCCCG

>RXN00980  
ATGCTGGCAGATGCATTCATGATCGCGGCTGCAATTGTTGCAGGTTGGCCGATCGCGCAG  
TCTGCATATCAAGCACTTCGCATTCGAATGGTGTGCGATTGACTTACTGGTCGTTGTGGCT  
GCCGTTGGTGCCATGTTTCATCAACAACTATTGGGAGTCTGCGGCGGTGACGTTCTCTTT  
GCCCTTGGCAAGGCACTGGAACGCGCGACAATGAACCGCACACGAAAAGCACTATCGGAT  
CTGGTGGATGCAGCTCCAGAACTGCAACAAGGCTCAACGCGGATGACTCAACAGAGGTA  
GTTGAGCTGTGGGAGCTTGAGCCCGGTGACATCGTCTTGGTACGCAATGGCGAACAAATT  
CCCGTCGATGGAAACGTGATTGCGGGTGTGCGGTGGAATTGATGAATCCAACATCACGGGT  
GAATCAATGCCGGCTGAAAAGGGTCAAGGCTCTGATGTGTATGCAGGAACCTGGCTGCGA  
TCTGGTGTTTTGAGAGTCGAGGCAACAGGAATTGGTTCAGACTCAACTTTGGCAAAAATC  
ATTCACCGCGTTGAAGACGCCAGGATGACAAAGCCCGCACACAAACATTCTTAGAGAAA  
TTCTCTAAGTGGTACACCCCGGGCGTCATGATCGCCGCGCAGTGGTGGGACTTATCACC  
TGGGACGTAGAACTAGCACTGACGCTCTTAGTGATCGGCTGCCCCGGCGCGTTGGTTATC  
TCCATCCCGGTGTCCATCGTCGCAGGCATCGGCCGTGCTGCACGCGATGGCGTGCTGATC  
AAGGGTGGAGAATACCTAGAAACCGCCGCGAAAGTCGACGTCGTTGTCTGTTGGACAAAAT  
GGAACGCTGACCACCGGCCGCCAGAACTCACAGACGTAGAAGTCATCGAGCCCGCCTAC  
AGCCAGGGCGAGGTGCTGGAGCTCGCCGCGCGCGCCGAGACGGCTTCAGAACATCCGCTT  
GCCGACGCCATCATCCGTGGTGGCCAGGATCGGGGGCTGTCCACAACATTGGTGGAAAGCA  
GCTGAAAACATCACCGGCCGAGGCATTATCGCAAATGTTGATGGACAGGCAGTTGCTGTT  
GGATCTGCTGAGTTACTTGATCATGAACCAGACTCGACCAGGATCCTGGAGCTAAATGCC  
GAAGGAAAGACCGCGATGTTTGTGCGAGTGAACGGACACGCCATTGGAATCGTGGCCGTC  
GCCGACGCCGTTCTGTTTCAGATTCTGCCTCAGCAATCGAATCGCTGCATAAGGCGGGCATT  
CAAGTTGTCATGGCGACTGGCGACGCTCACCGCGTTGCACAAAACGTGGCCTCCAAGCTG  
GGAGTGGATGAAGTCTACTCAGAGCTACTCCCTGAACAGAAATTAGAATGGTGCCTGAT  
CTGCAAGCTGCCGGCAAAACGGTTCGCGATGGTGGGTGACGGAGTCAACGACACCCAGCA  
TTGGCAGCTGCTGATATCGGAGTAGCGATGGGCGTGGCAGGTTCCCCTGCAGCCATTGAA  
ACCGCTGATATCGCACTCATGGCGGATCGTCTCCACGGCTGGCACATGCAGTGACCTTG  
GCAAAACGCACCGTAAGAACCATGCGCATCAATATTCTGATTGCGTTGGCTACCGTGATG  
GTGTTACTAGCTGGCGTCTTATTTGGCGGAGTTACCATGTGCGTTGGCATGCTCGTTTAC  
GAAGCAAGCGTGCTGCTTGTATCAGCATCGCCATGCTGTTGCTGCGTCCAACACTTAAA  
GAAGATGCTGCGCAAGCAAGTGATATTAAACGCTCGGAAATACAACAGATCGCA

>RXN00980-downstream  
TAACCAATGGCTGGGTACTGATG

>RXN01000-upstream  
CTTTCTATGCCTACGCGGATGTTTCCGTGATCATTCTGGAAATCCTCATCGTGGTGATTG  
TCATTGAAGTAATCTCCAACGCACTTCGAAAGAGGCTGGT

>RXN01000

ATGAGCACCTTAACCTCTCACCGCACAGTACCGGCCCCCAGCTCTCCCCCGGCGCGCCCC  
AACAAACTGGCGCGCAATATCGTTGCAATTGTCGCTGCGCTGATTGTCCTTATAGCTACC  
GGCACGCTCAAGATCGAGTGGAATGAGCTTCCGCAGATGCCCGCGCAGGTGTGGCATTAC  
TTAGAGCTGATGTTTAGCGATCCCGATTGGTTCGAAGTTTGGCCGCGCCGTCCAGGAAATG  
TGGCGTTCCATCGCCATGGCGTGGTTGGGTGCCATTTTATGCGTGGTGGTCTCTGTCCCT  
CTGGGAATGTTGGCTGCCCGCGGGGTGGGACCTTATTGGCTGCGTACCGTTTTACGGTTC  
GTGTTTCGCGGTGATTTCGTGCGTTCCCCGAAGTGGTTATCGCAATTATTTTGCTAACTGTC  
ACCGGCCTAACTCCTTTTACTGGTGGCTCGCATTTGGGTATCTCCGGTATTGGACAACAG  
GCAAAGTGGACCTATGAAGCCATTGAGTCCACTCCCACCGGCCCGTCAGAGGCAGTGCGT  
GCAGCGGGTGGAACTACGCCGGAGGTTCGTGCGGTGGGCGTTGTGGCCACAGGTTCGCGCA  
TCCATTGCATCTTTTGCCCTGTACCGCTTTGAGATCAACATCCGTACCTCTGCGGTATTG  
GGCATCGTTGGTGCAGGTGGTATCGGTAGTATGCTTGCCAATTACACCAACTACAGGCAG  
TGGGACACCGTGGGCATGCTGCTCATCGTCGTGGTTGTGCAACGATGATCGTCGATCTC  
ATCTCCGGCACCATCCGCCGCCGCATCATGAAGGGGGCTAGTGACCGTGTGCTGGCACCA  
AGCAAC

>RXN01000-downstream  
TGACGCTCCACCAAGCATCCGCA

>RXN01002-upstream  
GACTGCTGATACCGCACAGGATGAAATCACTCGTTACGGCGAGATCCTGAAGAAGTTCTC  
CAACTAATTTCCCTGTTTCCAATACTCAAGGTGTGCGCAT

>RXN01002  
ATGAATTCTGATGCTTCGGCTACCACCAACTCCTGGGCTATCAACTTCGACCATGTGTGCG  
GTGACGTATCCCAATGGGACGAAAGCCCTCGATGATGTTTCCCTCACCATCAATCCCGGT  
GAGATGGTTGCCATCGTGGGTCTGTGAGGATCGGGTAAATCCACGCTGATTTCGCACGATC  
AACGGTCTTGTCCGCGCTACGGAAGGCACCGTGACGGTGGGGCCGCATCAGATCAACACC  
TTGAAGGGGAAAGCACTGCGTGATGCCCGTGGGCAGATCGGCATGATTTTCCAGGGGTTC  
AACCTGTCGGAACGCAGCAGTGTGTTCCAGAATGTTTGGTGGGCCGCTTCGCGCACACA  
GCGTGGTGGCGTAACCTCCTCGGGTTTCCCACGGAGCACGACAAGCAGATTGCTTTTCAC  
GCGTTGGAGTCCGTGGGCATTTTGCACAAAGTGTGGACCCGAGCTGGTGCTTTGTGCGGT  
GGACAGAAACAGCGCGTTGCTATTGCGCGCGCCTTATCGCAAGATCCGTCTGTCATGCTG  
GCAGATGAGCCTGTGGCAAGCCTTGATCCGCCAACCGCGCATTCGTGATGCGCGATCTA  
GAAAACATCAACAACGTGGAAGGCCTCACCGTGTGGTGAACCTTGCACTTGATTGATTTG  
GCTCGTCAATACACCACAAGGCTTGTGGGTTTGCGTGCCGGCAAGCTGGTCTATGACGGT  
CCTATCTCTGAGGCCACCGATAAAGACTTTGAAGCTATCTATGGTCGCCCCATCCAGGCT  
AAAGACCTGCTAGGTGATCGCGCA

>RXN01002-downstream  
TGACCACGCCTTCTTCTACTT

>RXN01007-upstream  
TCTGAACCAATATACCGATCAGTCTAAAAGTGTGTTAAGTTCTGGAACATAAATTAGCTG  
ACACGTAAAGTAACTTAAAGATTCACTGGAGGTAAGCCTA

>RXN01007  
GTGTTTAAAAAGCACAGACACGGTCTCGGCTCCCCGAAACCAACCACGCTCAATAACC  
CGCCGGTTTTTACCGCGGGCCGCGCTACGCTGGCAGGATTGGCAGTCCTGTCCGGCTGC  
ACAGCACAACCCTCACAAGCAGAAGACAACACGCTCACTTACTTAGAGCCACAGTTCTTC  
CGCACCTGTACCCACCATCAGCGGGCTTTTACCCCAACGGCAGTGTGGTGAACAACATT  
GCAGACCGCTTGCTCTACCAGGATCCTGAAACCTTGGAACCTCAAGCCGTGGATCGCCACC  
GAACTCCCAGAAGTAAACGAAGACGCCACGGAATTTACCTTCAACATCCGCACCGATGTC  
ACCTACTCCGATGGCACCCCGCTGACGGCTGAAAACGTGGTGAAAAACCTTCGATCTCTAT  
GGCCTCGGCGATCAAGATCGACGCCTACCATCTCTGAGCAGATCACCACCTACGACCAC  
GGCGAAGTAGTAGATGAGGACACCGTCCGATTCCACTTCTCTGAGCCTGCACCTGGTTTTT  
GCTCAGGCCACCAGCTCCTTCAACGCTGGCCTTTATGCCGATTCCACCTTGGAGTTTCGCC  
AATGAGGATTTTCGCGCCAGGCAACGCCCAAACGTCATCGGCTCCGGTCTTTCGTGATC  
ACCGATGAAACCTAGGCACCAACCTCACCTTGACTGCGCGTGAGGATTACGATTGGGCA  
CCACCATCACGCGAACATCAAGGTGCGCGCAAGCTTGACGCCGTCAATTATGTCCTCGCG  
GGTGAAGAATCCGTCCGCATCGGAGCCATCGTTGCTGGCCAAGGTGATATCGCCCGCCAG

ATCGAAGCGCCAGTGGAGGCACACCTGAAGGATGCAGGCATCCCGATCATCTCCGCAGCC  
ACCAACGGTGTGAACAACAGCTTCAACTTCCGCTTCAAAAACGAGCTGCTCTCAGACATC  
CGTGTTCCGCAAGCTCTGATCCACGCGATCGACCGCGAAAAGATCATGCGTGTGCTGTTT  
AGTGATTCTATCCGCTGGCAACTTCTGTGCTTGGCGAAAATGCACTGGGCTACAAAGAA  
CAAGTAGATGCCTATGTCTACGACCTAGACAAAGCAACAGCTCTGCTTGACGAAGCCGGC  
TGGACCCTTGATAGCGACGGCATGCGTCGCAAGGACGGTGAAGTCTAGAGCTCACCTTC  
AACGAAGCCCTCCACAGCCTCGTTCACGCGAAGTTGTCACCATGGTCCAAGAACAGCTC  
GGTGATCTGGGCATCAAGGTCAACCTCAACCCAGGTGACCAAGCAGCCCAGGACGCTGAC  
TCCAAGGATCTCAACAAGATCCAGGTTCCGCCACACCATGGTGGGTCGCGCAGACTATGAC  
GTGCTGAAATCCCAGCTGTACTCCACCAACCGCAACGAGCTGTTGAACATGACCGTGGAA  
GGGGAGACCGCCGATATTGGCGATCCTCATTTGGAGGAACTCCTCATGGCTATTGCATCC  
AGCCACGCGAAGAGGACCGTGCAGCAGCATCTGCCGAGCAGCAGGATTACATCACCGAG  
CAGGCATATGTTCTTCCACTGTTTGAAGAGCCAGTTGTCTACGGCGTGCAGCCTTACGTG  
AAGGGCTTTAGCCCCGAAGTGATCGGCCGCCAGCTTCTATGAGACCTACATTGACCAT  
TCCAGCGACCATTCAGTGAGGAGGAC

>RXN01007-downstream  
TAAATGACTACCTCGCAGATTCT

>RXN01090-upstream  
GCCGGTTTGGGCTGGTTGGAGCTCTAGATCGTAAGTGGTGTGCTACCCATGACGTACCAT  
TAACCACGAACGTTTTAAAGAAGCCACGAAGGAGCCTGAC

>RXN01090  
ATGGCGTTACCACTACCCAGCAAGAGCGCTCGAGCACTTGTTACTGGGGCAAGCCAAGGC  
ATTGGCCTCGCCATCGCCAAAGATTTGGCGCGGTATGGGCACAACCTCATTTTGGTTGCT  
CGCCGCGAGGATGTCCTCAAAGAGATCGCCGAGATCTAGAGAAGAAGCACGGCGTGATC  
GTTGAGGTCCGCCCCGGTGGATTTGAGTGATGAGCCAGCCCGCAAGGTGTTGATCGATGAG  
ATCAAGACAAGGGAAATCAACATCATCATTAAGTCTGCTGGCATCGCAAGCTTTGGGCCG  
TTCAAGGACCAGGATTGGTCTTATGAGACTGCCAGTTCTCACTTAATGCCACAGCCGTT  
TTTGAGCTCACCCACGCGGTGTTGGGTGGCATGATTGACCGTGGCACGGGCGCTATTTGC  
AATGTGGGATCTGCGGCTGGCAATGTGCCAATCCCCAACAACGCCACGTATGTGCTCACC  
AAGGCTGGCGTGAACGCGTTCACCGAGGCAATGCATTATGAGCTGCGCGGAACTGGTGTG  
GCGTGACTTTGCTCGCACCGGGACCTGTCCGTGAGGCGGAGATCCCTGAGTCTGAGAAG  
TCGATCGTGGACAAGGTTGTCCCTGATTTCTTGTGGACCACCTATGAGTCCTGCTCCGCA  
GAGACCTTGCGTGCCTGTCTAAGAATCAGCGTCGCGTTGTTCCAGGTCCGCTGTCCAAG  
GCCATGAATTTTGTGTCCTCTGTTGCTCCAACCGCTGTGCTCTCCCCTGTTATGGGCTGG  
GTTTATAAGAAGATGGGT

>RXN01090-downstream  
TAGTTTTTAAAAGTGTCTGAATC

>RXN01114-upstream  
TTCGGTGGAAGATATCCGCAAGCTGGTGTGCGCAGCTTTTAGAAACGGCTCAAGCAAT  
TTCGACAGATCTCTCTGCACTCTAAATTAAGGATCAAAA

>RXN01114  
ATGAACCCTCAAGATATTGTCATCTGTTCCCCATTGCGCACCCAGTTGGTGCTTACGGC  
GGATCCTTCACCGGCGTCCCTGTTGAAGAATTGGCCACCACCGTGATCAACGCGATCGTT  
GAGGCAACCGGCATCACCGGCGACGATGTGGACGATCTGATCCTCGGCCAGGCATCCCC  
AACGGTGC GGCTCCAGCACTGGGCCGTGTTGTTGCTCTAGATTCCAAGCTTGGCCAAAAC  
GTTCCAGGCATGCAGCTTGATCGCCGCTGTGGTTCCGGCCTGCAGGCAATCGTCACCGCT  
GCTGCACACGTTGCATCCGGCGCTGCTGATCTGATCATCGCAGGTGGCGCAGAATCCATG  
AGCCGCGTTGAGTACACCGTGTCCGGCGATATCCGTTGGGGTGTCAAGGGCGGCGACATG  
CAGCTTCGTGACCGCCTTGCAAGACGCGAAACCGCTGGCGGACGCAACCACCGATC  
CCTGGTGGCATGATCGAGACCGCTGAGAACCTGCGTCGCGAATACGGCATCTCCCGCGAG  
GAGCAGGACAAGATCTCCGCAGCGTCCCAGCAGCGTTGGGGCAAGGCTGCTGATGCGGGG  
CTTTTCGACGACGAGATCGTGCCAGTCAACGTCCCTGCCAAGAAGCGCGGCCAGGAGCCA  
ACCATCGTTTCTCGAGACGAGCATGGTTCGACCAGGAACAACCGTCGAAAAGCTTGCTGCT  
TTGCGCCCCATCATGGGCCGCCAGGATGCGGAAGCAACCGTCACCGCTGGCAACGCGTCC  
GGCCAAAATGATGGCGCTGCTGCCGTCTCGTGACCACTCGCGCCAAGGCCGAGGAGAAG

GGCCTGCGCCCAGTCATGCGTTTGGCTGGCTGGTCTGTGGCTGCTGTTCCCCCAGAGACC  
ATGGGTATTGGACCTGTTCCCTGCCACCAAGAAGGTCCTGGATCGTTTGGGCCTTACCCTG  
GAGGACATCGGCGCGATCGAACTCAACGAAGCTTTCGCAGCTCAGGCACTGTCTGTGCTG  
AAGGAATGGAACATTTCTTGGGAAGATGAGCGCGTCAACCCACTGGGTTCGGGTATTTCC  
ATGGGACACCCAGTCGGTGCCACCGGTGCTCGCATGGCAGTAACCTTGGCTCACCGCATG  
CAGCGTGAAAACACTCAGTACGGACTGGCCACCATGTGCATCGGTGGCGGCCAGGGTCTT  
GCAGCTGTCTTTGAAAAGGAGAAC

>RXN01114-downstream  
TAAAAATGGCTATTTTGCACAGC

>RXN01139-upstream  
ACCACCGTGGCAGGCTTTTTTCAGTGGCAAGAAGATTAATTCTCCACCCCTTCATTTTCAA  
TAAGCTTTCAATAAGGGGAGAAGTGTGCTTAGCTGGGGTC

>RXN01139  
ATGGAAAGCCACGATCTTCAGCAGCGCAGTTATGCGCACAATCCCGATGGCCACGACCAC  
AGCCATGACGGAATCGGACACTCACATGCTCCCAGCTCCCTCAAGGCTCTTTTTGCGGTC  
ATCATTTTTCACCTCGATCATCTTCTAGCGGAACATAATCGCCGGCCTTATTTCCGGATCT  
TTGGCACTGCTGGCTGACGCCATGCACATGCTGTCCGACTCCACTGGCTTGATCATTGCG  
GCTGTGCGCCATGCTCATTGGCCGTCGGGCACGCACTTCTCGTGCGACCTACGGATACAAG  
CGTGCGGAAGTCTTGGCAGCGATGGTTAACGCCACCGTTGTTACAGCACTGTCTGTGTGG  
ATCGTCGTTGAGGCCATCATGCGTCTGGGCAAGGACCTGGAAATCCAGACCAACCTGATG  
CTCATCGTCGCGGTCAATTGGTTTTGTACCAACGGAATTTCCGCCCTGGTGTGATGCGC  
CACCAAGATGGCAATATCAATATGCGTGGAGCATTCCTTCACGTTCTCAGTGACATGCTG  
GGTTCCGTTGCCGTCATTATTGCGGGCCTGGTGATTTCGCTACACGGGATGGATGCCGGCC  
GATACCATTGCTTCGATTGCGATTGCTGCGATTATTATTCCTCGCGCATTACAGCCTCCTG  
AAGGAAGCTCTCAATATCTTGTGGAGCGTGTTCCTACAGGTGCGGAGCCTGCAGAGGTC  
GACGCAGCCCTTCGTAAAGTCCCAGGTGTCAGCGATGTGCATGATCTTCACATTTGGAGC  
ATTGACGGCAAGGAAATCCTGGCCACGGTGCATTTGGTGGTGGATTTCGTCTACAAATCAG  
CTGCATAGTTGTGGCGTGTGGATCGGGCAGAAGCGGAACCTATCCAAACTTGGGATCTTG  
CACTCAACAATTCAGCTGGAAAGCGCAGATCACAGTGATCATGAAAGTGTGTGC

>RXN01139-downstream  
TGATATAGAGTATGTCCCATGGG

>RXN01141-upstream  
AAAGAACACTCGGTATGGCACCTGATTTAAGGATGCTGCAATCGTGACACATATCCTCTT  
CGACAGCAGGCGTTTTCTGCAACTGGGCGCTTTTGCGTCC

>RXN01141  
TTGAGCACCGCATTGGCCGGAGCGGCCCCGCTACGTGACGTCGACAAGCAATAATGAACCT  
GCGGATAAACAATCCCCTGACCATTGGCTACGTGCCTATTGCGGGCTCGGCGCCGATTGCT  
ATCGCAGATGCGCTAGGGCTGTTTAAGAAACACGGCGTGAATGTCACGTTGAAGAAGTAC  
TCAGGCTGGTCCGACCTGTGGACCGCCTATGCAACAGAGCAGCTTGATGTTGCGCACATG  
CTGTGCGCCGATGACTGTGGCGATTAATGCTGGAGTGACCAACGCGTCGCGCCCCGACGGAG  
CTGTGCTTTACCCAGAACACCAATGGGCAAGCAATTACCTTGGCGTCAAAGCACTATGGT  
TCCGTCAATTCAGCGGCGGATCTTAAAGGCATGGTGCTGGGAATTCCTTTTGAATATTCA  
GTCCATGCGCTGCTCCTGCGCGATTATCTCGTCTCAAACGCGAGTTGATCCCATCGCCGAT  
CTTGAGCTTCGCCTGCTCCGACCTGCCGATATGGTTCGCACAATTGACAGTTGAGGGCATC  
GATGGATTCAATTGGGCCTGGGCGGTTTAAATGAACGCGCCATCAGCAATGGCTCCGGCCGG  
ATTTGGCTGCTGACCAAACAACGTGGGACAAACATCCATGCTGCGCCGTGGCGATGGCC  
AAAGAGTGGAAAGCTGAACACCCACGGCGGCTCAGGGTGTGCTTAATGCGCTGGAGGAA  
GCCTCCGCAATTTTGAAGCAATCCGGCACAATTTGATTCTCGGCACGCACGCTGTCGCAG  
GAAAATACCTCAACCAGCCTGCCACGTTGCTGGATGGACCGTCG

>RXN01141-downstream  
TAATCATCGGCATCACCGGCTTA

>RXN01142-upstream  
CTCCCCATCCACCGGCACAGTCAGCGCAGGCAACGAAGAAATTAAAGGACCAGGACCTGA



CCGAGGCATGGTTTTCCAAGACCACGCCCTCCTGCCCTGA

>RXN01142

TTGACCGCACGCGGCAACATCGACTTCGGGCTCCGCTCCGCGCGCCCTCCTTGAGCAAA  
ACCGAACGCGCCGACATCACCCGCACCCACCTCGAACAAGTAGGCCTCACCGACGCCGCC  
GAACGGCGCCCCGCCGCTCTCCGGCGGCATGCAACAGCGAGTCGGCATCGCACGCGCC  
TTCGCCATCGACCCACCAATCATGCTTCTCGACGAACCCTTCGGCGCCCTCGACGCCCTC  
ACCCGCCGCGAACTCCAGCTCCAATACTCAACATTTGGGAAGCCTCCCGCCGCACCGTC  
GTCATGGTCACCCACGACGTCGACGAGGCCATCCTGCTCTCCGACCGAGTTCTCGTGATG  
TCCAAGAGCCCCGAAGCCACCATCATCACCGATATTCCAGTGAATCTTCCCGCCCCAGA  
CACGAGCTGAGTGAAGACGCTTCTGTTGAAGCCGAGACCACAGCCCTGCGTAAGCGGATG  
CTGCATCTGCTGGAGCAC

>RXN01142-downstream

TAGTTTCTAACACGTCTTTTAAA

>RXN01164-upstream

GCCGATCGTGATTGATGAAGACGAGATCCAAGCCTGGACTTCTGATCTCAAACCTGAAGA  
TTTCACCAAAGGTAAAGATGAATCCGACGGTGAGAAATAA

>RXN01164

GTGACACTGTTTGTTCGGCTCGCCCTTGCTGCTGTGGGCGGGCTTTTTGTCTTTGCTTCC  
AATGAACCGATCGGCTGGTTTGTGCGGGGAATTGTTGGCACTGCATTATTTTTTATCTCC  
CTTGCGCCGTGGGATCTGGGAGTTCCCCAAAAGCGGCGGAAGAAGAATGAGCCAGTCCCA  
TTTTTGCAACAGATGTCCACGGGCCCAACTGTTGTACAGGGCATGCTTTTAGGTTTGTGTC  
CATGGCCTGGTGACATATTTGCAGCTGTTGCCGTGGATCGGTGAGTTTGTGGCTCACTG  
CCTTATGTGCGGTTGTGAGTTGTGAGGGCGCTTTATTCCATTGCTCTTGGTGCTTTCCGC  
GTGCTCATTTGCGGTTGGAGGGACTGGAAGGTTCTCCTGTTTCCGGCGATGTATGTGGCT  
GTGGAGTATCTAAGAAGCTCGTGGCCATTTGATGGATTCGCGTGGGTTCGCCTGGCATGG  
GGTCAAATTAACGGTCCGTTGGCTAATCTCGCAGCGCTTGGTGGGGTAGCGTTTGTCACT  
TTTTCCACGGTGCTGGCTGCCGTGGGTGTGGCCATGGTGATTATTTCCAAGAAGCGACTG  
GCCGGCGCAATCATCACCGCGAGTGATGCTATCGGCGCGGTGTCATCCCTGTACGTT  
GACCGCAATGGCACGAGCGATGAAAGCATCGAAGTAGCCGCAATTCAGGGCAATGTGCCT  
CGGATGGGATTGGACTTCAATGCACAGCGCCGCGCGGTGCTGGCGAATCACGCACGGGAA  
ACCCTCAAGCTGGATGAACAAGTGGATTTGGTGATCTGGCCGGAGAATTCCTCAGACGTC  
AACCATTTTCCGATGCACAAGCAAGAGCCATTATCGATGGAGCAGTGGAACATGTTTCAG  
GCACCTATTTTGGTGGGCACGATCACCGTCGATGAGGTTGGTCCACGCAACACCATGCAG  
GTATTTGATCCTGTTGAAGGTGCCGCGGAGTACCACAATAAGAAGTTCTTGCAGCCGTTT  
GGTGAATACATGCCGTTTTCGCGAATTCCTGAGAATTTTCTCGCCCTACGTTGATTCCGCT  
GGAACTTCCAGCCCGGTGATGGCACCGGCGTAGTGGAGATGAATGCTGCGAACTTAGGC  
CGCGCTGTGACAGTGGGCGTGATGACGTGTTACGAGGTCATCTTCGACCGTGCTGGCCGC  
GACGCCATCGCCAATGGGGCTGAATTTTGGACCACGCCACCAACAACGCCACCTTCGGA  
TTCACGGACATGACGTATCAGCAATTAGCAATGAGCAGGATGCGTGCCATCGAATTTGAT  
AGGGCGGTGGTTGTTGCAGCTACATCGGGTGTTCGGCTATCGTCAACCCTGATGGAAGC  
ATTTCCCAAAACACCCGAATTTTGGAGGCCGCCACCTTGACGGAATCCATTCCACTCAAG  
GACACTGTCACCATCGCAGCGCGGGTTGGTTTCTATGTTGAATTACTGTTGGTTATCATT  
GGTGTATTAGCTGGACTATTCGCCATTTCGAATGAATAGCCGTTCAAAGTCTGCGAAAGGT  
TCCGCTCGGCCCGCACAAAGTTCCGGGTTAAGAAGGTGCCTGCGAAAAAGGCAGCAACTAAT  
CGTCGAAAAGTAAAA

>RXN01164-downstream

TAAAAACGTCCCGAAGGGACGAG

>RXN01168-upstream

CCGCACAAGTTCGGGTTAAGAAGGTGCCTGCGAAAAAGGCAGCAACTAATCGTCGAAAAG  
TAAATAAAAAACGTCCCGAAGGGACGAGGAGGACAACACC

>RXN01168

ATGAGCAGTGAGGCAGTAGATGCTACGACGCTGGTGATTATTCCAACGTACAACGAGCTG  
GAAAACCTTCCACTCATCGTGGATCGCGTGCGCACCGCAACCCCTGACGTTACGTAATC  
ATCGTGGACGACAACAGCCCAGACGGCACCGGCGAGCGCGCAGACAAGCTTGCTGCTGAC

GACGACCACATTTTTGTCCTCCACCGCGAAGGCAAAGGCGGCCTGTGCGCAGAGTACATG  
GCTGGCTTCCAGTGGGGCCTGGAGCGCGACTACCAGGTCCTGTGCGAAATGGACGCCGAC  
GGCTCCACGCACCAGAACAGCTGCACCTGCTGCTCGCTGAGATCACCATGGCGCTGAC  
CTGGTCATCGGCTCGCGCTACGTGCCAGGCGGCGCGTAGTCAACTGGCCCAAGAACCGT  
TGGCTCTTGTCCAAGGGCGGCAACGTCTACATCAGCGTCGCGCTCGGCGCCGGCTTGACC  
GATATGACCGCAGGGTACCGCGCTTTTCGACGTGAAGTGCTAGAAGCACTGCCGCTTGAT  
GAGCTCTCCAACGCTGGGTACATTTTCCAAGTTGAGATTGCCTACCGTGCAGTTGAAGCC  
GGATTGATGTTTCGTGAAGTTCCCATCACTTTACCGAGCGTGAGATCGGCGAATCCAAG  
CTGGACGGCAGCTTTGTCAAGGATTCCCTGCTCGAGGTAACCAAGTGGGGCCTCAAGCAC  
CGCGGTGGCCAGGCCAAGGAACTGTCCAAGGAAATGGTCGGCCTGCTGAACTATGAGTGG  
AAGCACTTCAAAAAGCGCAACACCTGGCTC

>RXN01168-downstream  
TAAACTGCTTGCCGGTTAGTGAA

>RXN01191-upstream  
CGCTGCTTTACGCAACTGAAACCGCACCGGATCAAGTTATTTGGGGTTGTTCTTTGTGG  
CGTGTGGTGGCCGTCGCGGGGTTGGTAGGGCCCTGGGCG

>RXN01191  
GTGGGTGGACTCGTCGATAAGCTCCTTGCAACCCCGAGCATGCGCGACGTTGTAAGTGTTC  
GCGCTGCTTATCGTGGCTGGCGGCGTTGTTTCGAGCCTGGGCACGTGGTGGGGCAGCGCG  
CTGATGGCGCGCGGTTGGAGCCGGCGATCGCGGGGCTGCGCGAGGATGTGTTGCGCGCG  
GCGGTGAGTTTGGATGCGAACACGATTGAAACGGCGGGGCGCGGCGACGTGATTTGCGGT  
ATCGCGGATGATTCGCGGGAGGTGTCCACTGCGGCGAGCACCGTGGTGCCGCTGATGGTG  
CAGGCGGGCTTTACCGTGGTGATTTCCGCGTTTGGCATGGCGGGCGGTTGATTGGCGCCTC  
GGCCTTGTCGGTTTGGTCGCGATCCCGCTGTATTGGACCACGTTGCGCGTCTATTTACCC  
CGCTCAGGTCCGCTTTATACGCGTGAGCGCGAGGCCTTTGGGGTGCGCACGCAGCGGCTT  
GTCGGCGCAGTCGAAGGCGCGGAAACCTTGCGCGCTTTCCGCGCAGAAGATACAGAATTA  
AAGCGTATCGACGCAGCCTCCGGCGAAGCCCGCGACATTTCCATTTCTGTTTTTCAGGTTT  
CTCACATGGGCATTTTCCCGCAACAACCGCGCGGAATGCATCACCTCGTGCTCATCTTG  
GGCACCGGCTTTTACCTGGTCAACATCGATCTGGTCACCGTCGGCGCAGTCTCAACCGCC  
GCACTGATCTTCCACCGACTCTTCGGTCCAATCGGCACGCTCGTGGGCATGTTCTCCGAC  
ATCCAATCCGCCAGCGCATCGCTGATCCGCATGGTGGGCGTTATTAACGCGGCATCGAAC  
CAGGTGAGCGGCACCTCGCCGGCGTCTGCCAGCACCGCTTTAACGCTTTTCGACGTCTCC  
CACCCTATCACACTGCACCCGTCATCAAGAATGCATCCGTGCAGCTGGAACCAGGGGAA  
CACATCGCCATTGTGGGTGCGACCGGCGCTGGTAAAAGCACGCTCGCCCTCATTTGCGGCA  
GGCCTGCTCAGCCCAACTTCCGGGCGAGGTGGCTCTCGGCGGATCGAGTTTTTCTAACGTC  
GAACCGGAAGCATTTGCGCCAGAAGATCGCGATGGTCAGCCAAGAAATCCACTGCTTCCGA  
GGATCTGTTTTAGATAATCTTCGTATCGCACGCCCCGAAGCCACCGATGCGGACATCCAC  
GCCGTTCTCGCCGATATTGGTGATTCCTGGTTGGAGCGCTTACCGCAAGGCATAGACACC  
ATCGTGGGTGATGGCGCTTTCCGTTTAACTCTGTGGAAAACCAGATCATGGCGCTTGCT  
CGCGTACATTTGGCCGACCTAGCAATCGTCATCCTTGATGAAGCAACGGCTGAATCAGGC  
TCTGATCATGAAAACAGCTTGAAGATGCAGCCCTTAAAGTCACTGAAAACAGATCAGCC  
ATCATCGTGGCTCACCGCCTCAACCAAGCGAAAACCGCCGATCGCATCATCGTCATGGAC  
TCCGGAGAAATCATAGAATCTGGAACCCATGAAGAGCTTCGAGCGATCGGCGGCCGATAT  
GAACAACGTGGACTGCGTGGTCTGCGCGC

>RXN01191-downstream  
TAATTAGCCACCCAAGACCACGC

>RXN01212-upstream  
TTTAGAAGCCACATGACATATGTCATGAAAATTATGTGCAAAGTGCAGTAATACTCCTGA  
CATATGGCTCTACCAGCGCCAATGCGAAGTAGGAAGAATT

>RXN01212  
ATGCCTATGACAACGACACCAGCAATCGACGTAACAGACCTCGTGAGAACCTACGGCGAC  
TACACCGCAGTCAAGGGCCTGAATTTCCATGTACAGCGCGGTGAAGTATTTGGTCTGCTC  
GGCACCACGGGGCCGGCAAAACCTCCACCTTGGAAGTCATCGAAGGACTTTCCGCACCC  
AGCTCCGGCACCGTGCGCATCTCCGGGCTTGACCCCGTTGCCGACCGCGCGATCCTGCGC

CCCGAGCTCGGCATCATGCTGCAATCAGGCGGCCTGCCATCACAGCTCACCGTCGCCGAA  
 ACCATGGACATGTGGCACGGCACCTGCACGTATCCGCGCGCCATTAAAGATGTGCTTGCC  
 GACGTCGACCTCCTACACCGCGAAAACGTCAAGGTCGGCGCGCTTTCCGGAGGCGAACAA  
 CGACGCCTTGATTTGGCCTGCGCACTGCTTGGCGACCCCTCAATTTTGTTCCTCGACGAA  
 CCCACCACCGGCCTCGACCCAGAATCTAGGCGCCACACCTGGCAACTCCTGCTGGACCTG  
 AAACAGCGCGGCGTCACCATGATGCTGACCACCCACTACCTGGAGGAAGCCGAATTCCTC  
 TGCGACCGGATTGCCATCATGAACGCCGGTGAGATCGCAGTGGAAGGCACCTTGGATGAA  
 CTGGTGGCCCGCGAGAAGTCGATCATCAGTTTCGTGCTGCGTGGCGGGCAGGTGGAGTTG  
 CCGGTCTTGAGTGGGGCTGAAATCATCCGCGACAACAACACGTCCGCATCGCCACCACC  
 ACCCTGCAGCAGCACACCTTAGAAATACTTACCTGGGCTGCAGAGACCGGGATCGCGCTG  
 GAAGGCTTCGCTGCAAACCCGCCACCTTGGAATCCGTATTCATGGACATCGCCTCACTC  
 GAGAACACCTCGCTGCAAACCGCC

>RXN01212-downstream  
 TAGAATCTTTAAGGAGACCACAA

>RXN01285  
 CTCAACGTCACCATCCCCGACAACACCTTCACCGCCATCATCGGCCCAACGGCTGCGGC  
 AAATCCACCCTGCTCCGCGGTTTCTCCCGCGTGCTCAATCCGCAGCACGGCAAAGTGCTT  
 CTCGACGGTCGGCAACTCGATTCAATTCAAGCCTAAAGAGATCGCCCGAGAAGTGGCCTG  
 CTGCCACAGACCTCCATCGCCCCAGAAGGCATCCGGGTTTACGATCTCATCGCGCGCGGG  
 CGCGCTCCCTACCAAAGCCTCATAACAATGGCGCACCTCCGACGAAGACGCCGTCGCG  
 CAAGCGCTCGCCTCCACGAATCTCACCGAAGTTGAGCTCGCCTCGTCGATGAACTCTCC  
 GGTGGCCAGCGCCAACGAGTGTGGGTGGCCATGTTGCTCGCCAGCAAACACCGATCATG  
 CTTCTCGACGAGCCCACCACCTTCCTCGACATCGCCCAACAATACGAAGTCTTGGAATTG  
 CTGCGCGCATTCACGAGGCCGGGAAAAGTGTGGTCACTGTGCTTCACGATCTCAACCAA  
 GCCGCCCGCTACGCCGACCACCTCATCGTGATGAAAGATGGGCACGTACATGCCACGGGC  
 ACACCGGAGGAAGTCTTAAGTGGCGAGATGGTTCAAGGAGTTTTTGGCCTGCCCTGCATC  
 ATCTCCCCAGACCCCGTCACAGGAACCCCAACCGTCGTTCCCTCAGTCGGTCTCGCGCA  
 GGAGCT

>RXN01285-downstream  
 TAAGTAGCTACCCCTCCAACGGA

>RXN01298-upstream  
 CTTAAACGTCACCTTATTTATGCATTATGTTGGTTTCAGACTCGAACAATTCAATTAGAA  
 AACACTAATCGGACATTTAGGTCACATAACATTTCCGCTC

>RXN01298  
 GTGTCCACATTAATTTCTGAACCCGAGGTGGATAAGCTACGTAAACGTGCCAAGAGATCA  
 AGGCGGACAGAATGGTGGCTTGCCGCGCACTTCTTGCCCCAACTTGCTTCTCTTGCC  
 ATCTTTACGTATCGGCCACTGTTAGATAACTTCCGGTTGTCTTTTCAACTGGAACATT  
 TCCTCGCCACATCAACCTTCATTGGGTTTGATAACTACGTTGAGTTCTTCACTCGTAGT  
 GACACTCTCCAAGTTGTTTTAAACACCGTCATCTTCACGGCATGTGCTGTGATCGGATCG  
 ATGGTGTCTCGGTTTGCTCCTGGCCATGTTGTTGGATCAGAAGCTTTTCGGCCGTAACCTT  
 GTGCGTTCCATGGTGTGTTGCCCGGTTTGTTGATTTCCGGTGCTGCCATTGGTGTGCTTTC  
 CAGTTCGTTTGTGACCCTAATTTTGGTTTGGTTTCAGGACTTGCTGGGACGCATCGGCGTT  
 GATTCGCCACAGTTCTACCAAACCCCTAAGTGGGCATTGTTTCATGGTGACGTTCACTTTC  
 GTGTGGAAGAACTTGGGCTACTCCTTTGTTATCTACCTGGCTGCATTGCAGGGGCTAAAC  
 AAGGATTTGTCTGAGGCCGACCGGTGGATGGCGCGAGCGCGTGGACACGTTTTTGGGAAG  
 GTTACTCTTCCGCAGCTTCGCCCAACCACGTTCTTCCTTTCTATTACTGTCACGCTGAAC  
 TCGGTTACGGTCTTCGACATCATTCACACCATGACTCGTGGTGGCCCTTGGGTAAACGGT  
 ACGACCACCTTGGTTTACCAGGTGTACACCGAGACTTTCACCAACTATCGCGCGGGATAT  
 GGTGCAACAATCGCAACGATTTTGTTCCTGTTGCTGCTGATTATCACTGTTATCCAGGTT  
 CGATACATGGATAAGGAGAACAAGCAGAAA

>RXN01298-downstream  
 TGATCTCGACTGATAGAAACGTT

>RXN01338

AAACTTATACCCCAAATCCCTGGATGTTATTTCATCCGCTCATTTGATGGCATCATCACT  
 GTCGCAGCCCTTGTGGCCATCGCAATACATCTCATTTTATGGCTGGCTCTAGATCTAGAT  
 GGCCTTGCTAAAACTGGCCTTTAATAGCCATCGTTATCGTAGGTGGCATTCCGTTGATG  
 TGGGATGTGCTGAAATCAGCCATTAAACTCGCGGTGGCGCGGATACTTTAGCAGCAGTC  
 TCCATCATTACTTCTGTGTTGTTAGGGGAGTGGTTGGTTGCCGCGATCATCGTGCTCATG  
 CTCTCTGGTGGTGAAGCGCTAGAAGAGGCAGCATCACGGCGAGCCAGTGGCACCTTGGAC  
 GCACTTGCCCGGCGCGCACCAAGTACAGCTCACCGCCTGTTGGGTGCAACCATTCTTGAT  
 GGAACCGAAGAGATCGCCGTGGAAGAGATCACGGTTGGTGATTTAGTGGCGGTGCTCCCG  
 CATGAACCTTTGTCCCGTGGATGGTGAAATCGTGGCAGGCCACGGCACCATGGATGAGTCT  
 TATCTCACGGGTGAGCCCTATGTGGTGAGTAAATCTAAAGGTTTCGCAAGCAATGTCGGGT  
 GCAGTCAATGGTGATACTCCGCTGACGATTGTTGCCACAAAGCTTGCCCATGATTCCAGA  
 TACGCCCAAATTGTTGGTGACTCCATGAAGCAGAAAACAACCGCCAGAAATGCGCAGG  
 ATGGCTGACCGTCTTGGCGCGTGGTATACGGTGATTGCACTTGCCCTCGGTGGTCTTGGC  
 TGGATTGTCTCCGGCGACCCAGTGAGGTTCTTGGCTGTTGTCGTTGTCGCCACCCCATGT  
 CCATTGCTCATTGACAGTGCCAGTGGCGATCATCGGTGCGATTTCTCTTGCGGCTCGTCGG  
 GGCATCATCGTGAAGAACCCTGGAATGCTGGAAAACGCTTCAGGAGTAAAGACAGTGATG  
 TTCGATAAGACTGGAACGCTCACCTATGGCAGGCCAGTGATTACTGATATCCACACTGCT  
 CCCGGAGTTGAGGAAGATACAGTCCCTAGCTTTGGCTGCTTCAGTAGAGCGCTACTCCAGA  
 CACCCGTTGGCTGACGCGATTCTGTGAGGGCGCAAAAGCCAGGGAACCTTCATCTGCCTGAT  
 GTAGTGGAAGTATCGGAACGTCCAGGACAGGGACTAACCAGGCACGGTGGGCGAGCACCTG  
 GTTCGAATAACCAATAGGCGCAGCACACTAGAAATTGATCCAGACAGCAAGAACTACATT  
 CCGGTGACAAGTTCCGGCATGGAATCTGTGGTGCTTGTGATGATAAATATGCAGCACTC  
 ATTCGCCTCCGGGATGAACCTCGTGCATCTGCCAGTGAGTTTCATCGCGCACTTGCCCAAG  
 AAGCACAAAGTGGACAAGCTCATGATTATCTCTGGTGATCGCGCATCTGAGGTTCTGTTAC  
 CTTGCGGACAAGGTTGGCATTGATGAGGTACACGCAGAGGCCTCACCGGAAGACAAGCTG  
 AACATTGTTAATCGGCATAATGAGCACGGCGCCACCATGTTCTTAGGTGATGGAATCAAC  
 GATGCGCCAGCCATGGCCGTTGCCACCGTTGGTGTCGCGATGGGAGCAGACTCCGATGTC  
 ACGTCCGAAGCAGCAGATGCTGTGATTTTGGATTCTTCCCTGGAACGTCTCGACGATCTG  
 CTCCACATCAGTGCACGGATGCGTGAATAGCGTTGCAATCTGCGGGCGGTGGCATGGCG  
 TTGAGTGTATAGGAATGATCCTCGCGGTATTTGGATTCTTGACGCCACTGATGGGTGCG  
 ATCTTCCAAGAGGTCATTGACGTGCTGGCTATCCTCAATTCCGCTCGGGTCGCACTGCCA  
 CGCGGAGCGATTAGTGATTTTGATACGCAAGAAAAAGTTTCT

>RXN01338-downstream  
 TAGCAGGGTAACCTAAATGTCGT

>RXN01382-upstream  
 AAAGGATGTACCTCATGAGCACCACGATTACTCGCCGCAATTTCTCCGAGCAACCGGAA  
 TCCTCGGTGTCGCAGCTGGCATCGGCGCAACACTTGCTGC

>RXN01382  
 ATGTGCACCAACAACACCGGCACCAGCGGATCCACCTCCACCGCAGCTGGCACCGGAACT  
 GCAATGAAGAAGGCACCATCACCGCAGCCATCTCCTACGAACTGGGAACCAACGGCTAC  
 GACCAATGACCACCACCTCGGCTCTCACTGTGGCAGCCAACCTGGCACACCCTTGAAGGC  
 CTCACCGAAATCGACCCAGCCACCGGCGAGGTCTACGCAGCACTCGCCAGCGCACTGCCT  
 TCAGCCGATGCGACCTCCCTAGACATCAAGCTTCGCGACGGCGCCACCTTCCACAACGGC  
 GACGCAGTCACCGCAGACGACGTAGTCTTCTCTTTGAGCGAGTCTCGATCCAGCCAAC  
 AACTCCCTTTACGCATCCTTCATCCCATTCATCAAGTCAGTCACCAAGAAGGATGACACC  
 ACCGTACCATCGACCTCGACTACGCAACCGGCATCATCAGCGAACGCCTCGCAGTAGTA  
 AAGATCGTGCCAAAGTCCGTCTGGAAGCAGACGCATCCGGATTTCGACGCCAACCCAATC  
 GGCTCCGGGCCATACAAGATGACCGACAACGGTGATCCAAGGTGGTCAAGTTCGAGCGC  
 AACGACGACTACAACGGCCACGCCAGCACGTGCCGCCAAGATGGAATGGCAGATCATC  
 CCCGACGCCTCCACCCGCACCAACTCCCTTCAGTCCGGCAGCACCATGGCCATCGACTCC  
 GTTCCATACCTGTGATCCCACAGCTTGAAGCCACCAGCACCGTAGAATCCGTCCAAGGA  
 TTCGGCCTCCTGTTGCGCATGTTTCAGCTGCTCCGAAGGCAACCCCTTCAACGACGTCCGC  
 AACCGCCAGGCATTCTCTACGCACTGGACATGGACAAGATCGTTAAGACCGGCATGTCC  
 GACCAGGCAACCCAGCCACCTCCTTCGTGCAGAAGGAACACCCCAACTACAACCAGGCA  
 TCCACGGTCTACTCCCTCGACGCCGACAAAGCCAAGGCGCTGTTGCTGAAACCGGCCTT  
 ACCAGCCTCAACCTCCTGTGCACCGACACGACTGGGTCAAGAACTGCACCCCACTGATC  
 CAGGAATCCCTC



>RXN01411-upstream

CTTATCGACGTCCCCATCCCCCTCGCCAATGCTTCGGCGAGGGGTTCTATTTATTGTGTG  
TGCTAGCCTTTTCGCAATCGTTCAGCCCGCCCCGACGTCA

>RXN01411

ATGTTGGGAGTGGGCTGGCGCATTCCATTCCCTGATGGCCGTGCCACTAGGGCTTATCGGC  
TGGTGGATCCGCACCGGTGCCAGGAAAATGTACGCCCCGCATCCGAACGCCCCGAAGCT  
CCTATTAAGCAGGCATTGCGTACTGAGTGGAAGATGATGTTGCGGGTAGGTGGCTTTATC  
TCTTGCACCGGTCTGAGCTTCTACATTTTCACCACGTACATGACCACTTTCCTGCGCAGC  
ACCGTCGGACTGGAGGGCACGTTAGTGCTGGCTGGAAACATCATCGCTCTCAGCATGGCA  
GCAATTGTGGCCCCATTTGTTGGCCGCGCAATTGATAAATTCCCCCGCCGGAACATCATG  
GCTTTCGCTACCTTAAGCACAGTAATTATGGCGATCCCGGCCCTACATCATTGCAGGTCAA  
GGTACTTTGACTGCTTCTTTGATTGCGCAGGTAATGCTTGGAATCGGCGCGGTTACCGCT  
AACTGCGTTACCTCAGTAATGATGGCCGAGGTCTTCCAAGAGGTCACCCGCGGTACTTCC  
GCCGGCATTACCTACAACGTCACCTACGCAATCTTCGGCGGGCTCGGCTCCATTTATCTCC  
ACCGCATTGGTCTCCTGGACCGGCAGCCCGCTGGCCCCCTGCGGTATACATGATCATCAT  
GCGCTCTTCGCCTTCACCGCGTCCCGCTTCATTTCCTGAAACCTCCCCAGTTTTTGTACC  
GCAACCCCGGCCATTAAGGCACCAAAGGTGCTGGTCAACCCGGGT

>RXN01411-downstream

TAAACCACGCTTTTCGACGAAAA

>RXN01421-upstream

TTGATGCACGTGCAGAAATCGTCGGCGGTCCGTGGCACCCATCTGTTAAGGGAGACTCGG  
TTACTGCAGGGATCCTGCGAGATCGAGTAAACGCCTAAAG

>RXN01421

ATGACGTCGAAAAGCATTAGCGGCAAGCGCCCGAATCTGCCGTCGCTCACTGGAGCGCGG  
TGGCTCGCGGCGCTCGCTGTTTATTTTTTGCATGCGTTGGTGTTTTTGTGCGGTGTATCCG  
TTCCAGCAGTCGGAACGTGTTTGCCACAATCCATAAATTTGTCCCCATGCAGCTGGGTTCA  
GCTGGTGTAACCTTCTTCTTTATCTTGTCCGGATTTTGTATCTATTGGTCAAATAGCCAG  
CTCAAGGGCATGAAGAATGTGCTGTATTACTGCAAGCGCCGCATACCAAGATTTATCCC  
ATGCACTTGATTGCGTTGCCGATGTTTATTGAGGCGTCGGCGAAGTTCACGACTACAGGC  
ATTACCTGGGTGCTGATTTTGCGCGAG

>RXN01421-downstream

TAAAGCTGTGGCTGCGGAATGCG

>RXN01602-upstream

TGCAGGCCACATGCCTCCCAGTGCCGTCTCTGCACGTTGATTTTCCCCTGCCACGACTGG  
TCGCAGGGCGACTTTCTAGCACTTTTAAAGGAATTTTTTA

>RXN01602

ATGGCTAAAACCCATATTCGGTTACAGGACCTTTCCCTGTCATACACCTCAACCCCGTTA  
ATTACGAAGCTCAATATCACTGTTTCTTCTGGACAGTGCGCAGTGATTGTTGGTGAGAAT  
GGTCGAGGTAACACCACTTCTGCGAGCACTGGCTCGAGAATTCCCGCCATCTGCAGGT  
GAGATTCTCACTCATGGCACGGTAGCAATTGCTCATCAACACATGCCTGCAGGTGATCTG  
TCCGTGCGGAGAGATCTGTGATGAGGCAATTCGTGATTCAAAGAATGCTCTCGAAGAGCTT  
GAGAGAGCTGGAGCTCTACTTGAGACAAACACTGCGCACGCACTTGATGGATATCAACAA  
GCCCTTGATGCCGCTGAAGTGCTTGACGCATGGAACGCTGAACATCGATTAGAAAAAGCT  
CTGCGCAGCTTTGGCGCGATCACCGATAGATCCCGTGCACTCAGTGAGCTATCGATCGGG  
CAAAGGTATCGGGTACGGCTGGCCTGCCTCATCGGTGGCGATGCTGATATTTTGCTTCTC  
GATGAACCCACCAATCATCTTGACCGGGGCGCGCTTAACCTATCTCACCAGAGCCATAACC  
TCCCACAAAGGTGTGGTACTTGTTGTTTCTCATGATCAAGCACTGATCAAAGATGTCGCG  
GATTTTCATCATCGATATTGATTCAACCCAGACGGCCTACCACGGATCTATCATGAGGGT  
TTTGATTCTTATCGACGCCAAAGGAGTGCGCTTCTTGAACTTGGAGGCAGGATTATGCC  
GCTGCACAAACTGTGCAACAGCAATTGCAGGAGGATCTAGAGCACGCACGCCAGCGGGTG  
AATTCTTCGTGGAAACCTCCAAAAGGAACGGGAAAACACACTCGCGCATCTCGGGCTCCC  
GGAGTGGTGCAGGCCTTAAAGCGAGCACAGGATGCGTTGGATAGCAAAGCGTTGGACGTT  
CCCCCGGCTCCGGCCCCATTGCTTCTGCCTACCTTGAAAGTGCGACCAGATAAACCCATG

GTGGACTTTTCGGACCTTTTGTACCCACCGCTTGCCTCTGCCAGGCTCACATTCAGTG  
GTATCAGGTGACAAAATAGTGATCACTGGTGACAACGGCGCTGGCAAATCAACGCTCATC  
GAAGTCTTGTCTGGGGTTTGTACTCCGGCAAGTGGTTCGGTTGCAAACCATGCCCCGAAC  
GGGGTTCTCGGCCAAGAATCACTTGTCTGGCGAGGTGCCATCAATAGCACGAGATCACGCA  
GTTAAGTGGGGACTTTTAAGTGTGAGGAGAGCCGATTTGCCCTACAGGAATTCTCAATT  
GGTCAACGCAGAAGACTAGATTTGGCCATGTCGTTAGCTGGCAATCCTGAACTGTTGCTT  
CTCGATGAACCTTCGAACCATCTGTCTATGCACCTTGGTTTCCGCACTTACAGAGTGGCTG  
GACACGACCGCGGGCTGCAGTGATCATGGTAACGCATGATCGACAGCTACTCCGCGATACG  
GCTCATTTGGAGGCACATCGAGTTGAAATCT

>RXN01602-downstream  
TAAGAATTCGCAAGGGCTTTCAC

>RXN01604-upstream  
CTCTCATGTTGTTGTCCTCTAGTTGACAGCGGGGGTGGTGGTGGTCCTAAAATAGCCTAC  
GATAACTGATAGTGTTTCTCCACTTACGGAAGAAGATAC

>RXN01604  
ATGAATACCCCTCTTTTGAGAAGCTCTGGGCTCTCCATCCGCGACACACCCTTCGCCGAT  
GTTGAGATAGCTCCAGACAGCGGACTCACTTTGCTGAGCACCGGGCGGAATCCCAATCC  
AGTTCCTTTTCTTTGGTACTTTCGGGCCGATGCGCGCCTCCACCGGAACCATCGAATTA  
AACGGCGAACCATCAAGGCAACCAAGCTGGCCAAGCATGTGGCTTTGGCGGGCATCCCT  
GAAATCGATTCACTCGAGCGACTTGTCACTGTGCGCACCGTTGTCCGTGAACAACCTCGCC  
TGGTCAAGCCCTTGGTACCTGATGGTGCCAGGGATATTAGTGATTCCGGGACGGTGGGT  
GACGTCGAAAAGCATCTTGGCCTGAACCTGAACCCTAAAACCTTAATCGGCGACCTCAGC  
GTGCTCGAGCGTTTAAAGCTGCGCATCGCGCTGGCGCTGCTGGCGCGGCCAGAGGCGCAA  
CTGTTGGTTCGTGGATGATCCCGATCAAGTGCGCAGCATGGAATTGCGTGCGGAGGTGTTG  
CACGCATTGAAAGGCGTTGCAGAGGATCTCCCTGTGGTCGTGGTATCCACCAACCCAGAT  
TTTGATTCTTGGCCGATACCGCTTTGACCATTACGGGGGCTGGAAAC

>RXN01604-downstream  
TAATGGCATTTTTTACACTTTGGC

>RXN01722-upstream  
CTCATTTCCCTCGCTAAAAGCTGCATAAAGTTTCGACGTTTTCAAAGTTGATTGCTTGCA  
CTGTCGTTGCGTGTCGCATGCCCCGGCTATTGTTGATTGC

>RXN01722  
ATGCTCAGCACGATGCAGGACGTCCCACTGTCATTAACCAGAATCCTCGAGTACGGGTCC  
ACTGTTACGGTGATACTTTGATCACACGCTGGGGCGGTGCCGATGGCATTGAACAAGCA  
CAGCAAACCTTTAGTGCTGTGGGGGCTAGAGCTGCGGCTTTGGCTCATGCGCTGCATGAT  
TCTTTAGGTATTACTGGGGATCAGCGAGTGGCGTCGATGCTCTATAACTGCGCGGAACAC  
ATGGAAACTATGTTTGCAGTCGCATGCATGGGTGCCGTGTTAATCCGCTGAACAAGCAG  
TTGATGAATGATCAGATTGTGTTCAATCACTCTGAAGCTGAAGTGGTTATCGCT  
GATCCGCGCATGGCTGAACAATTGGGTGAGATCTTAAAAGAAACACCAAAAGTTCGTGCC  
GTGGTGTTTATTGGACCGAATGATTTCTCTAGCGCGGCGGCCACATGCCGGAGGGAATG  
AAGCTGTATTCTATGAAGCGCTCCTTGACGGCCGTCCACTGTTTACAACCTGGCCCGAG  
CAGGATGAACGCACTGCTGCTGCAATTTGCTATTCCACCGGTACATCGGGACCGCCGAAG  
GGTGTGGTGTATTCCACCGCTCGCTTTATTTACAGTCGTTGAGCTTGCGCACACCGGAT  
TCCCTCGCAGTGGAACACGGCGAAACGTTCCCTGTGCTGTGTGCCGATTTACCACGTCCTC  
AGCTGGGGCGTGCCGATCGCAGCGTTTATGTCCGGCACTCCCCTGGTGCTTCCTGGACCG  
GATCTTTCTGCGCCGACATTGGCAAAGATCATTTCCACCACGCTGCCTCGCGTGGCGCAT  
GGCGTGCCCTACTCTCTGGATTGAGCTGATGGTTCACCTGAAAAATCCCCAGAGCGT  
ATGTCTCTGCGTGAGCTATACGTGGGCGGTCTGCGGTGCCCTCCAATCGTGATCACCATG  
TGGGAGCAGCGCTATGGCGTGGATGTTGTCCACGTGTGGGGTATGACGGAAACCTCCACC  
GTGGGTACTGTGTCTCGCCACCATCAGGTGTTTCTGGTGAAAGCCGGTGGAATTATCGA  
GTCTCCAGGGCCGATTCCCCGCTCCCTGCAGTACCGCATTGTCAACGACGGCCAGGTC  
ATGGCGTCCACCGACCGCAACGAGGGCGAGATTGAGGTCCGCGGTCCGTGGGTGACTGCA  
AGTTACTTCCACCCCGATGTGGAAGAAAGAGGTGGCACCGCCTCAACATTCCGCGACCAT  
GACGTTGAAGAGGAAACGATGAGCTCTTACCGCCGACGGCTGGCTGCGCACCGGGGAC  
GTTGGATCTGTCACCAGCGATGGATTCTCACCATCCAAGACCGCGCCCGCGATGTCATC

CGTTCTGGCGGCGAGTGGATTTACTCCGCTCAGCTGGAAAACCTCATCGTGGCTACGGAA  
GAGGTTGTCGAATGCGCCGTCATTGGCTTCCCCGATGACAAGTGGGTGGAACGTCCCCTC  
GCAGTCACCATGCTCTACCCCGGCATTGAACGCACCCGGGAAACCGCCGAGCGCCTCCGC  
GATCAACTTCGCGACCGCCTACCCAACTGGATGCTGCCAGAATATTGGACATTTGTTGAT  
GAGGTGGATAAAACCTCCGTCGGTAAATATGACAAGAAGGACCTCCGCAACCACCTGCGC  
AACGGCGATTTTCGAAGTAATTAAGCTTAAAGGGCCAGGTGAAAAA

>RXN01722-downstream  
TAACTTCCCTATTTATTCCGGCT

>RXN01732-upstream  
GATTCTATCGCTGATCTCCCTCTCCTTGCCTGGGTTTGTTCCTCCGGTCTCCTCTTCTTAA  
CTTTCTTGTCTCATGTCGCTGAAAGGTTTTTAAAGATCTC

>RXN01732  
ATGTTCAAGCTCTCTAAGCCATCCAAGTCCATGCGTGTTGCTGTTTCTACGCTTGCGATC  
TCTACCCTTGCTCTAGTTGGTTGTTCTCTTCCGATGAGTCTTCTTCTCATCATCTGCG  
TCTTCTTCTTCGGATGCTGCAAGCCAGTGGCCTGAGTCCATTACTTTGTCTCTTGTTCCT  
TCTACTGAGGGTGAGGATTTGGCTGAAGCGTTGGCTCCTTTGACTGATTACCTGTCTGAG  
AACCTTGGTATTGAGGTCAATGGTGTGGTGGCGTCTGATTACGCTGCAACCGTTGAGGCT  
TTGGGTGCTGATCAGGCTCAGGTGATCATCACTGATGCGGGTTCCCTGTATAACGCGATT  
GAGCAGTACGATGCGCAGCTGATTCTGCGTGATGTGCGTTTCGGTGCCACCTCGTACTCT  
GCTGTGGCGTACACCAACAATCCTGATAAGTACTGCGACGATGCCCCAGTGGCTGCGTCT  
TATGCTGCGTCCGATGTAGACATGCTTTACTGCAACGGTATTGAAACTGAGGGCCAGGCT  
GCTACCGGTGAGGGCCCAGCAGCTCTTGATGCGCTGGAAAAGATCGAGTCCGGTGACAAG  
GTAGCGCTGCAGGCTGCAACCTCTCCTGCGGGTTACCAGTACCCTATCGTCGCTATGCAG  
GATCTGGGCATGGATAACGATTCCGCTTTTGTTCAGGTTCCAGTAGAGGGCAACAACAAC  
GCTGTGCTGTCTGTCTGAACGGTGACGCGGAAGTGTCTTTCGGTTTCTGGGATGCGCGT  
TCCACCGTGCTGTCTGAGGCTCCTAACGCAGCTGAGGATGTCGTAGCGTTTGCCTACACC  
GAGATGATCCCTAACGGTGGCGTGCAGCGTCCAAGTCCCTTCCATCCGACCTGGTGGAA  
AAGCTCACCGAGTTGATGGATGATTACGCAGATTCTCCGAGGAAGCCAAGGATGTCATG  
TTCGACATGGTTGGTCTATCTGACTGGACTGCTGATACCGCACAGGATGAAATCACTCGT  
TACGGCGAGATCCTGAAGAAGTTCTCCAAC

>RXN01732-downstream  
TAATTTCCCTGTTTCCAATACTC

>RXN01762-upstream  
TGGAGTGATGAATTTTCTATAGAACGTTTTTTAAACGATTGACTTTTTTAAACGTTTACG  
CTTTTAATGACTTCAAACGTGATCTAAAGCACAAAGGAGA

>RXN01762  
ATGAAAGTGAACCTCGGAATAGGAAGCTACCCACGACGCAGGGCAACTGTTTCGACCAGAG  
TCCACTGCAATCGAATTCGAAGGCACCAGCATCACCTACGGAGAATTCAGCAAACGAGTC  
AATCGGCTTGACATGCTCTTCTAGACCTCGGCGTTGCGCACCAAGATCGAGTAGCTTAT  
GTCGGATTCAACCACCCTGCCCTGCTAGAAGTGTCTTTTCAACGAACCTCATTTGGGGCA  
ACACCCGTGCTTGTTAACCCTCGCCTATCGGCAAACGAAATCGATTACATCATCCAAGAC  
AGCGGTGCGAGCATCGTGTTTTACGGAATCGACCTCATCGAGCACGCCACTTACCTCCAA  
GAACTCCATCCAGAGATCATCATGGTGGCCGTTGAAGGCGATGAGGGTCCAGGTTTGCCT  
CGAAAAGCGCTTATTGAAGCGGCGAGCGACGCCGACATCGACCTAGAAGTCAGCGATGAT  
GACCTGGTGCTGCTCATGTACACCTCCGGAACCACTGGCCGCCCAAAGGGCGCCATGTTA  
TCCCACCGAAACCTCTTCTTTAACTACTTCAATGCCCTGCTCAGCCAGGAAATTGAACAA  
GGCGCGGTACTTTTTATCCACTGCGCCGTTATTCCACATCGCGGGCCTCAACATGACCACC  
ATCCCGGTGATGATGAAGGGCGGAAAGGTGATCATCCACCGCGAATTCCGGGCAGAGCAC  
GTCCTCGACGAAATCGAACGCTCCAAGGTATCCGAATCCTTCATGGTGCCAGCGATGATC  
GACATGTTGTCCAACCAACCATCATTTGCCGAACGCGACCTTTCTTCCCTTCGCGCCATC  
ATGGTGGGCGGCTCTCCCCTTAGCGAACGTGCGCTGCGAATCTGGCAAGGACGCGACGTA  
AAAATTGTCCAAGGCTTCGGCATGACAGAAACCGCACCGGGCGCCTGTATCCTCGAGGCA  
ACAGACACAAGCACACACCTTGGAACCGCAGGTCGAGCCCACTTCTTCACCGACATCAAA  
CTAGTGGAACCCGAAAACCGGCGAAGAAGTCCCCACCGGAGAGGCCGGCGAAGTTCTCATC  
CGCGGACCACATGTGATGACCGGATACTGGAACCGACCAGAAGACACCGCCAGCGCACTA

CAAAATGGCTGGTACCACTCCGGAGATATCGCCATCAAAGATGAAGACGGCTACTACACC  
ATCAAAGACCGCATCAAAGACATGTACATCTCCGGCGGCGAAAACATTTACCCCGCAGAA  
GTCGAACAAGCACTCCAGGAAGTGGAGCAGTCCTTGATGCCGCAGTCATCGGAGTCCCC  
GATGAACGATGGGGCGAAACTGGCATCGCCTTTGTCTCCATCCGAGAAAGCTACCTGACC  
AACCACCAACCGGACCGGAAGTACGAGAACTACTAGGCAGTGTCTAGCCAGATACAAA  
CTTCCACGAGAAATCCACATCATCGAAGAACTCCCCCGCAACGCCACAGGCAAAATCCAA  
AAGAACATCCTGCGAGACTTCACCATCCCCGTTTCA

>RXN01762-downstream  
TAAACCCCCAACGTCACTTTGA

>RXN01881-upstream  
ACCGGCCCTGCGGCCTCAACCGCCGACCAGCGCGGCGCACACATTTTGACTGTTTCATAA  
TAAAGACAAACTTAAGTATCGGAGTCGAAGAAAAACCACA

>RXN01881  
ATGGCCAATCTGATTAATCTCGAGAACGTCTCCAAAACCTGGGGATTAAAAACGCTTCTC  
GACGGTGTCTCCTTAGGTGTTCAAACCGGCGACCGCATTTGGCGTCGTCGGCCTCAATGGT  
GGCGGAAAAACCACCTGCTGGAAGTACTTACTGGCATCGAAAAGCCGGATCAGGGCCGT  
GTGTCTCACAACCTCTGACCTGCGCATGGCTGTGGTGACGCAGCGTGCTGAACTCAATGAT  
GACGACACCGTCGCTGACGTGGTGCTTGGACCTTTGGGTTTGAAGTTTTTGAATGGGCA  
TCAAACGCCACGGTGCGCGACGTCTCGGTGGCTTGGGCATTGTGATCTTGGCCTTGAC  
ACCAAGGTGGGCAAACCTTTTCCGGTGGGCGAAGCGCCGACGCACCAACCTGGCCGCCGC  
GCTGGTTCGCGACCT

>RXN01881-downstream  
TGACCTGATCGTGCTCGACGAGC

>RXN01936-upstream  
GCGCGGTGACACCACAGCCGTTGTCAGCGGCGCTTGGTCTGTGGAGGATCGCCGAGGTTA  
CTAACAAATAGGCCCAACAAAGAGGTCTAAGCTCTACCTG

>RXN01936  
GTGAGTTTCCGAGATATTTTCGCTGACACCAGACCGCTGAAAGAACCGGCCTTCAAACGC  
CTCTGGCTTGGCAATGTTGCCACCGTCATTGGTGCCCAATTAAGTGTGTTGCCGTTCCG  
GTGCAGATTTACCAAATGACTGGGTCTCCGGCTATGTGGGCTTGACCGGGCTTTTGGC  
CTTATTCCTTTGGTTATTTTGGCCTTTATGGTGGATCCATTGCGGATGCTTTTGATAAA  
CGCATCGTGCTGATCTGCACCACGATCGGCATGTGTGTCACCACTGCCGGTTTTTGGGTG  
CTGACCATTTTAGGCAATGAGAATATTTGGCTCCTGTAAATAAACTTTCTTTACAGCAG  
GCATTTTTCGCGGTGAATCAACCCACCCGAACGGCGATCCTTCGAAGTATTTTGCCGATT  
GATCAATTAGCGTCGGCAACATCACTGAATATGCTGCTCATGCAGACCGGCGCAATCGTT  
GGCCCGCTGATCGCAGGTGCGTTGATTCCGCTGATCGGTTTCGGGTGGCTGTATTTCTT  
GATGTTGTCTCCATCATCCCCACACTGTGGGCTGTATGGTCACTGCCTTCGATCAAGCCA  
TCCGGCAAGGTGATGAAGGCTGGTTTCGCCAGTGTGGTGGATGGCCTGAAGTATTTGGCT  
GGCCAACCCGTGTTGTTGATGGTGATGGTGCTGGATCTTATCGCCATGATTTTCGGCATG  
CCACGTGCGCTTTACCCCGAGATCGCAGAAGTGAAGTTCGGTGGGGGTGACGCCGGTGCA  
ACGATGCTGGCGTTCATGTACTCATCCATGGCTGTTGGCGCAGTTCTTGGCGGCGTGCTG  
TCTGGTTGGGTGGCCCGGATTAGCCGCCAGGGTGTGTCAGTTTATTGGTGATCATCGCC  
TGGGGCGCAGCCGTTGCTTTGGGTGGTGTGGCAATTGTTGTGAGCCCCGGCGCGGTGACT  
GCGTGGGCGTGGATGTTTCATCATCATGATGGTCATTGGTGGCATGGCTGACATGTTTCAGC  
TCGGCAGTTTCAAACGCTATTTTGCAGCAGTCTGCTGCGGAACATGTGCAGGGCCGAATC  
CAAGGTGTGTGGATCATCGTCGTGGTGGGTGGACCTCGTTTAGCTGACGTCCTTCACGGT  
TGGGCCGCTGAGCCCCTCGGCGCAGGTGGACGGTATTATGGGGCGGAGTAGCGGTGGTT  
GTACTCACTGCAATTTGTATGGTGGCGGTGCCTAAATTCTGGAAATACGAGAAACCAAAA  
ATTACCGGCATC

>RXN01936-downstream  
TAAATACTTATCCATGCCCATTT

>RXN01946  
ATCCGCAAGTACTCCAGGCTCGAGGAACAATTCCAGTCGCTCGGCGGCTACGAAGCTGAC



GCCGAAGCAGCCCAGATCTGCGACAACCTCGGCCTCGAGGCACGCATCCTCGACCAGCAG  
CTTAAAACCCCTGTCCGGCGGCCAGCGCCGCGGTCGAGTTGGCGCAGATCCTCTTCGCC  
GCCACCAACGGCTCCGGCAAATCAAAAACACATTTGCTTCTCGACGAGCCCACCAACCAC  
TTGGACGCAGACTCGATCACCTGGCTCCGTGACTTCCTGGCGAAGCACGAAGGTGGACTG  
ATCATGATTTTCGCACGACGTCGAACTGCTTGGCGCCGTATGTAACAAGATTTGGTACCTC  
GACGCAGTACGCAGCGAAGCCGATGTCTACAACATGGGCTTTAGCAAATACGTTCGATGCA  
CGTGCACTCGATGAAGCACGCCGACGCCGTGAGCGCGCAAACGCCGAAAAGAAGGCCGGA  
GCCCTCAAGGACCAGGCTGCACGCCTCGGCAGCAAAGCAACCAAGGCTGCCGCAGCTAAG  
CAGATGATCGCCCGTGCAGAACGAATGATCGACAACCTCGACGAAATCCGCGTAGCTGAC  
CGCGCCGCCAACATCGTTTTCCAGAACAGCACCTGTGGAAAAACCCCACTCAACGCC  
AAGGGCCTGACCAAGATGTACGGCTCCCTCGAAGTCTTCGCCGGCGTCGACCTAGCCATC  
GACAAAGGCTCCCGCGTAGTCGTCTCGGATTCAACGGTGCAGGTAAAACCACCCTGCTC  
AAACTCCTCGCCGGTGTGGAACGCACCGACGGCGAAGGCGGCATCGTCACCGGATACGGC  
CTCAAATCGGCTACTTCGCCAGGAACACGACACCATCGACCCCGACAAATCCGTCTGG  
CAAAACACCATCGAAGCCTGCGCCGACGCCGACCAACAAAGCCTCCGCAGCCTCCTCGGA  
TCCTTCATGTTCTCCGGCGAACAACCTCGACCAACCAGCAGGAACACTCTCCGGCGGTGAA  
AAAACCCGCCTCGCACTGGCCACCCTCGTGTCTCCCGCGCAAACGTCCTGCTTCTCGAC  
GAGCCCAACAACCTTGACCCGATCTCCCGCGAACAGGTCTCGACGCACTGCGCACC  
TACACCGGCGCAGTCGTCTGGTTACCCACGACCCGGGTGCAGTCAAGGCCCTTGAGCCA  
GAACGCGTCATCGTGCTTCTGATGGCACCGAGGATCTTTGGAATGATCAGTACATGGAA  
ATCGTGGAATTGGCG

>RXN01946-downstream  
TAGGTTCTAAGGCTGTTTATGCT

>RXN01995-upstream  
CCGACGCAAAGGCATGCGCCTGCGTGTCTCGAGTAGTCTCCTCCCCTTCCTCGTCCCCAA  
CCTCGACCATTACGGTCGCCCTCTCCTAAAGGAGCCTGGC

>RXN01995  
ATGGATATCCGCCAAACAATTAACGACACAGCAATGTGCGAGATATCAGTGGTTCATTGTA  
TTTATCGCAGTGCTGCTCAACGCACTGGACGGCTTTGATGTCCTCGCCATGTCTTTTACT  
GCGAATGCAGTGACCGAAGAATTTGGACTGAGTGGCAGCCAGCTTGGTGTGCTGCTGAGT  
TCCGCGCTGTTCCGGCATGACCGCTGGATCTTTGCTGTTCCGGTCCGATCGGTGACCGTTTC  
GGCCGTAAGAATGCCCTGATGATCGCGCTGCTGTTCAACGTGGTGGGATTGGTATTGTCC  
GCCACCGCGCAGTCCGCAGGCCAGTTGGGCGTGTGGCGTTTGATCACTGGTATCGGCATC  
GGCGGAATCCTCGCCTGCATCACAGTGGTGATCAGTGAGTTCTCCAACAACAAAACCGC  
GGCATGGCCATGTCCATCTACGCTGCTGGTTACGGCATCGGCGCGTCCTTGGGCGGTTTC  
GGCGCAGCGCAGCTCATCCCAACATTTGGATGGCGCTCCGTGTTGCGAGCCGGTGCAGATC  
GCAACTGGTATCGCCACCATCGCTACTTTCTTCTTCTGCCAGAATCCGTTGATTGGCTG  
AGCACTCGCCGCCCTGCGGGCGCTCGCGACAAGATCAATTACATTGCGCGCCGCCCTGGGC  
AAAGTCGGTACCTTTGAGCTTCCAGGCGAACAAAGCTTGTGCGACGAAAAAGCCGGTCTC  
CAATCGTATGCAGTGCTCGTTAACAAAGAGAACCGTGGAACCAGCATCAAGCTGTGGGT  
GCGTTCCGGCATCGTGATGTTCCGGCTTCTACTTCGCCAACACTTGGACCCCGAAGCTGCTC  
GTGGAAACCGGAATGTCAGAACAGCAGGGCATCATCGGTGGTTTGATGTTGTCCATGGGT  
GGAGCATTCGGCTCCCTGCTCTACGGTTTCTCACCACCAAGTTCAGTCCCGAAACACA  
CTGATGACCTTCATGGTGCTGTCCGGCCTGACGCTGATCCTGTTTCTTCCCTCCACCTCT  
GTTCCATCCATCGCGTTTGCCAGCGGCGTTGTCGTGGGCATGCTGATCAATGGTTGTGTG  
GCTGGTCTGTACACCCTGTCCCCACAGCTGTACTCCGCTGAAGTACGCACCACTGGTGTG  
GGCGCTGCGATTGGTATGGGTGCTGTCGGTGCGATTTCGCGGCCACTGCTGGTGGGTGGC  
CTGCTGGATTCTGGCTGGTCCCCAACGCAGCTGTATGTTGGTGTGGCAGTGATTGTTATT  
GCCGGTGCAACCGCATTGATTGGGATGCGCACTCAGGCGGTAGCCGTGAAAAGCAGCCT  
GAAGCCCTAGCGACCAA

>RXN01995-downstream  
TAGGGCCGCGATTCTAGCATGC

>RXN02062-upstream  
TTGTCTAAACATCGTTTTGGGGTCCGAATGATAGCCCCTTTTAATGCCCCCATTTTCGGTA  
TCGCTGCGCAACTGTTTTTAGATGGCTAATCTTTGAAATT

>RXN02062

ATGAGAGTCGGAATGATGACAAGAGAGTATCCACCAGAGGTTTACGGCGGCGCTGGCGTG  
CACGTCACCGAATTGACCCGATTCATGCGTGAGATCGCTGAAGTTGATGTTCACTGCATG  
GGTGCACCTCGCGATATGGAGGGAGTTTTTCGTCCACGGCGTCGATCCTGCCTTGGAAGC  
GCGAACCCTGCGATTAAGACACTGTCCACCGGTTTACGCATGGCAGAAGCTGCAAACAAC  
GTGGATGTCGTGCACTCACACACTTGGTATGCAGGTCTTGGCGGCCACCTTGCAGCTCGT  
CTCCACGGCATTCTCCTCACGTGGCTACCGCGCACTCTTTGGAGCCAGATCGCCCATGGAAG  
CGTGAGCAGCTTGGCGGTGGATACGACGTGTCCTCCTGGTCTGAAAAAATGCCATGGAA  
TACGCTGACGCGGTTCATCGCTGTGTGCGGCTCGCATGAAAGATTCCATCCTCGCTGCGTAC  
CCTCGCATCGAGCCGGACAACGTGCGTGTGTCTCAACGGCATCGACACTGAGTTGTGG  
CAGCCTCGCCCGACTTTCGATGACGCGGAAGATTCCGTACTCCGCTCCCTAGGCGTTGAC  
CCACAGCGGCCCATCGTTCGCATTTGTGCGGCCGCATCACCCGCCAAAAAGGCGTCGAGCAC  
CTCATCAAGGCAGCAGCGCTTTTCGACGAGTCCGTGCAGCTTGTGCTCTGTGCCGGCGCG  
CCAGACACCCCCGAAATCGCAGCTCGCACCACCGCCCTGGTGGAAGAACTCCAGGCAAAG  
CGCGAAGGCATTTTCTGGGTTCAGGACATGCTGGGCAAGGACAAAATCCAAGAGATTCTC  
ACCGCTGCTGACACCTTCGTGTGCCCATCCATTTACGAGCCACTGGGCATCGTGAACCTTG  
GAAGCAATGGCCTGCAACACCGCAGTTGTGCGCATCCGACGTTGGAGGCATCCCTGAGGTT  
GTTGTGACGGCACCACCGGCGCCCTCGTTCACTACGACGAAAATGATGTGAAACCTTC  
GAGCGCGATATCGCCGAAGCGGTGAATAAAATGGTCTGATCGAGAGACCGCAGCCAAA  
TTTGGTCTCGCAGGGCGCGAACGTGCTATCAATGATTTCTCCTGGGCAACGATTGCTCAG  
CAGACCATTGATGTGTACAAATCCTTGATG

>RXN02062-downstream

TAAAACCGAAAGCCGGGGAACCT

>RXN02074-upstream

CGGGGGAAGGCCGTGTCGCATGCTCGGGCTAGCCTTGGATCTCAAGAAGAATTCGACTGG  
TTTAAAGTCTGGGCTTTAAGTGCAGAAAGGTTGTGGATTG

>RXN02074

ATGCGCTCCCTGCTTCGTGATATCCCTGCGGTGGGTGGCTAATCACCGCGACGATTGTT  
GTGCGCACGCTCGTTGTTGCGCTGGTCATCGTTGGGATCGGCTTGCTTATCGACGTCCCC  
TCGCCCGCTCATTTCAGCCATGTTGTGGTGGGTCTGGCAGGTGCCACGGCAGCAGCTGCG  
CTGCTGTGCGCGGAAGCGGTGCTCCCCCAACGTATTCGTGCACGAGTTGAACGATCCTGG  
CGGCGGCAGTTGGCTGCTAAAAATCTGGAGCTGAATTCCAGTTTCGTGAGATGATGCCAG  
TTGATCACACTGGCAACTGAAGCCACCTCAAAGCATCCACTTACACAGTGATGTTTCTG  
GGGCCTTACTTTGCAGTATTTTGGCCCCACTGACAGTTATTGCCGTTGTGCGCGCGGCT  
ATTTCTGCGCGATTGCGGGGATACTGTGCTCGGGTTGTGCGTGATACCTTTCGTTATT  
TCTTGGGCACAGCGCATGTTGAAAGGCGCTGGCGCGGGATACGGGCGAGCATCTGGGCAG  
TTGGCAGGCGTGTTTTTGAATCGGTGCGCACACTAGGCACCACGATGATGCTGAATGCC  
GCTGGGCAGCGCAGGCAGATCATCACACAGCGCGCAGAGAATATGCGCTCCCAAGTGATG  
TCATTGCTGTACCGAAATCAGTTGATGATTCTGGTGACCGACGGCGTGTTGGAGTTGCC  
ACCACAATGGTTGCTGCGGTGTTTGCCATTGGAGGATTCTTTTCAGGCTCTCTTACTCTC  
GGCCAAGCTGTAGCACTCGTATTGCTGGCCAGGCTGCTTATTGATCCCATCAACCGCATG  
GGTCGCACGTTTTACACCGGCATGGCAGGCAAACCTCGCTGATCGCCATTGAAAAAGCC  
CTCGCGACAACCTTTACTGATCAGCCAACCAAGGGACAGCGCCACGATGGGGATCTG  
GTGGTCAACAACCTGAAGATCGCCCGCGATCACAGGGACATTGTGCACGGTATCTCTTTC  
AGCATTTCCCGCGGTTCCACATCGCGGTGGTAGGTCCAGTGGCGCTGGTAAATCCTCT  
GTGGCTCTAGCGTTGTCCGGACTTTTAGAGTTTGATGGTGCGATTTCCTCGGCGGCCAC  
AACTGTGAGATGTTAGATCTTCGCGCCTCAGTCAGTTTCGTGCCCCAATCCCCACGCTG  
TTTAGCGGAAGCATCAAAGCAATATCGATCTGGCGCGCACGGGTGTTGATTCTGATCAC  
ATCCACGCAGCACTTTTAGGCGAAGAACTCCCCGCGGACCTCAAAGTCGGTGAAACCGGC  
AAAGGTGTCTCCGGCGGCCAAGCAGCAGCATTTCCATTGCCCGAGGTTTAGTAAAGAAT  
GCTGCCGTGATTGTTCTCGACGAGGCGACCGCACAACTCGACTACACCAACGCCCGCCAG  
GTTTCGACATCTTGCCAAATCCCTTGAGTGCACGTTGGTTGAGATCACCCACCGCCCATCA  
GAAGCCCTCGATGCAGACTTCATCATTTGTTTTAGAGGATGGCCAATTGACCATGATGGAT  
ACACCCAGCAACGTTTCCAGCACAAATGCGTTTTTCCGCACCGCTGTGATGGAGGAAGAA  
CAA

>RXN02074-downstream

TGATTTCCCGACTTCTCCAATTG

>RXN02096-upstream

CGCTTCGACGACCTCACCCACAGCGATATCCGCAGGAATCTCATCGCGGTTTTTGATGAG  
CCGTTCTTGTACTCCTCCTCCATACCGCGAGAACATCTCG

>RXN02096

ATGGGTTTGGATGTCAGTGATGAGCAGATCGAACACGCAGCCAGGCTTGCCCAGGCTCAT  
GATTTTATCGATCGCCTTCCAAACAAATACGAGGAAGTCATTGGCGAACGCGGCCTGACG  
CTTTCTGGTGGTCAACGCCAACGCATCGCCCTCGCACGGGCTTTCCTGGCGCATCCCAA  
GTGTTGGTGCTTGATGATGCCACCTCTGCCATTGATGCCTCCACTGAGGACCGCATTTTC  
CAGGCCTTGCGCGAAGAAGTGCACGATGTCACCATTTTGATCATCGCGCACCGCCACTCC  
ACTTTGGAGCTCGGCGATCGGGTTGGTCTGGTCTGAAGATGGACGGGTAAACAGCACTGGGA  
CCGTTGAGTGAGATGCGTGATCACGCTCGTTTCTCGCATCTGATGGCTCTTGATTTCCAG  
GATTCTCACGATCCGGAATTACCCCTCGACAACGGTTCACTACCCAGCCAAGAGCAATTG  
TGGCCGGAGGTCTCCACAGAAAAGCAGTACAAGATTCTTGCGCCTGCCCCTGGTCGAGGC  
CGTGGCATGTCCATGCCAGCAACCCCTGAGCTGCTCGCCCAGATTGAGGCGCTGCCAGCA  
GCAACGGAAGAAACACGAGTTGATGCCGGGAGGCTACGCACCAGTACCTCCGGTTTCAA  
TTGCTCAGTTTATTCAAGCAGGTCCGTTGGCTCGTCGTCGCGGTTCATCGCGTTGTTGCTG  
GTGGGCGTAGCCGCCGATCTAGCATTTCCAACACTGATGCGCGCAGCCATCGACAACGGT  
GTGCAAGCACAAAGCACCTCCACGTTGTGGTGGATCGCCATCGCAGGCAGCGTAGTAGTC  
CTTCTGTCTGGGCCGCCGCCGCGATCAACACGATTATCACGGCACGCACCGGTGAACGG  
CTGCTTTACGGCTTGCGTCTGCGCTCATTTGTGCATCTATTGCGCCTGTCCATGAGCTAT  
TTCGAACGCACCATGTCCGGCCGCATCATGACGCGCATGACCACCGACATCGACAACCTC  
TCGTCTTCTCCAATCAGGTCTGGCGCAAACAGTTGTCTCTGTGGGCACGCTCATCGGT  
GTGGTCACCATGCTCGCCATCACCGACGCACAACACTAGCACTCGTTGCGCTGTCCGTGGTG  
CCGATCATCATCGTGCTCACTCTCATTTTCCGACGCATCAGCTCCAGGCTGTACACCGCT  
TCACGCGAGCAAGCCAGCCAGGTCAACGCGGTATTCCACGAGTCCATCGCCGGTTTACGC  
ACCGCGCAGATGCACCGCATGGAAGACCAAGTCTTTGACAATTATGCGGGCGAAGCAGAG  
GAATTCCGACGCCTGCGTGTGAAATCCCAGACGGCCATCGCCATCTACTTCCCCGGCCTT  
GGCGCGCTCTCTGAAATCGCCCAGGCACTCGTCTCGGTTTCGGCGCACTGCAAGTAACG  
CGCGGCGACATCTCCACCGGCGTACTCGTGGCATTCGTGCTGTACATGGGCCTGATGTTT  
GGCCCCATCCAACAATAAGCCAAATCTTCGACTCCTACCAACAAGCCGCGCTCGGCTTC  
CGTCGCATCACCGAACTGCTCGCAACGCAGCCCAGCGTCCAGATCTGGGCACCAACAGGC  
ACGCTAGGCAGGCTGCCACGCAGCCTTTATTGCTTGACGACGTACCTTCGGCTATTTCAG  
ACGATCCGATCC

>RXN02096-downstream

TAGACAACGTCACCGTCCAGATC

>RXN02148-upstream

GCCTCAGACTACGGAATCCCTGTGCAGGTGGTATCTGTTGATTCAGCACCGTTTTATGGT  
GCGCGTCGCTACTAAGAAATAGTTCGTCAGGAGAATCTTT

>RXN02148

GTGTCTGCATCCCGAAAACTCTCGTTGTGACCAATGATTTTCTCCACGGATCGGCGGA  
ATCCAAAGCTATTTGAGGGATTTTCATCGCTACTCAAGATCCTGAGTCGATCGTGGTGT  
GCGTCGACTCAAACGCTGAGGAAGCGCATGCCTACGACAAGACTTTGGACTATGAGGTC  
ATTAGGTGGCCTCGTTCGGTGATGCTGCCCACCCCAACAACGGCACACGCTATGGCGGAG  
ATCATTCGTGAGCGAGAGATCGATAATGTGTGGTTCGGTGCTGCGGCTCCGTTGGCGTTG  
ATGGCAGGCACAGCGAAGCAGGCAGGTGCGAGCAAGGTTATTGCCTCCACTCATGGGCAT  
GAGGTGGGGTGGTCAATGCTTCCCTGGATCGAGACAATCGTTGCGCAAAATCGGCACTGAG  
GTGGACGTGCTGACTTATATCTCGCAGTACACGCTGCGCAGATTCAAAGTGCTTTTGGA  
TCGCACCCGACTTTTGAACATTTGCCTTCCGGCGTGACGTTAAGAGATTCACTCCGGCC  
ACGCCAGAGGACAAAAGCGCAACAAGGAAAAAGCTAGGATTCACGGACACCACCCCGGTT  
ATTGCCTGTAACCTCGCGTTTAGTGCCGAGGAAAGGCCAGGACTCGCTGATCAAGGCGATG  
CCACAGGTGATTGCGGCGCGCCAGATGCGCAGTTGCTCATTGTGGGCAGTGGGCGATAC  
GAGTCGACTTTGCGGCGCCTTGCCACTGACGTGAGCCAGAACGTGAAATTCCTTGGGCGC  
CTTGAATATCAAGATATGATCAACACGCTTGCCGCGCAGATATTTTCGCGATGCCAGCG  
CGCACCCGCGGTGGCGGACTTGATGTTGAAGGCTTGGGCATTGTCTATCTCGAGGCACAA  
GCCTGCGGAGTGCCGGTGATAGCCGGCACCTCTGGCGGCGCGCCAGAGACGGTGACTCCG  
GCAACTGGCCTGGTTGTGGAGGGGTGCGACGTCGATAAGCTGTCTGAGCTTTTAATTGAG



CTTCTCGACGATCCGATCCGCCGCGCCGCGATGGGCGCTGCAGGTAGGGCGCATGTGGAG  
GCCGAATGGTCGTGGGAAATCATGGGGGAGCGGTTGACCAATATTTTGCAGAGTGAACCA  
CGA

>RXN02148-downstream  
TGATGGTTGGACAGCTGTTGATA

>RXN02168-upstream  
AGGGTTTAGTCATCTATTTTCGGCTACGCTCACGTAACCTACGCATTCGTAAGTGGTCATG  
GGTCCAAGAAGCCCATTTCCAAGACTTAGGAGCTTTATTTTC

>RXN02168  
GTGAGTATTTCTTCACTGACACCGCTGCACTCTTTCAAAGAGCCAGCAATTCTGTACGCC  
GGTCAGGCTTCTGCCTGGCAGCAGGTGATCGCTGATTCCAGCGAAGACCACATCACCGCA  
ACGCACCTGCGCGAGCTCCTGTCTCGCTCCCGTGCAAAGACTGCACCTTTTCGCTCGCCAA  
ATCACCGCCATCGTGCCTGGCTCACTTGCTCGTCTTGAGGAACTGACCCGCGAAGACGCA  
CAAATCGGTGCAGACATCGACGCACAGCCTGCCGTTTCCATTCCAGGCATTCTGCTGGGA  
CAGATCGCTGCAACCCGTCAGCTGCGTGACCTCGGACTCGATGTCGCAGCAGCTTCCCGC  
CTTGAGACTCCAGGGCATTTTGGGCGTTGAAGCAGTAGACAATGAAGAAGACGTTTTTA  
GCTTTTCGCCATCCTGCTGGGCGCAGCAGCTTCCCAGTTTCGCTGGCAAGGGCGCACATATG  
CTCTCTGTTTCGCGGCCTGTCCCGTGAGATCATCCAGGACACCATCGCTGGTGTTCGATGGG  
GTAGAGGTCTCCCTGCGCAACGCTCGTGACACTTTGTTGTCTCTGGTAAGCCAGAGGCA  
CTGAAGAAGGCTGCTGCTGCTCTACAGCGCGCAGCTGATGTTTACAACGAAGACATCAAC  
GAAAAGCGCAAGGGTGGATCCCTGGCAGAGCCTAAGTTTGACTACTTGATGTGGCCATT  
CCTTTCCACCACTCCTCCATGCAGGACGCAGCCGACTTGGCTGTCGAGTGGGCAACCACC  
TGTGGCCTAAACGTCAACGCGCGCGCGTTGGCAGAAGCAATTCTAGTTAACCCAGCTGAC  
TGGGTTGAGCAGATCGCAAACCTCAAGGCTGATTACGTTCTTTCCCTCGATGCAGGCGTC  
AGCCGTTTTCACCGCTCCATTGCTAGACGGTCGCGGAATCTCTTTGGTTCTTGCCTTCTCC  
GCTGCAGAGCGCGACAACCTTGGCTCGCCCTGGCTTCCACGTTTCTACCGCTGAGGATTGG  
TCCGAGTTTCGCTCCAAAGCTGGTTAAGCTTCCAAACGGTGAGCACAAGGTTCTCACCGGG  
TTCTCCCGCCTGACTGGTTATTCCCCAATCGTCTTGGCTGGCATGACCCCAACCACCGTT  
GATCCTGAGATCGTTGCAGCTGCAGCGAACGCTGGACACTGGGCCGAAATGGCCGGTGGC  
GGACAGTACTCTGAAGAAGTCTTCAACCAAGAACAAGGAAAAGCTCGTTTCCCTGCTCAAG  
GTTGGACGCTCCGCACAGTTCAACTCCATGTTCTTCGACCGCTACATGTGGAACCTGCAG  
TTCGGTGCACAGCGCATCGTTTCCAAGGCACGTGCAACCGGTACCTCCATCAACGGTGT  
GTTGTCTCCGCTGGTATCCCAGAGGTTGAGGAAGCAACTGAGCTGATCAACGATCTGAAC  
GCTGATGGCTTCCCATACGTTGCATTCAAGCCAGGCACCGTGGATCAGATCCGCGCAACC  
CTGAAGATTGCTGATGCAAACCCAGAGACCAAGATCATCATCCAGATCGAGGACGGACAC  
GCTGGTGGCCACCACTCCTGGGTCAACTTGGACGATCTGCTCCTGACCACCTACGCAGAG  
CTGCGTTCCCGCAAGAACGTTGTCGTCATGATCGGTGGCGGCATCGGAACCCCTGCAAAG  
GCTGCTTACTACCTGACCGGTGAATGGTCCACCGATTTGGGCTTCCCAGCAATGCCAGTG  
GACGGCATCCTCGTGGGTACCGCTGCCATGGCAACCAAGGAAGCAACCACTTCTCCTCAG  
GTCAAGCAGGCACTGGTCGACACCCAGGTGTTGATCCACACGACGCTGGCGGCTGGGTT  
GGCCGTGGCGATGCTCGTGGTGGCGTGACCTCTGGTCTGTACACCTGCACGCTGACATG  
TACGAGCTGGACAACGATTCTGCTGCAGCTTCCCGCCTGATCTCTTCCATCGATTCTGAT  
GATTACGCAGATCACCGCGAAGAGCTCATCGAGGCTATCAACAAGACCGCTAAGCCTTTC  
TTCGGCGAGGTGCAAGAGATGACTTACGCAGAGTGGATCCAGCGTTGGGTTGAGCTTGCT  
TACCCAACCTCAGGACCCAACCTGGGATGATCGTTTCCCTCGATTTGGTTACCGCATTTGAA  
GCTCGTCTCAACGAGGCAGAGCACGGCGCCATCACCACTGTTCCCAGACCATGCGTCT  
GTGGAAGAAATGAGGAAGAGGCCGTCGAAAAGCTTCTTGCTGCTTACCCGCAGGCCCGCGAG  
ATCCAGGTCTCTGCGCGCGACGCCGCGTGGTTTATTGGTCTGTGCCGCAAGCACCACAAG  
CCTATGCCTTGGGTTCCAGCAATCGATGCTGACCTAGCACGCTGGTGGGGCCTTGACACC  
CTGTGGCAGTCCCAGAACGAGCGCTACGGCGCGAACTCAGTCCGCGTTATCCCAGGACCA  
GTCTCCGTGCGCCGGCATCGACCGTGTTGACGAGCCAGTTGCAGAGCTGCTCGGCCGCTTC  
GAAGCTGCCTGCGTTGACGCTCTCGACGGCGAGCCAGAAGAGATCTTCGCTCGCCTCAAT  
GAGTCCAAGAACGAGCGCGAATTCCTGCTGGCTACCCACACATCGTGTGGCACGGCAAC  
CTGATCGACAACCCAGCTCACGTCTCAACGAGGGTGCTTTTCGAGCTCATCGAGGAGGAT  
GGCTACTGGGTCTATCCGTATCCTGGCTGATTCTTACTTCGACGATCTGCCAGTTGAGCAG  
CGCCCATACCTGGTTTACGATGTTGACATCCCAGTTGAGCTGGGTGACGCTGGT



>RXN02168-downstream  
TGAACCGGTGGTTTCCCAATTGG

>RXN02233-upstream  
ATCCCCACCCAATTGGCCCAAGAGCTGCAGAGTTACGTTGTAGAACCCACCTCTGCCTAA  
CTGTTCGATTTCCCAAGAGCCCCCTTGGGAGTCGATAATTA

>RXN02233  
GTGCTCGTGACTTCAACATGGGGATGGACCGTCCACGGAGACGGCAAAAAGATCGAACCC  
GGCGCAGTTGTCTGCTCCTAAAGAGCGCCTGAGCTGGGGGCGCACAATTGGAATCGGTATG  
CAGCACGTGATCGCCATGTTTCGGCGCCACGCTCCTGGTTCCACACTCACCGGATTTCCG  
GTCAACACCACACTTTTATTCTCTGGTCTGGGAACAATCCTGTTCTGTTGATCACCAGA  
AACCGACTACCTCTGTACCTGGGTAGTTCTTTTGCTTTTCATTGCACCTTTAACCGCAACC  
CAAGTCCATGGCATTGGCGTGCAGATCGGTGGCATTCTTGTCTGCAGGTCTCGTGCTCGTC  
GCCATTGGATTTGTGGTGAAAGCAGCGGGCAAACGCGTTATTGATGCTGTCATGCCACCC  
GCTGTCACCGGTGCGATCGTGGCACTCATCGGCCTGAACCTGGCACCAACCGCGGCAGGA  
AACTTCTCAGCCAACCACTGGTTGCCACGGCGACCTCTTTGCCATTTTGATCGCTACC  
GTTGCAGGCCGCGGAATGATTGCTCGCCTGGGCATTTTGATCGGTGTGGTGATCGGCTGG  
GTTTTCTGCAGCTATCACCGGCAACCTCTCAGAAGGCGCAGCAGACACCATCCGTGAAGCA  
GCATGGTTTCGGACTGCCACAGTTCCACAAGCCGGAATTCAGCTCTCTGCCATTTTGGTG  
ACACTGCCAGTCATCATCGTGCTCATCGCTGAAAACGTCGGCCACGTCAAAGCAGTCTCA  
GAGATGACAGGGGAGGACCTCGACGACCTCGCCGGCGACGCACTTATCGCAGACGGATTC  
GGCACCAACCTCGCAGGTGCCCTTCGGTGGATCCGGCACCAACCACTACGCAGAAAACATC  
GGCGTCATGGCGGCCACCCGCGTATATTCCACCGCTGCGTACTGGGTTGCCGCGTGCACT  
GCCATCGCCCTTGCCTTCATCCCCAAATTCGGTGCATGATCTTCACCATCCCCGCCGGC  
GTGCTGGGTGGGGCATGTTTGGTTCTTTACGGCCTAATCGGTATGCTCGGCATTCGTATC  
TGGCAAGACAACAAGGTCAACTTCAACAATCCAGTGAATCTGACCATGGCTGCCGTTGCT  
TTGGTTGCAGGCATTGGTAACCTCACCTCACCGTTTTTCGGAGTCACTCTTGAAGGCATC  
GCATGGGGCTCTGTAGGCATCATTGTGCTGTACCCAATCATGAAGCGCCTGTACCTTTCC  
ATTGGGGAAGGCAAGAACGCAAAGTTC

>RXN02233-downstream  
TAGTACGCTGCTAAAGTATGCAG

>RXN02309-upstream  
GTGCCTTCCGTCGACTACGGTTAAACAAAAAGCTTTTTGTCCATTTCACTGGATTACCG  
AAAGAATGAATCCACACTCGATCACCAAAGGTAGCGATGA

>RXN02309  
ATGAGTAGCGGCCGAACCGTTCCAACCCGTTCCACGGGCTCGGAAAAGAAGGTGTATCC  
ACCACAGGAGCATCTCAGGTCGAGTTTGGTGATCCCGAGCTAACGGCCAGGATCAATGAC  
GCCATGGTGCAGGTAGAAGAACTCCTGCACACTGAACTATCGTCCGGGGGAAGACTTCCTC  
GTCGATATCGTCATGCACCTAACACGAGCCGGCGGCAAACGATTCCGCCCCATGTTTGCA  
CTGCTGGCCTCCGAGTTTCGGTGAAAAACCACTCTCCGAAAACGTCATCAAAGCCGCCGTT  
GTCGTAGAGATCACCCACCTGGCCACCTGTACCACGACGATGTCATGGACGAGGCATCC  
ATGCGCCGCGGCGTCCCAAGTGCTAACGCGCGATGGGACAACTCCGTAGCCATCCTCGCA  
GGCGACATCCTCCTAGCACATGCATCAGGTCTGATGAGTCAGCTGGGTACCGACACAGTC  
GCCCACTTTGCCGAAACATTCGGCGAACTAGTCACCGGCCAAATGCGCGAAACAGTCGGG  
CCACGCGACACCGACCCGATCGAGCACTACACCAACGTAATCCGTGAAAAAACTGGTGTC  
CTCATCGCCTCCGCGAGGCTATTTGGGAGCCATGCACGCGAGGCGCCGCACCTGAACACATC  
GACGCCCTGAAGAACTTCGGCGCAGCCGTGGCATGATCTTCCAAATCGTCGACGACATC  
ATCGACATCTTCTCGGAAACCCACGAATCCGGAAAAACGCCCGGCACCGACCTCCGCGAA  
GGTGTATTACCCCTCCAGTGCTCTACGCACTCCGTGAAGACACCCCCGTTCGGCGCAGAA  
CTCCGCGACATCCTCACCGGCCCTCTAGAAGACGACGAGACCGTCAACCACGTCTCTGAG  
CTCCTCTCCCAATCCGGCGGACGCCAAGCAGCCCTCGACGAGGTCTACCGCTACATGGAC  
ATCGCCAACGCAGAACTCGACCGCCTCCAGACAGCACCGTCAAGGAAGCCCTCCGCAAC  
CTTGCAACCTTCACAGTCAAGCGCGTCGGA

>RXN02309-downstream  
TAACCCCGTAATCCACCACTTAA

>RXN02321-upstream

TTTAAAACTACCCGCACGCAGCACGAACCTGTTCAAGTATGTAATCACCGCGGAAATA  
TTGTGGACGTTACCCCCGCCTACCGCTACGATTTCAAAC

>RXN02321

ATGACCATTTCCTCACCTTTGATTGACGTCGCCAACCTTCCAGACATCAACACCACTGCC  
GGCAAGATCGCCGACCTTAAGGCTCGCCGCGCGGAAGCCCATTTCCTCATGGGTGAAAAG  
GCAGTAGAGAAGGTCCACGCTGCTGGACGCCTCACTGCCCGTGAGCGCTTGGATTACTTA  
CTCGATGAGGGCTCCTTCATCGAGACCGATCAGCTGGCTCGCCACCGCACCAACGCTTTC  
TGCTTGGGCGCTAAGCGTCTTGCAACCGACGGTATCGTGACCGGCTGGGGCACCATTGAT  
GGACGCGAAGTCTGCATCTTCTCGCAGGACGGCACCGTATTCTGGTGGCGCGCTTGGTGAG  
GTGTACGGCGAAAAGATGATCAAGATCATGGAGCTGGCAATCGACACCGGCCGCCATTG  
ATCGGTCTTTACGAAGGCGCTGGCGCTCGTATTACAGGACGGCGCTGTCTCCCTGGACTTC  
ATTTCCAGACCTTCTACCAAAACATTACGGCTTCTGGCGTTATCCACAGATCTCCGTC  
ATCATGGGCGCATGTGCAGGTGGCAACGCTTACGGCCAGCTCTGACCGACTTCGTGGTC  
ATGGTGGACAAGACCTCCAAGATGTTCTGTTACCGGCCAGACGTGATCAAGACCGTCACC  
GGCGAGGAAATCACCCAGGAAGAGCTTGGCGGAGCAACCAACCCACATGGTGACCGCTGGT  
AACTCCCACTACACCGCTGCGACCGATGAGGAAGCACTGGATTGGGTACAGGACCTGGTG  
TCCTTCCTCCCATCCAACAATCGCTCCTACGCACCGATGGAAGACTTCGACGAGGAAGAA  
GGCGGCGTTGAAGAAAACATCACCGCTGACGATCTGAAGCTCGACGAGATCATCCAGAT  
TCCGCGACCGTTCTTACGACGTCCGCGATGTCATCGAATGCCTCACCGACGATGGCGAA  
TACCTGGAAATCCAGGCAGACCGCGCAGAAAACGTTGTTATTGCATTCGGCCGCATCGAA  
GGCCAGTCCGTTGGCTTTGTTGCCAACCAGCCAACCCAGTTCGCTGGCTGCCTGGACATC  
GACTCCTCTGAGAAGGCAGCTCGCTTCGTCCGCACCTGCGACGCGTTCAACATCCCAATC  
GTCATGCTTGTGACGTCCCCGGCTTCTCCAGGCGCAGGCCAGGAGTACGGTGGCATT  
CTGCGTCGTGGCGCAAAGCTGCTCTACGCATACGGCGAAGCAACCGTTCCAAAGATCACC  
GTCACCATGCGTAAGGCTTACGGCGGAGCGTACTGCGTGATGGGTTCGAAGGGCTTGGGC  
TCTGACATCAACCTTGCATGGCCAACCGCACAGATCGCCGTCATGGGCGCTGCTGGCGCA  
GTTGGATTTCATCTACCGCAAGGAGCTCATGGCAGCTGATGCCAAGGGCCTCGATACCGTA  
GCTCTGGCTAAGTCCTTCGAGCGCGAGTATGAAGACCACATGCTCAACCCGTACCACGCT  
GCAGAACGTGGCCTGATCGACGCCGTGATCCTGCCAAGCGAAACCCGCGGACAGATTTCC  
CGCAACCTTCGCCTGCTCAAGCACAAGAACGTCACTCGCCCTGCTCGCAAGCACGGCAAC  
ATGCCACTG

>RXN02321-downstream

TAAATCGGCGAATCCATAAAGGT

>RXN02342-upstream

CAGGTTCTGTGCTGCGTGCGGGTAGTTTTTAAAGGTAAACCTTTTTGGGCGTGTCGCCCTT  
AAAGCGCGCTTTTCGACGCGACCCCACTACATTGGCTTCC

>RXN02342

ATGAACGTTGACATTTACGATCCAGAGAGCCGCTAAACGTTGAGCTCCTGAAGGAAAAA  
TTGCTCCAAAACGGTGACTTTGGCCAGGTCATTTACGAAAAAGTGACAGGCTCCACTAAT  
GCTGACTTGCTGGCACTTGCAGGTTCTGGCGCTCCAAACTGGACGGTGAAAACGTGTCGAG  
TTTCAAGATCATGCGCGTGGGCGACTCGGCCGCCCGTGGTCTGCCCCTGAGGGTTCCCAA  
ACAATCGTGTCTGTGCTCGTTCAACTATCTATTGATCAAGTGGACCGGATTGGCACTATT  
CCACTCGCGGCGGGACTCGCTGTCATGGATGCGTTGAATGACCTCGGTGTGGAAGGTGCC  
GGACTGAAATGGCCCAACGATGTTCAAATCCACGGCAAGAACTCTGCGGCATCCTGGTG  
GAAGCCACCGGCTTTGATTCCACCCCAACAGTTGTCATCGGTGGGGCACTAATATCAGC  
CTGACTAAAGAGGAGCTTCCTGTTCTCATGCAACTTCCTCGCATTTGGAAGGTGTTGAA  
GTCGACAGAACCACATTCCTTATTAATATGCTCACACATCTGCATACTCGACTGGACCAG  
TGGCAGGGTCCAAGTGTGGATTGGCTCGATGATTACCGTGCGGTATGTTCCAGTATTGGC  
CAAGATGTTGAGTGCTTCTACCTGGGGATAAAGAACTCTTAGGTGAAGCGATCGGTGTC  
GCGACTGGCGGAGAAATTCGTGTTGCGGATGCTTCGGGCACCGTTCACACCCTCAACGCC  
GGTGAAATTACGCACCTTCGCCTGCAG

>RXN02342-downstream

TAAGGTGACGGTATGGGGAATTC

>RXN02348-upstream

AAAGACCCGAGCCGAAGCCCTGGCCTGCGCATACTTCCTTGTCAACGCTCGCTGGGATTA  
GGTCTTTTCTGAGCGCTAGCATTTCTCCACTCAAAGGAGC

>RXN02348

ATGCTTAACCGCATGAAAAGTGCGCGGCCAAAATCAGTCGCTCCAAAATCCGGACAAGCT  
TTACTCACTCTCGGTGCCCTAGGTGTTGTGTTTCGGCGACATCGGCACCAGCCCCCTGTAC  
TCACTTCACACTGCATTTCAGCATGCAGCACAACAAAGTCGAAGTCACTCAGGAAAATGTG  
TACGGCATCATCTCCATGGTGTGTTGTGGACCATCACTTTGATCGTCACCGTCAAATACGTC  
ATGCTGGTCACCCGAGCTGACAACCAAGGACAAGGTGGCATCCTGGCGCTCGTTGCTTTG  
CTGAAAAACCGTGGGCACTGGGGAAAATTTCGTGGCAGTAGCCGGCATGTTGGGCGCCGCA  
TTGTTTTATGGCGATGTGGTGATCACCCCGCGCATCTCTGTTCTCAGCGCAACAGAAGGC  
TTGACGGTTATCTCCCAAGCTTTGAGCGCTTCATTCTGCCCCTATCTCTCGCAGTTCTG  
ATCGCTATTTTTGCAATCCAACCGCTCGGTACAGAAAAAGTCGGCAAAGCCTTCGGCCCC  
ATCATGTTGCTGTGGTTTGTCAACCTTGCAAGATTGGGAATTCCGCAAATCATCGGGCAC  
CCAGAAATCTTGCAAGAGCTTGTCTCCACATTGGGCCCTGCGCTTGATTGTGGCTGAGCCT  
TTCCAAGCATTTGTGCTGCTTGGTGCCGTTGTCCTGACAGTAACGGGTGCGGAAGCGCTC  
TACGCTGATATGGGCCATTTTGGGGCGAGGCCAATCAGAGTGGCGTGGTTTTGCGTCGTC  
ATGCCTGCTTTAATCTTGACGTATTTGGGGCAGGGCGCCTTGGTGATCAACCAGCCTGAA  
GCGGTGCGCAACCCCATGTTTTATCTCGCGCCGGAAGGTCTGCGGATTCGGTTGGTTATT  
TTGGCGACCATCGCTACGGTGATCGCATCGCAGGCCGTGATTTCTGGTGCGTATTCATTG  
ACCAAGCAGGCCGTGAATTTGAACTGCTGCCACGCATGGTGATCCGGCATACTCCCGC  
AAAGAGGAAGGCCAGATCTATATGCCACTGGTTAATGGATTGCTGTTTGTATCCGTGATG  
GTTGTGGTGCTGGTATTCCGATCCTCTGAAAGCCTCGCCAGCGCGTACGGACTTGCAGTG  
ACCGGAACCTTGGTGCTGGTGAGCGTCTGTATCTGATCTATGTTTACACCACATGGTGG  
AAAACAGCGCTGTTTCATTGTGCTCATCGGTATTCCAGAAGTACTTCTATTCGCCTCGAAC  
ACCACGAAAATTCACGACGGTGGCTGGCTTCCACTACTTATTGCGGCCGTGCTCATCGTG  
GTGATGCGGACCTGGGAGTGGGGAAGTGACCGCGTCAATCAGGAACGCGCAGAGCTGGAA  
CTTCCCATGGATAAGTTCTTGGAGAACTCGATCAGCCACACAATATTGGTCTGCGTAAA  
GTTGCCGAAGTGGCAGTATTTCCACATGGCACCAGCGATACTGTCCCGTTGTCATTGGTT  
CGCTGCGTGAAAGACCTCAAGCTTTTATACCGAGAGATCGTGATCGTTTGAATCGTCCAA  
GAACACGTTCCGCACGTGCCACCAGAGGAACGCGCGGAAATGGAAGTGCTCCATCACGCC  
CCGATCAGAGTCGTGCGAGTTGATCTGCACCTTGGTTATTTTGATGAGCAGAACCTGCCT  
GAGCATCTCCATGCCATTGACCCAACATGGGATAACGCCACCTACTTCCTGTCTGCCCTG  
ACTCTTCGGAGCAGGTTGCCTGGAAAGATTGCTGGCTGGCGTGATCGTTTGTATCTTTTCG  
ATGGAACGTAATCAGGCATCTCGAACTGAGTCTTTCAAATTGCAACCAAGCAAAACCATC  
ACGGTTGGAACAGAGCTGCACCTT

>RXN02348-downstream

TAATCAGGCAGTTGCTGGCCAAC

>RXN02372-upstream

GACAATACTGATGGATAAAATTTTCATATCGAGGACGAAGGGACAACCCCGAACGCCGTGAC  
AACATCAACCACAACCCGGGTGAAACATCCGGTAGACCAG

>RXN02372

GTGCCACCCGCACCCAACTTGCAGCCCTAGGGCTCCAACACGTTCTTGCTTTCTACGCA  
GGAGCCGTCATTGTTCCGCTGCTGATTGCACAGTCGCTGAACTTGGACACTGCGACCACC  
ATTCACCTGATTAACGCTGACTTGTGACATGTGGCATCGCCACGTTGATTTCAGTCTGTG  
GGCATTTGGTCGCCACATTGGTGTGCGCCTACCGATCGTTCAAGGTGTCACCACTACTGCT  
GTTGCTCCCATCATCGCCATTGGTTTGGGCGTTACTGATGGTCAAGGTGGCGTTGCGTCG  
CTGCCTGCCATTTACGGTGCACTGATTGTCTCCGGCATTTTCACGTTCTTTGCAGCGCCG  
GTGTTTGCAGCGTTTCTCAAGTTCTTCCCACCAGTTGTCACCGGTACTGTGCTGTTGGTT  
ATGGGTGCTTCCCTGCTGTCGGTATCTGCAAATGACTTTGTGAACTACGCCGATGGGGTG  
CCTGCTGCCCGCGATCTTGCTTACGGTTTTGGCACCTTGGCGGTGATCATTTTGGCGCAG  
CGCTTCTTCCGTGGATTTCATGGGCACCTTGGCTGTGTTGATCGGCCTGGTTGGTGGCACC  
GCAGTTGCTCTGATCTTGGGCGATGCCAACTTGGATGAGGTGGGAAATGCTGAAGCGTTC  
GACATCACCACTCCGTTTTATTTTGGTGTTCAGAAATTTAACGCTGTTGCCATTTTCTCC  
ATGATTATCGTCATGATCATCACCATGGTGGAGACCACCGGTGATGTGTTTGCAACGGGG  
GAAATCGTCGGCAAGCGAACTCGCCGAGTGATGTACCCGCGCACTGCGCGCTGACGGC  
CTGTCCACCCTGATGGGTGGCGTCATGAACTCCTTCCCGTACACGTGCTTCGCGCAAAAC  
GTTGGCCTGGTGCGCATCACGGGCGTGAAATCTCGCTGGGTGCGGCAGCTGCTGCCGGC

TTCATGATCATCCTCGGTGTGCTGCCCAAGGCTGGCGCGATCGTCGCTTCCATCCCTTCC  
 CCAGTCCTCGGTGGCGCATCCTTGGCACTGTTCCGCAACGTTGCATGGGTGGGCATCCAG  
 ACCATCGCCAAGTCTGACCTCGCTGATAGCCGCAACTCCGTCATCGTGACCTCCGCACTT  
 GGCCTAGCCATGCTGGTGTCTTCCGCCCCGATGTTGCTCAGGCGTTCCCTGAGTGGGCG  
 CGTATCTTCGTCTCCTCCGGCATGTCCGTGGCGCGATCACCGCGATCCTGCTTAACCTG  
 CTGTTCTTCCACGTGCGACGCCAATCCGGTGGACAAGTCGCTACCTCAAATCCGGTGAG  
 CGCATCAATTTGGATGCGGTCAACAAGATGGATCGCACCGACTTCGTAGAAACCTTCGCA  
 CCGCTGTTCAACAGCAAGACCTGGCCTTTGGAAACCGCATGGGAATCCCAGCCATTCGCC  
 AACGTCACGGAAGTGCAGCAAGCCATCCAAGTCGCTGTGCTCACCGCACCGTTGTCCGAC  
 CGCGAAGAGCTCATCCACGACTACCCCGACATGGCACAGCTCATTTTGGCCACCGAAGAG  
 GAAGCCGCCACCATCTCTCAAGACCGTGGTTCGATCGGTCTTGATGATCTCGATGACGTG  
 GATCAAGAAAAGCTCATCACCGTCACCGAGCAGTACCGCGAACGGTTCAACATGCCGTAT  
 GTTGCCTACTTCGACACCATGGATTCTGTGGATACCGTCGTAGCCGCCGGCTTGCGCCGC  
 CTCGACAACCTCCGACGAGCAGGAGCACCGCCAAGCGCTATCGGAAATCATTGAGATTGCC  
 AATGACCGCTTCGATATATTGCTTGCCGACGCTAACCCAGCCCGTTTCAGCTTTTCGATCGC  
 AAGTTTACCGAGACTGACTTCCTCGGC

>RXN02372-downstream  
 TAAACACCAAAAACAAATTAAG

>RXN02395-upstream  
 AAACAGGAATATTTAACTCGACTTCTTAAAAAAGCTCTATACGTAAATATCTTGCCCATC  
 CAGCACCACTCATTGTGGTGCACAATGGAGAGGACACAC

>RXN02395  
 ATGTCCACCAACTCTGGCAATAACTTGCCTGAATCCCAAGAGTCACCCGAGGAACCTCAT  
 TATCCTCAGCACACCCACCCAGGCCTAGTTCCCTGGCATTTCGGTCGATGCTCAACGCAAC  
 AAGTTCGGACTCGACAAAACCGTTTTTCGGCGTCACCGCAGCATTAATTCTGGCGTTCATC  
 GCCTGGGGCATTTCCAGCCCTGATTCGGTTTCTTCAGTATCGTCCACGATGTTTCAGTTGG  
 GCTATGACGAATACTGGTTGGCTCCTCAACTTTGTCTATGCTGATCGGCATTGGCACCATG  
 CTCTACATCGCTTTTTTCGCGCTACGGCCGCATCAAGCTGGGCACGGACGAAGACGAACCA  
 GAATTCTCTCGCTTTTCCTGGATTGCGATGATGTTTCGGCGCCGGCATCGGTGTGGGTATC  
 TTCTTCTTCGGTCTTCCGAACCGCTGTGGCATTATCTCAGTCCCCACCTCACACCGTG  
 GAAGGATCTACACCTGAGTCTTGCACCAAGCACTTGCGCAGTCCCACTTCCACTGGGGC  
 TTATCCGCCTGGGGGCTGTATGCCTTGGTCGGCGGCGCGTTGGCGTACTCCAGTTACCGA  
 CGCGGCCGCGTAACCTTGATCAGCTCCACCTTCCGGTCACTTTTCGGTGAGAAAACCGAA  
 GGTATCGCGGGTGCCTCATCGACATGATGGCGATCATCGCCACGCTGTTTGGAACGGCT  
 GCAACCTTGGGCCTTTTCAGCAATTTCAGGTTGGTCAGGGCGTGCAGATTATTTCTGGCGCT  
 TCGGAAATCACCAACAACATCTTGATCGCCATCATCGCGATCTTGACCATTGGCTTCATC  
 ATCTCCTCAGTATCTGGCGTGTCCAAGGGCATTTCGTTATCTTTCCAACCTCAATATTTCC  
 TTGACGCTTGATTGGTCTTGTGTTTCATCACCGGCCCCACCTTGTTCTCTGCTCAAC  
 TTGATCCCATCGAGTGTGTTGGAATATGGCAGTGAGTTCTTGTTCAATGGCTGGCAAGTCT  
 TTGTCTGGGGTGAGGAAACCATTTGAATCCAAGCTGGTTGGACGGCGTTCTACTGGGCA  
 TGGTGGATCGCATGGACTCCATTTCGTGGGTATGTTTCATCGCGCGTATTTCTCGCGGCCGC  
 ACCTTGCGTGAATTCGCGCTCATCACCATGGCTATCCCTCCTTCATTTTGATCCTGGCG  
 TTCACCATTTTCGGTGGAACTGCCATCACGATGAACCGCGAGAACGTAGATGGTTTTGAC  
 GGCAGTTCATCCAAGGAACAGGTGCTGTTTGATATGTTTCAGCAACCTTCCGCTGTACTCG  
 ATCACACCGTTCATTTTGATCTTTGTGCTGGCAGTATCTTTGTTACCTCTGCCGATTCC  
 GCCTCCGTGGTGATGGGAACGATGAGCTCCCAAGGTAACCCTGCACCAACAAATTAATC  
 GTGGTGTCTGGGGACTGTGCATGATGGGCATCGCGGTGGTCATGCTGCTTACTGGTGGC  
 GAATCCGCGCTGACTGGTCTGCAGAACCTCACCATTTTGATCGCCATTCCGTTTGCGCTG  
 GTGTTGATCGTGATGGCTATTGCCTTTATTAAGGACTTATCCACAGACCCAGCCGCTATT  
 CGACAACGCTATGCAAAGGCAGCCATCTCTAACGCGGTGGTTTCGTGGCTTGGAAGAACAC  
 GGCGACGACTTCGAGCTCTCCATCGAACCTGCAGAGGAAGGTCGTGGAGCGGGTGCTACC  
 TTCGATTCCACCGCTGATCACATCACCGACTGGTATCAGCGCACCGACGAAGAAGGCAAT  
 GATGTTGATTATGACTTCACACCGGCAATGGGCCGATGGTTGGACACCGGAATCGACC  
 GAAGAAGGCGAAGTGGACGCGAAAAAGGAT

>RXN02395-downstream  
 TAAAAAATAACGACTGGCTGGGA



>RXN02424-upstream

AGCCAATGCTCAACTGCCCTTCAAAATCGATTTTTGTGCGCTTCAAAAATACACCTTCGA  
ACATAGCATCGAACAAGGTGTTTCCGCTAGTCTGAACCAC

>RXN02424

ATGACTAACGAGCTCACTCTTCACCATATTTCCGTGTCCCAAATGGACAACAATTGCTAC  
CTTTTGGCCGCAAATGGCAACGGTTTACTCATTGATGCTGCAGATGACGCAGCTGCACTA  
CTTAAATTAGCCGAAGATGCCGGTGTGACCATCACCAAAGTGTTGACCACCCACCGCCAC  
GCAGACCACGTCCGTGCATTGCCGGAGGTTCTCCAGAAGACCGGAGCAACTCACTACGCG  
CCTTTCCTTGAGGTGCCAGCTTTGCCCTCCGCTGTTGATGTGGAAGTGCATCATGGTGAT  
TCAATTGAATTTGAGGGTCATGTATTCCCTATCAGCATTCTGCGCGGCCACACCCCAGGC  
GGTGCAGTACTCACCGCTGAGATCGACGGTAAACTCACCTTTTCGTGGGTGACAGCCTC  
TTCCCCGGCGGTTTGGGCAAACAGCAGCGAAGGCGACTTCGTCCGACTGTTCAACGAT  
GTCAAAGAGCGCATCTTTGACACCTACGACGATGACAGCATCGTGTGGCCAGGTCACGGC  
AAGGAAACCACCTTGAGCCGAGCGTCCACAGCTGGAAATCTGGTGGGAGCGTCGCTGG

>RXN02424-downstream

TAAGCGCTTTTCTCAACCAGGCA

>RXN02442-upstream

GCCGTGATGTTGTTGAGCGCGATGTGATTGCCGTATGTGCATGTGAGATTCCGGACGCTG  
AGTTCTGCCATTCCTTAATGATAACGGTTATCATTTTCAA

>RXN02442

ATGAAGTTTTTTACTGACGCCCTCATAGTGCTTTTTGACGTTTCATTCATCTCCCGCGCC  
CTGGTCGCCGGATGCCTGGCCGCAATTTTATGCTCACTCATTGGAACGTGGGTTATTTTG  
CGCAGGCTAACCTTTTTTCGGCGACGCTATGTCGCACGGCTTGCTCCCCGGAGTAGCCACG  
GCATCACTATTGGGCGGAAATCTCATGTTTCGGCGCAGCAATCAGCGCATTAATCATGTCA  
GCCGGAGTGGTGTGGACCAGCAGAAAATCCAGCCTCTCCCAAGACGTCAGCATTGGCCTG  
CAATTTATTACCATGCTTTCCCTCGGCGTGGTTATTGTGTCCCACTCCGATTCCCACGCC  
GTAGACCTCACCAGTTTCCTTTTTGGAGACATTCTTGGCGTGCGACCCTCGGATATATTC  
ATCATCGCCATTGCAACAGTGTTGGGTGGATTGACTATTTTTCTCTTCCACCGACAGTTC  
ACTGCACTCGCTTTTCGACGAGCGTAAAGCTCACACCTTAGGACTCAATCCCCGCTTTGCA  
CACCTACTCATGCTGGCACTGATCGCATTAGCTACGGTGGTGTGCTTTCAGGTGGTGGGA  
ACGCTTTTAGTGTTTGGACTTCTCATTGGTCCGCCCCGCCACGGCTGCACTTTTAGTGCAA  
GACAAAGCAAGTATTTCACTGATCATGATCGTCGCGTCGCTTCTTGGATGCGCGGAAATT  
TACCTCGGGCTTTTAATCAGCTGGCACGCAAGCACTGCCGCGGGAGCCACTATCACTTTG  
TTAAGTGCTGCGATATTTTTTTGCCACCTTATTGACAAAGAGTGCCATTAGTAGGTAAAC  
TTCACCGCG

>RXN02442-downstream

TGATACTGAAAGACATTTTCAAT

>RXN02443-upstream

CAAGCACTGCCGCGGGAGCCACTATCACTTTGTAAAGTGCTGCGATATTTTTTGCCACCT  
TATTGACAAAGAGTGCCATTAGTAGGTTAAACTTCACCGC

>RXN02443

GTGATACTGAAAGACATTTTCAATAATGGGGAGCTCTTTGGGGCTTCCTCCGCGAAAAAT  
TTCCGAAACTACTAGCTGTTCCAGCCGTTGCCGCCTCACTAGCTTTTGGTATCACCGCC  
TGTTCCGCTGTAGATGACACCCCTGACATTGTGGTCAACCAACATCCTGGGTGATGTT  
GTAAGCCATATCGTGGGAGATTCCGCAGATGTCCAAGTACTCATGAAACCCAACGCAGAT  
CCACATTCCTTCGGAGTCTCAGCACAAGACGCCGCTGCCATGGAACATGCCGATCTCATC  
GTGGCCAATGGACTAGGACTTGAAGAGGGCCTTCAATCCAATGTGGACAATGCCAAAAGC  
CAAGGGGTTCCCGTCTTGGAAGTCGGCGAACACATCGATGTCAATTGACTACTCCCCGGC  
GTTCCAGATCCTCACTTTTGGACAGACCCGGCGCGCATGATCGCCGCCACGGAAGTTATA  
GAAGCTGAAGTATGATCAAAGAACTCGATCCTTCCCTGACTGAATCGATCACACAATCAGCC  
CAGCACTACCGTGAGGAAGTTGTTGCCCTTGATGAGGAAGTCACCGAATTGCTCAGCGGC  
GTGGCCCCAGAAAACCGCAAGCTGGTAACCAATCACAATGTTTTTGGATACCTGGCCAGC  
CGGTTTAATACTACACCGTCATTGACACCATCATCCAGGTGGAAGCACATTGGCGGCGCCT  
TCAGCATCTGACCTCAATGACATCTCCACCGCCATCGAAGACAACAATGTTCCCGCAATC

TTCACCGATACCTCAAGCCCACAACGGTTAGCTGAAGTGTGGCCAGCAACGCTGGCATT  
GATGTTCAAGTGGTGTCCATTTTCACGGAATCACTCACCGATGCAGATGGTGAAGCACCC  
ACCTACATCAGCATGCAAAAAATCAATGCCGAGCGCATTGCAAGCACTTTGTCC

>RXN02443-downstream  
TAAACAGTCCTAACAGTCTTAA

>RXN02447  
ACAGTAGTTCCGGTGTACCTCGCTGAACTCGCACCCTAGAAATCCGCGGCTCCCTGACC  
GGCCGAAACGAGCTTGCTATCGTCACCGGCCAGCTGCTTGCCTTCGTGATCAACGCGCTT  
ATCGCCGTCACCCTACACGGAGTTATTGATGGAATCTGGCGCATCATGTTCCGCGTCTGT  
GCCCTCCCTGCCGTCGCCCTCTTCTCGGCATGCTGCGGATGCCGGAATCACCACGCTGG  
CTGGTCAACCAGGGGCGTTACGACGACGCCCGCCGCGTCATGGAGACCGTCCGTACCCCT  
GAGCGTGCGAAAGCCGAAATGGATGAAATCATCGCGGTGCACTCTGAAAACAATGCGGCA  
CTTCTGTTGTTAAGCAGTCTTCGGGCCAGGCTTCAGGCCAGGTTTCTAGCAAGCACACC  
CACATGTCCATCGGCGAAGTCCTCAGCAACAAATGGCTGGTTCGTCTGCTCATCGCCGGC  
ATCGGTGTTGCAGTTGCCAGCAGCTCACCAGCATCAACGCCATCATGTACTACGGAACC  
CGCGTCCTCGAGGAATCCGGCATGAGCGCAGAAATGGCTGTGGTTGCCAACATTGCTTTC  
GGTGGCGTTGCCGTCATCGGTGGACTGATCGCACTGCGCAACATGGACCGCCTGGATCGC  
CGCACCACTTCATCATCGGCCTGTCACTGACCACCACCTTCCACCTTTTGATCGCAGCT  
GCCGGCACTCTCCTTCCAGAAGGTAACCTCCATTTCGACCATTCGCCATCATGATCCTTGTT  
GTTGGGTTCGTGCTCTCCATGCAGACTTTCCTCAACGTTGCAGTGTGGGTGTGGCTGGCG  
GAAATCTTCCAGTCCGAATGAAGGGTATCGGCACCGGTATTTCCGTATTCTGCGGTTGG  
GGCATCAATGGCGTCCTAGCGTTGTTCTTCCAGCACTGGTCTCCGGCGTGGGTATCACC  
TTCTCCTTCTTATCTTCGCAGTCGTGCGAGTCATTGCCCTGGCGTTCGTACCAAGTTT  
GTTCTGAAACCCGTGGCCGCTCACTTGAAGAACTCGATCACGCAGCATTACCGGCCAG  
ATCTTCAAGAAGGCT

>RXN02447-downstream  
TAAACCCCTCCGATCTCTTTGG

>RXN02487-upstream  
TCATAGCTACGCGCATGCCACATTCTAGATCGCCGAAGAAAGCAGCGGGACGTCTCTAT  
ATACTAAAGGGCACTAAAGCAACGCAGTTGAAGGGACACC

>RXN02487  
ATGTCAGCATACGAAACCAAAGAATGGCTCCAGCACTACCCAGAGTGGACGCCCACTCG  
CTGGAATATGGCGACACCACCTGCTGGACGTTTACGACAACAACCTGGCCATTAAACGCA  
GACAAGCCAGCCACCTACTTTTTCGGTTCGTTACAAACCTACGGTGAACCTGGACAAAGAA  
GTCCGCAAAACTGCCGCTGGCCTGCGCGCACTAGGTGTCCGCCCCGGCGATCACGTAGCG  
ATTATCCTCCCCAACTGCCACAGCACATCGCAGCTTTCTACGCAGTGCTGAAACTCGGC  
GCAGTAGTCATTGAGCACAACCCGCTCTACACCGCCACGAACTGCTCGAACCTTCAA  
GACCACGGTGGCCGCGTTGCCATCGTCTGGGACAAAGCCTCCCCACCGTCGAACAGCTA  
CGTGGACAGACCCAGTTGGAAACCATCGTGTGCGTCAACATGATCAACGCGATGCCACCA  
CTCCAGCGCCTAGCACTTCGGCTCCCAATCCCTGCACTGCGCAAGAGCCGCGAATCCCTC  
TCCGGCGCAGCCCCAACACCGTTCCCTTTTGAAACCCTGACCAGCGCAGCAATGGGCGGC  
GACGGCGACGACGTAGTTTCAGAACCCACCGTGACCAAAGAATCCGTGCGGCTGATCCTC  
TACACCTCCGGCACCAACCGGACGCCCCAAGGGTGCCAGCTACCCACGGAAACCTGTTC  
TTCAATCTTCTTCAAGGAAAGCACTGGGTTCAGGTCTCGGAGACAAACCAGAACGCATG  
CTTGACGCCCTACCAATGTTCCACGCATACGGTCTGACCATGGTCCGGCACACTGTCCGTG  
TTCATCGGTGGCGAAATGGTGCTACTTCCACCCACGCATCGACCTGATCATGAACGTA  
ATGAAAAAGCACACCCCAACCTGGCTACCAGGCGTGCCACCCCTTTACGAAAAAATCGTC  
GACGCTCCGAAAAAGAAGGAATCCCCATCAAGGGAGTCCGCAACGCCTTCTCCGGTGCA  
TCCACACTCTCCAGCGCACCGTTGAACGCTGGGAAAAGCACACCGGCGGACGCCTCGTC  
GAAGGCTACGGCCTCACCGAAACCTCCCCATCATCGTGGGTAAACCCATGAGCGATCAC  
CGACGCCAAGGCTACGTAGGAATCCCTTCCCCGACACCATCGTGCGCATCGCAAACCCA  
GAAAACCTCGACGAAACCATGCCCGACGGCAGCGAAGGCGAAGTCCTAGTCAAGGGCCCA  
CAGGTGTTCAAGGGTTACCTCAACCAGGAAGAAGCCACCAAGAACAGCTTCCACGGCGAG  
TGGTACCGCACCGGCGACGTGCGAGTGATGGAAGAAGACGGGTTCATCCGCCTAGTTGCT  
CGCATCAAGGAAGTCATCATCACTGGCGGTTTCAACGTGTACCCAGCTGAGGTTGAAGAA

GTCCTCGCAGAGCACCCAGACATTGAAGATTCCGCAGTCGTTGGTATCCCGCGTGAAGAC  
GGCTCCGAAAACGTCGTTGCTGCCATCACTTTGGTGGAAGGTGCAGCGCTGGATCCGGAT  
GGCCTGAAGGAATTCGCCCGCAAGAACCTCACCCGCTACAAGGTTCCGCGCACTTTCTAC  
CACTTTGAGGAGATGCCGCGGGATCAGATGGGCAAGATTAGGCGTCGTGAAGTGCAGGCG  
GAGTTGTTGAAGAAGCTCGGCAAG

>RXN02487-downstream  
TAGACGCCGATTTAAGAGGTCGA

>RXN02512-upstream  
GCTGGAAAGTCCCCATTGGCTAAGGAATTTACCAAGGCACCAGCAGGTGCGAAGGCAGAT  
TACAGCAACACCAAATAAAAATTAGCCGAGGGAGCATCGC

>RXN02512  
ATGAAGCCGAAGGATTTCTGCACAGCGGAAAATTGGGCGGAGAATTTAAGCGCACTGGGC  
TATCTAGCTGGTTGGCGTTTTGTCCGGATGCTCCCTTTGCCTATTGCTCGCCGGGTGTTT  
GACCTTGGGGCGGATCTGGCGTCGAAAAGCGGAAAAGGCATGGGGCAGCTACGCGCTAAT  
CTGGCGCGGGTGGTCGGTGCAGGAAAACGTTACGCAGGCGCTGGTGAAGCAAGCAACGCGC  
AGCTATGCGCGGTATTGGCTGGAAGCGTTCCGGCTACCGGCGATCGCGCGAGATCCTGAG  
CTGCTTGCGCGGTTGCGTAAGGGAAGTGTGGCCTAGATTTGTTGGATGAATCTTTGGCT  
GCCGGCAAGGGCGTAGTTTTGACGCTCCACACAGCGGCAACTGGGATATGGCTGGCGCT  
TTTCTGATTAGCCATCATGGGCAATTCACCACCGTTGCAGAAAGGGTCAAGCCGGAACGC  
TTGTTTGAAGCGTTCGTGGAGTTTCGAGAAAGCCTTGGATTTGAGGTGCTGCCTCTCACC  
GGTGGCGAGCGTCCGCCGTTTGAAAAGCTGAAAGAGCGCCTGACATCTGGAGGTATCGTG  
TGCTTTCTTGGGGAGCGTGACCTGCGGCATTCCGGCGTGAGAGCACTTTTTTTGGTGAG  
AAGACCTCCATGCCAGCAGGACCTGCGCAGCTGGCCATTGAAACAGGTGCGGCGCTGCAC  
GTGGTGATCCATGGTTCGATGACGACGGCTGGGGTCTCAGCGTATCCGATGCCGTGACC  
GTGGATAATTTATCCGACACGGTGACGCGGATCGCACATCTTTTTATGGCAAATATTACG  
GCGCACCCCGCTGATTGGCATATGCTCCAACCCCTGTGGTTTGGTGATTGGATCCGGAG  
CGTCTCAAGCGCTCTAGGGAGCAGACAAATGTTCACAAACCGGTGGCATTACAGGAGGAC  
AAT

>RXN02512-downstream  
TAGGTGCGAATTGGAATGGTCTG

>RXN02515-upstream  
GTGGCTAAGCACAGTTACTTGGCCAAGCTGGGCGGCAGAAAAACCGGCCAGCTAATACT  
TCAGTTTAAAATTCGCTTCAACCCTGAAAGATTGTGACAG

>RXN02515  
ATGAGCACTCTTGAAATCCGTAACCTGCACGCACAGGTCCTGCCGTCCGATGAGTCCGCT  
GAGCCTAAGGAAATCCTCAAGGGCGTCAACCTCACCATCAACTCTGGTGAGATCCACGCC  
ATCATGGGCCCTAACGGTTCCGGCAAGTCCACTCTTGCTTACACCCTTGGTGGACACCCA  
CGCTACGAGGTAACCGCAGGCGAGGTCCTCCTCGACGGCGAGAACATCCTGGAGATGGAA  
GTTGATGAGCGTGCACGCGCTGGTCTCTTCCCTGGCCATGCAGTATCCAACTGAAATCCCT  
GGCGTTTCCGTTGCTAACTTCTGCGTTCCGCAGCGACCGCAATCCGCGGCGAGGCTCCT  
AAGCTTCGCGAGTGGGTTAAGGAAGTCCGCACCGCTCAGGAAGCTCTGGCAATTGACCCT  
GAGTTCTCCAACCGCTCAGTCAACGAAGGTTTCTCCGGTGGCGAGAAGAAGCGCCACGAG  
GTTCTGCAGCTTGATCTGCTGAAGCCAAAGTTCGCGATCATGGATGAGACCGACTCCGGC  
CTTGACGTGGATGCACTGCGCATTGTTTCCGAGGGCATCAACTCCTACAAGCAGGAGACC  
GAAGGTGGCATCTTGATGATCACCCACTACAAGCGCATCCTCAACTACGTTAAGCCTGAC  
TTCATTACGTTTTTCGCGAATGGCCAGATTGTGACCACCGGTGGCGCTGAGCTTGCTGAC  
AAGCTCGAGGCTGACGGCTACGACCAGTTCATCAAG

>RXN02515-downstream  
TAACATGTCCGATTTCCCTCAATG

>RXN02547-upstream  
GGGGCCGTCGATAAGCGAAGAACAATTAGCACTGCGCGCGCTGGTCTGACGCATTGGTTA  
AGGGGCTGGCGGTCCGGCGCCGGAATCGGCGGAGGAGCTT

>RXN02547

TTGGAGCTCAACAACGCTGCGCGGCTGACCGTGGATGAGTATCCGGCGGCGAGGGAAGCG  
CTTGAATCTGCAGGTCAGAGGAATGTAGAGGACCGAACCCGTGCGGTTGATGAGTTCAAA  
GCGGCGGATCAAGAGCTGTCTTCTTTGAGTAAAGGCAGCAGTAATATTGAGTACCGTTTG  
CTGCAGGTGCGGGAAAATTTGTGTGAGGATTTGGGCGTGAGCCCGCGGGATATGCCCTTT  
GCCGGTGAGCTGATTGATCCGAATAATGCGGAATGGGAACCCGTTGTGCAGCGCATTTTG  
GGTGGTTTTGCTGCGGAAATGTTGGTTCCTCATGGGTGTTGCCACGGGTTTCGGGATTGG  
GTAAATGCCAAACATTTGGCAGCGCTGCTGAAATTC AACGGCGTGGTGACAACGGGGGAG  
TACAAAACCTCGCGTTTTCCGGCGGATTCCCTGATCCGAAAAGTTGATGTTGTGGAGTCG  
CCGTTTTCGCGATTGGGTAAATCAAGAATTAGGCAAGCGTTTTAATATTCGGTGCGTGCGC  
ACTCCTGAGGAATTGTGCGCGCTGGGGCCACGCGATCAGGGCGTGACCATTTTGGGTGTG  
CGAAAATTTGCGCAGCAGACAGGCGATCCGACGACGCGTTGGGAAAAAGATGATCGCCGA  
AAGCTGGGGGATCGTTCCACATAACCGTTTGGGTTCACCAATGATGCCAAGGTGGAAACG  
CTTCGGGAAACCGTGAAAGCTGGCAAAGCAGTTGTGCAGGCAGCTGATAATCGCATTGCT  
GCAAACCGCGCTGAGCTGCGGGAACCTGAACGGCAGTATCAAGCTTCGCAAGAAATTTTG  
AAAGTGTCGTGGGCTCAGATTGATGTGAATCAGCCGACGCGGCGATTGCTGAGCTGGAC  
CGATTGCTGGAAGAGCTGAACAACACTCCAGAGGCCACCGAGCTTTCCGCGCGGCATGAG  
GCGGCGAAGCAGACGCTCGCGAGGGTTTCTGACTTGCTTGTGCGCAGCTCAGAGTGAGGAA  
ACCGTGGCGTCGATGAACCTGAAACGCGCCGAACTGAATTGAAACGGCTCGAAAGCCTG  
CCGGTTGCGGAGGTTTCTGAAGAAATCGCGCGGGAAGTGGAGAAACTATTTCTTGCCAAC  
ACCCGCCGGGTTACGCGCCCAACGTGGATGAGCAGACCATTTGCGCTGCGCGAGGATCTG  
GACAAACAAATCGATGCCAATGAGGCAGAACTTCGACGTTGTGAAAACCAAATTGTTGGC  
ATTTTGCGCAGCTATATTGAAACGTGGCCTGCGAACCGCGCTGACTTACAAGCCGAACCT  
GAGTTTGTGTTGGTGAGGCCATCAACCGCCTCGGCGAGCTTCGCGAGCGATCGTTTGGCAGAA  
TTCACGGCCAAATTCCTAGGGCTCATGAACGAGATGTCCACCCGAAACCTCGGCCAAATC  
TCGCGGCGTCTACGTGATGCGCGCCGGGAAATCGAGGAGCGCATCGAGCCGATCAACGCC  
TCCTTGGCGCAGTCGGAATTC AACGAAGGTGCGTTCTTGCACATCGACATCCGTGATCAA  
AGTGGTCCGATTGTGAGGGAATTCAGCAGAACTTGATGCCGCTACCAGCGGTGACCTG  
GGAACCAGTACCGAGAAACAAGCCTTCGCCCCGTTATGCGCTGATCGCTGAAATCATTTC  
AAACTCGCCTCCCACGACTCCGCGGACGCCCCGCTGGCGCAACACCGTTCTAGACACCCGC  
CGCCACGTTTCGTTTCATCGGCCTCGAGCGCGATTCCGACGGCGCAACCGTCAACACCTAC  
GTCGACTCCGCATCACTTTCAGGCGGACAAGCCCAGAAGCTGGTGTCTTCTGCTCGCC  
GCTGCCTTGCCTTACCAGCTAGCCGAACCCGGCGCCCATTTATCCACCTACGCCACCGTC  
ATTCTGGACGAAGCCTTCGACCGCGCCGACCCCGCCTTCACCCGCCAAACCATGAACGTC  
TTCCACAGCTTCGGCTTCACATGGTGCTCGCGACCCCGCTGAACTTATCCAAACCCTC  
GGCGATTATGTCGGCTCCACCATCGTGGTCAGCTACACCGAAAAACCAAACGCCAGGGC  
GCAATTCAGGGCAATTCCAGTTTCTCTAGGATCGAGAAA

>RXN02547-downstream

TAACATGCCATTGTTTATCGACG

>RXN02566-upstream

GACTCCGGATGATCAAGCAGCGAAACCTTTGTCAAGAACATAGCTCCCCACCCTAGACAA  
AAGCCCAAATAAATCTGCTCAATAACCTAACCTAAAGTCC

>RXN02566

ATGCACGCCTCGTCGCCCCAACCTCACCTCAGCGCACCCGTGTTCTCAGCGGCCTGATT  
TTCGCCCCAAATCATGGTTGGTGCATCCAATGGCGTGACGCTATCGATGGGAAGTTTGCTG  
GCAGCACACTTGGCGGGAGCTTCGTGGGGAGGATCAGCCGCCACATTGACCACGATCGGC  
GCAGCTATCTTTTCGATTCCCCCTTGCCCGCATGGTCTCCACATACGATCGCCGAACCTCA  
CTCAGCACGGGCATGTTGCTTGGTTGCGTGGGCGCACTACTGGCGATCCTCGGCGCACAA  
TTCGGCTTGTTTCCAGTAGTACTTTTGGCATTTTTGTTCTCGGATCCATGTCGGCGGTT  
AACCTCCAAGCACGTTTCGCGCGAACCGACGTGGCCAGTGAAGAAACCCGCGGCCGCGAC  
CTCTCGATCGTTGTGTGGTCCACCACCATCGGCGCAATCGCCGGACCAAATTTATTTGAA  
CCAAGCGCCCGATTTCAGCGAAACCTGGGCCTCGAACAAACATGCCGGCGCATACCTGCTG  
TGTTTATTTGGCCAGCTCATCGCCATCGCAGTCTGGCGATTACCCCTCCCCAAAGGCCTC  
AAACCCGAAGCCACCCCAAATGCACCAACAGAAAAGAAGCGCCTCACCCCGAAAGCCCTC  
CAAGCCATCACATCGGTTGCAACCGCACACTTCTCCATGGTCTGCTCATGTCCATGGCC  
GCCATCCACATGCAAGGCCACGGCGCCAGCCTCACCATCATCGGCTTCACCATCAGTTTG  
CACGTCGCCGGAATGTACGCACTCTCACCAGTGTTTCGGCCTGCTCACAGACAAACTCGGC



CGCAATGTCACCATCTATTCCGGCTTCGCCATGCTCGCCACATCCGCAGCATTTCTTATC  
 ATTTGGCCCGAACCACAGTGGGCCATGATCACATCCATGATCCTGCTTGGGCTCGGCTGG  
 AACTCTGCCCTCGTCGGTTCTTCAACATTGCTTGTGACGCCACCCCATCCACCACCGC  
 ACCTACGCCCAGGGGCGCAGCGACCTAACGATGAATCTTGCGGGAGCTTCAGGCGGGTTG  
 ATCGCCGGACCGTTAATTGCCATGGGCGGAATGCCCTTGTGAGGCGGTCGTTCTTGCA  
 GTTGTGGCGCTTCAAACGGTGCTTAGTTTCAGAACCCGTTCAATTGAAAAGACTCCTGCT  
 TCATGTTTT

>RXN02566-downstream  
 TAGCCTAGGAATTCACGCACGAC

>RXN02571-upstream  
 TGGACAGGCCGGGGCCGCGTACGGTGTGTTGAGGTGGTGGAGGGGCGCGTCGAAAAGC  
 ATTGTCGCTGGTTGTTGCCGCTTTTGGCAGTCGGGATGGC

>RXN02571  
 GTGGTGGCTCTAACTCAAATCGTCGGACCGTCCGGCTCCGGGCTCACGCGGGAATTGGAA  
 AAACGCTACCGGGAAACGCCCGGAGCGGTGATGCTGACCGCCGACCCGCGCGCATATC  
 ACCTACCTGCGCGCGACAGTCGCCGAGGAGCTGGCCTTTGGGCTGGAACAACGCGGCATC  
 GTACCCGCGCAGATGTGGGAGCGCGTCCGAAACATCGGGCTCGGCCTCGAGAATCTGCTA  
 GACCGCGCACCCGCGCAACTTTCCGGCGGGCAAACACGGCGGCTGGCGATCGGCACCGTC  
 GCCATCTTAGAGGCGCCAACGATGCTTCTCGACGACCCCTCTCCGGTCTTGATACCTCC  
 TCGCGAGCCCAACTCATCACAATGTTGGAATCATATGAGGGCGATGTCATCGTCGCTGCG  
 CACAAGCGGTGGCTCGACGCGCCGACTGTGTACTTAGGGGATTTGGAGGAGCTGTCCCTG  
 CCTGCGCGGGTGGAAATTTCCGGTCCATCGCGAACGTTTTTCAGCGATTACAGGAACCCGC  
 GGACAACAACGCCGACGCTGGTGGCAATTCAACGAATCCCAACCACAGTTTCAGATCGGC  
 CCCCTGGATATTACTGTTTCTGCAGGTCAAGTGCTGTGGTTGCAGGGTCCCAATGGTTCA  
 GGGAAGTCCACACTCCTGCGTGGTCTTGCCAATGAACCCGGCACTGAATTGATGCTGCAA  
 AACCTAGCGATCAAGTCATTGACTCCACTGTTGCTAATTGGGTGCCAGGCAGTAACAGT  
 GAAGAACATCCGCTGGATTTATCGCAACGCGAACTCCGCCTTGCCCAATGCGACGCAGCC  
 CTGGGTAATAACCCGGAAGTTTGTCTGCTGATGAACCCGACGTCGGCCTTGATGTCGGC  
 GGTCGAAACGCCATCCACCAGCGCTTTGCGGATTTCTTAGGGAATGGGGGAGCGCTGATC  
 CTGACCTGCCATGATGAAACCTTCGTGGCAGAGGTAGCTGAATACGCGATAGTGAAGGAA  
 ATGGGGCTC

>RXN02571-downstream  
 TAGGTTTCTTTGGACCAAACCAC

>RXN02581-upstream  
 ACGGTCACTCGCTCAAGTAGTGTTAGTTTGCAAAAGTAATAAAATGTTTCATCTTTGTGCA  
 TGGTCACAATAGTCATTAAAGAATTGTAAGAGGGGTTAC

>RXN02581  
 ATGGATTTAGATAAAGCGATTGGTTCATTCTTCGATGAGAATGGAGAAATCAACCTTCCT  
 CCATTCCTAACTTTGGCAGCCATGGGTGAGTTCATGTACCAGGCTGACATCGCTGAAGGC  
 GGCGGGGATAAACCACGCATGCATTTCTGGGACTTCTCCGAAGACCGCGATGGCAAGCTG  
 ATTCAGTACACCCGAAACGAGATCGATACTCGTATCAAGGCTGTAGCAGGCCGTTTGCAG  
 CAGGTGCGCACCCCTGGGTGATCGTGCAGCGATCCTGGCTAACAACAGCCCTGAGTACATT  
 TTCAGCTTCCTCGGCGCGATCTACGCTGGCATGGTCCCTGTGCCGCTTTATGATCCAAAC  
 GAGCCAGGACACGCAGACCACCTCAACGCTGTTTTCGCAGACAGCGAGCCAGTTGTCGTT  
 CTGACCAACTCCAAGTCCGCAGGTGCCGTGCGCAAGCACTTCTCCAGCCTTCCAGCTGCA  
 GAACGCCACGCATCCTCTCTGTAGATTCTTGCTGATTCTCTCGCGGATTCTTACGAG  
 AACCCAATGCTGACCGAAGCCGGCCGCGCCTGGCTGCTCTGCGCCAGTCCGCGCCCAT  
 GATCTGACCGCATTCCTGCAGTACACCTCCGGCTCCACCCGAACCCAGCTGGCGTTGTT  
 CTGACCAACCGCTCCATCCTGACCAACGTCTTGCGAGATCTTCAGCGCCGCACAGCTGAAA  
 ACCCCACTGCGCCTGGTTTCATGGCTGCCACTGCACCACGACATGGGCATTATCCTCGCG  
 GCGTTTGTCACTATGCTTGGCCTGGACAACGAGTTCATGAACCCACGCGATTTCGTGCAG  
 CAGCCTTCCCGCTGGATTAAGCAGCTCAACCGTCGCGAAAGCGACGTGGACGTTAACGTC  
 TACACCGTGGTTCCCTAACTTCGCCCTCGAGCTTGCGAGCACGCTACGCAAAGCCAGCAGAG  
 GGAGAGACCCTGGATCTTTCCGCATTGGATGCCATCATTATCGGTTCCGAGCCAGTCACA  
 GAAAACGCTCTGACCACCTTCCGTGAAGCTTTTCGAGCCTTACGGCCTGCCTGTTTCAGACC

CTGCGTCCTTCCTACGGTCTTGCAGAAGCATCCCTGCTGGTCACCACCCACAGACCGAA  
AACCGCCCACTGATCTCCTACTTCGACCGCGAGGCCTTGGCCGAAAACCGCGTTGAGCTT  
GTAGAAAAGGGCAATAACAAGGCTGTTGCTTTCGTCTCCAACGGCCAGGTTGCAGCCCCA  
CAGCAGCTGGTCATCGTTGATTCCGAAACCGGAACCGAGCTGGCAGACGGCCAGATCGGC  
GAAATCTGGACCCACGGCGAAAACACTGCTGCAGGTTACCTCGACCGCGAGGAAGACACC  
GCAGAAACCTTCCGCAACCGTCTGACCACCCGCCTGGAAGAAAACCTCCCGCGCAGAAGGT  
GCTGCCGACGACAACTACTGGATGGCCACCGGTGACCTCGGCGTCATCGTAGACAACGAG  
CTCTACATCACCGGTCTGTGAAGGACCTCATCGTTGTGCGAGGCCGAAACCACTACCCA  
CAGGACATCGAGTACACCGTCCAGGCTGCTTCCGACACATCCGTGCAGATTCCGTGCGA  
GCATTTCGCAGTCCCAGGCGATGACATTGAAAAGCTCATCATCCTGGCAGAACGCGACACC  
ACTGCAAACGAAGCCGACGATGCAGCTGCTGAAGAAGCAATCCGCTCCGCCGTTGGCACT  
GCACACGGTGTGTTCCAGAAGAGATCCGTATCCTCGCACCTGACGAGATCGCGCGTTCC  
TCCTCCGGAAGATCGCACGCCGCGTCAACCAGCGCAACTACATTCAGGAACAAGCTAAC

>RXN02581-downstream  
TAGTTCTTTGCAGACACCGCAGG

>RXN02595-upstream  
GTGGGTAAAGGGGACTCCGAGGAAGTCCACGTCGTCTTCTTTCGCGGCGCTGAGGATGGT  
TTCGCGGATTTGTGCGGGGGAGTGGGTGGGAGAGAAAACG

>RXN02595  
GTGATCGTTGTGGCCATGGCTTCCATTATGGCTTGTTTAAAAGCAGCTAGACTGAATAAC  
CCTATGAAGATCCTTTTGTGTGCTGGCGTGATACTCATCCTCAAGGTGGCGGAAGT  
GAACGCTATCTGGAGCGGGTGGGTGAGTTTTTGGCGGATCAGGGCCATGAGGTGGTGTTT  
CGTACTGCTGGGCACACGGATGCGCCACGGCGTTCTTTCGCGATGGTGTGAGGTATTCC  
AGGAGCGGTGGGAAGTTTAGTGTGTATCCCAAGGCGTGGGTGGCCATGATGTTGGGTCTG  
GTGGGGATTGGCACGTTTTTCCAAGGTTGATGTGGTGGTGGATACGCAGAATGGCATTCCG  
TTTTTTGGAAAGTTTTTCTCCGGTAAGCCGACTGTGTTGCTCACGCATCATTGCCATAAG  
GAGCAGTGGCCGGTGGTGGGTGCGGTGCTGGCGAAGGTTGGTTGGCTGATTGAGAGCCAG  
ATCGCGCCGCGCGCTTACAAAACCTGCGCCGTATGTGACTGTTTCAGAGCCGAGCGCTGAG  
GAGCTCATTTGCGTTGGGTGTGGATCAGCAGCGGATTCATATCGTGCAGCAATGGCGTGGAT  
CCCGTGCCGCTGCACACGCCGAAGCTGGATCGCGATGGCCAGCATGCGGTGACGTTGTGCG  
CGCCTGGTTCCGCACAAGCAGATTGAGCATGCGATGGATGTCGTGCGGGCGCTCGACGGC  
GTGGTGCTGGATGTAGTCGAAAGCGGTTGGTGGCAGAAGGAACTGGTCGATTATGCCCCG  
ACGCTGGGTGTGAGCGATCGCGTGGTTTTCCACGGCCAGGTCGCCGAGGATCACAAGCAC  
GCCCTGTTGGAGCGCGCCACGATTCATCTCATGCCTTCGCGCAAGGAAGGCTGGGGCCTG  
GCGGTACAGGAGGCGGCGCAGCACGGCGTTCCGACGATCGGTTACCGAAGCTCAGGCGGC  
CTGCGCGATTCCGTGTCGACGGCGAAACCGGCCTGCTTGTCGACTCCAAGGCCGAGCTT  
ATTTACAGCCACCAAAACCTGCTTATCGACGCCTCCCTCCGCTCCAAGCTCGGCGCCAGC  
GCGAAGCAGCGCGCCGAAAACCTACAAGTGGGACACCGCGGGAGCGCAGTTTCGAGGAACTA  
CTTCTTGGTCTTGCCTCGAAAAAG

>RXN02595-downstream  
TAGTCCCAGCGGCAACGCCATCC

>RXN02613-upstream  
AGATATCCCCGGCGATCGCCGCACCCACCCCTCCTTTGCCTCCTACACCGCTCAACTCCT  
TGAGTGGCTCGAAATCACACACCTGCCTAGAAAGAAATC

>RXN02613  
ATGAAATTTAAGAAAATCGCCCTCGTTCTCGCCTTCGGTCTAGGCCTTGCATCCTGCTCA  
TCAGCTTCTGGCGATCCCGCCACCAACGCCGATGGATCCATCGATCTGAGCAAAGTAACC  
CTTAACATCGGTGATCAAATCGCCGGAACAGAACAAGTGCTCCAAGCTTCAGGGGAGCTA  
GATGATGTCCCTTATAAAATCGAATGGTCATCATTTACCTCTGGACCACCCCAAATCGAA  
GCATTAAACGCAGGTCAAATTGATTTGCGGATCACCGGAAACACCCACCGATCATCGGC  
GGCCCCACCAACACCAAAGTGGTCTCCGCCTACAACAACGATGCTTTAGGTGATGTCATC  
TTGGTTCGCCCCGATTCTTCAATAACCTCGGTGGCTGACCTTGCTGGAAAGAAAGTGGCT  
GTCGCCCCGCGGATCCAGCGCCACGGACACCTCATCCAACAACCTAGAAAAAGCAGGCGTG  
AGCGTTGACGACGTAGAAATCAACCTCCTCCAACCTCCGACGCCAAAGCCGCTTTCCAA  
AACGGCCAGGTAGATGCGTGGGCAGTGTGGGATCCCTACAGCTCACAGGCGGAACTGGAA

GGAGCTCAAGTTTTGGTCAGGGGAGCGGGACTGGTCAGTGGGCATGGATTTGGTGTGCGCA  
AGTGATGAAGCGCTCGATGACCCCGCAAAGGAAGCCGCCTTGGCAGATTTCTTCGATCGC  
GTGGCCGACTCTTATGAATGGGCTGAAGACAACACCGATGAATGGGCGACGATTTTCAGC  
CAAGAATCCGGCTTTGATCCGGAGGCCTCTCAACTGAACACCCGCAGCCTGCGCCATCAG  
GTGCCGCTCGACGAGTCCGTCAACACCTATCAGAACGCGCTTATCGACGCTTTTCGTCTCC  
CGGGGTCTCGTTGAGGACTTTAATTTTCGAGGACACCGTAGACACCCGATTTGAGGGC

>RXN02613-downstream  
TAAGTATGTCTGAGTATGGCAA

>RXN02614-upstream  
TCATTGTATACGCCACCCTCGGTCTGCTGTCTGAAGCGCTGATCAGAGCTTGGGAACGTC  
ACACCTTCCGCTACCGAAACGCATAAGAAAGTTGCTCGCC

>RXN02614  
ATGACTGCCACATTGTCACTCAAACCCGCAGCCACTGTCCGTGGATTGCGCAAATCATAC  
GGAATAAAGAAGTCCTCCAAGGAATCGACCTCACCATCAACTGCGGCGAAGTAACCGCG  
CTGATCGGACGCTCAGGTTCAAGAAAATCCACCATCCTGCGCGTGTGGCGGGCCTATCT  
AAAGAGCATTCCGGCTCTGTAGAAATTTCCGGAAACCCGGCCGTTGCCTTCCAAGAGCCT  
CGCCTGTTGCCGTGGAAAACGGTGCTCGATAATGTGACCTTTGGCCTCAACCGCACTGAT  
ATTTCTGGTCAAGACACAAGAACGCGCCTCGGCACTGCTTGCAGAAGTCAAACCTCCC  
GACTCCGACGCCGCTGGCCCCCTCACGCTCTCCGGCGGCCAAGCCCAGCGCGTCTCCCTT  
GCGCGAGCGCTCATCTCCGAGCCAGAGCTTTTGCTTCTCGACGAACCCTTCGGCGCCCTC  
GATGCTCTGACAAGACTGACAGCCCAAGACCTGCTGCTCAAAACCGTGAACACCCGAAAC  
TTGGGAGTTCTGCTGGTCACCCATGATGTTTCCGAGGCCATCGCCCTGGCCGACCACGTC  
CTTCTTCTTGACGACGGCGCCATCACACACAGTTTGACTGTAGATATCCCCGGCGATCGC  
CGCACCCACCCCTCCTTTGCCTCCTACACCGCTCAACTCCTTGAGTGGCTCGAAATCACC  
ACACCTGCC

>RXN02614-downstream  
TAGAAAGAAATCATGAAATTTAA

>RXN02638-upstream  
CTCTGTTGTTGTTTCCTGAGGCGCTTCGTCCATTTCGTGGGCAAAGACGTGCTCAAGCCAGT  
GAAACAAGCCGGTTAATTAAGCGGAAAGCTCGTGGTCGAC

>RXN02638  
ATGGTCAAAAGGTTTGGCTTTTTTCGTAGAGGATTCCCTGCCTAAGGTTCCGCTGCATCCC  
GAAGAGTCACGGGAGACGTTTTATGGGCGCATCATCATTAGTGCTGTGCGGACGGTGATG  
AAAGCCCAGGATGTGCAGATTTCCATCTTCGGTGCGGAGAACATTCCGACCACCGGCGGC  
GCACTTTTCGCATCAACCACACTGGTTATTATGACTTCATTCTGGGTGGTATCCCCCGCA  
TTCGTGCGGGGTAAGCGCCTGGTTCGATTTCATGGCGAAGAAGGAAATTTTCGACACCCCA  
GTTGTGCGCACCCCTCATGCGCTGGATGAAGCACGTCTCTGTGGACCGCTCCGCAGGTGCC  
GGTTCATGGAAGATGCGCGGAAGCGTCTCGACGCGGCGAGCCTCGTCGGTATCTTCCCT  
GAGGCGACGGTGTCACGGTCTTTTGAATCAAGGAACATAAACTGGCGCCGTCCGCATC  
GCCGACAGCGCTAACGTTCCGCTGCTGCCACTTATTATTTGGGGCGGCCAGCGCATCATC  
ACCAAAGACATCGAGCGCGACTTCGGCCGCTCCACATCCCCGTATTCATCAGCGTGGGT  
GAACCCGTCGACGCCAGCGGCGATCCCGACGAAGCAACGGAACGCCTCTACGAGGCTATG  
AAAAAGCTTCTCGACGAAACCCGCACCGCCTACGAACAAAAGTATGGCCCATTCGAAGGT  
GGAGAATTGTGGCGCCCGAAATCCCTCGGCGGCGGCGCCCCAACGTTGGAGCAGGCGAAA  
ATGTTGGAAATCGCCGAACGGGAACGTCGACAAGCAAAACGCGCGGCAAAGGTCGCCAAG  
AAACGCACCACCTTTATAAGGAAAATCTTTAAAAAA

>RXN02638-downstream  
TGATTGCACTGGGTTTCAGCGCCC

>RXN02662-upstream  
CCAAGGTGTCACCCTCACCCTGTCATCGCCTTCATCATCGTCAATATCGCCGTGGACCT  
GCTCTACGTCCTGGTCAATCCACGTATTAGGAGCATCTAG

>RXN02662

ATGCGCCGTAAACTAACCACCACATTAGAAAACAAGCCCGGTGCACGACTTGGTGGCTTC  
CGCGCACTTGCACCAACTTCAAAAATCGCGCTGGTTTTCTTCTCCTGATCTTCCTCCTC  
GCGATCTTTGCCCCACTGATTGCTAAATACGATCCACTGGCCTCCGGAACCTCCAGTCCAG  
CCTCCAAGCGGTGAGCACTGGTTTGGTACCGACGCCATCGGCCGCGATATTTTCTCCCGC  
GTAGCCACGGCGCCAGAGCCTCCC

>RXN02662-downstream  
TGATCATTTGGTCTTTTCGCTACG

>RXN02794-upstream  
GCGCCCACTCATCGGCGAGCTTCAGGAGATGAGGTTGATGCTCCATTGATAATTTCTTTC  
GCTAATAGTCAAATGATCATTTGAGTGTTAGTGTTTTCTC

>RXN02794  
ATGCTTCTTTCCGCCCCGACACACACGAGTTTCCAAGAACTTGGACTCAATGCTAGTCGG  
CGCAAAGCAATCAACTGGACACTGGCACTCACTGTGGTGCTAATTGCCTCCATGTTTGTT  
GGCGTGCTCATCGGTGCATCCGGGACCTCAGTGTTTTCCACGTGGACCGTAATTAGCCAC  
CATCTTTTTGGCACTGAGCTAGGTGGCTCCGACACTGCCGACGCCATCATTTGGTACATC  
CGCACCCACGCGTCTTGCTCGCTGCCATTGTGGGCGCAGGCCTTGCCCTGGCAGGTGCC  
ATCATGCAAGTACTGGTCCGAAACATGCTGGCAGACCCCTATATCCTCGGGGTGAACTCA  
GGTGCCAGTTGCGGTGCGGCCGCTGCCTTACTGTTTCGGAGTGGGCGCTGGATTTGGCGAT  
TACGCCCTCCAAGGCAGCGCGTTTCTCGGCGCAATGGCAGCTTCCGGATTGATCTTCTTC  
GTGGCGCGCGCAGCGGGGCGCATCTCCTCGACCCGCTTGTTGATGTCCGGCGTAGCGATC  
GGATACATGCTCTCTGCGGCAACAAGCTTTCTCATCTTCTCCTCCGACTCCGCCGAAGGC  
AGCCGCTCCGTGTTGTTCTGGCTGCTTGGATCCTTAGGACTTGCCGCATGGAATGGGCCG  
ATGGCGATCATCTTCTCATCGTGGGCATTGCCCTGGCGTTGCTCATGGTGTGGGTCCG  
CAATTGGATGCCTTAAACTCCGGCGATGAAACCGCACTTACCTTGGGAGTATCCCCTGAT  
CGCCTCCGCATTCTCCTCCTGGTGATCACCTGCCTGCTGGTGGGATCCATGGTTGCCATG  
GCCGGCAGCATCGGATTTCATCGGCCTTGTCATCCCCACCTGGCCAGGCGTTTTGTTAGT  
GGAAAACACCGACTCATGCTGCCTGTATCCGCGTTGATGGGCGCAATTTGCTCATCTGG  
GCTGATATCGCCGCCCCGACCCCTGCTTGCGCCCCAAGAGATTCCCATCGGCATCATCACC  
GCACTCATCGGAGCACCCCTTCCTCCTGATTCTGGTTTCGCCGGATGCACACCTAC

>RXN02794-downstream  
TGATTTTTAAGGAATTATGCGTA

>RXN02809  
AACCTCTCCGTCCCAGCAGCACTAACCAACGCCCTTTCTTACCTCTCCGCAGAGTGGAAC  
AACAAGGCTGCAGGCATCGTCTCCTACGGCTCCGCAATGGGCGTTTCGCGCAGCTGAGCAC  
CTCCGCGGCATCCTTTCCGAGCTTCAGATCGCACACGTTCAAAGACCGGCCTGCTGAGC  
ATCTTCACCGACTTCGAATACCCTAACTTCAAGCCTTCCGAGCAGGGCATCTCCTCTGTG  
GACGCTATGCTTGAGCAGCTTGTTGTCTGGACCAAGGCAATGTCCACCATTGCGGAGTCT  
GCGAACGTCTATCACTTAAGAACCCTCACAAAAGTGGCGAGCTCCCCGACTGGGACTCG  
CCTCTTTTCGTATTC

>RXN02836-upstream  
CCATCACTCGGCTTCACCGTCTACGGTGCTGCCCCGAGGACAGAGCGCCCCCAAAGCTC  
GCTTCAGACGGGATCCACCCCTCGAGATGGACGTCACCG

>RXN02836  
ATGACAATCGATGAAGGCCGTCGCCAGTTCGAGGTCAATGTATTCGGCGCGATGGCCCTC  
ACCCGACTCGTCCTGCCCCACATGCAGAAACAAAAGTGGGGGACGATCGTGAACATCACA  
TCGATGGGCGGGAAGATCTACACGCCTCTCGGCGGCTGGTATCACGGCACCAAGTTCGCC  
CTCGAGGCCCTCTCGGACGCCCTCCGCCTGGAGGTGCCCCATTTCGGCATCGACGTTGTT  
GTCATCGAACCAGGCGGCATCGCCACCGAGTGGGGAGGAATCGCTGCCGACAATCTCGAC  
GCAGTGTGAAAGACAGCGCATAAAGCGCCAGGCTGACGCAGTATCGAAGTCGTTGCGA  
TCTGAGGCGAACAGCAACCGCAACTCACCACCGTCGGTTGTCGCCGATGCGATTGGAAAG  
GCCGTGACGGCACGTCACCCCAAGACCCGCTATGCCATCGGCTTCGGTGCCAAACCGCTG  
ATTGCCTCGCGCAACATCCTCACCAGTCGCCAGTTCGACCCAGTGATCACTCGAGCGACT  
GGCGTCCCCCGCGAC



>RXN02836-downstream  
TGACCACTCTTCTGCGCCCGTCA

>RXN02922-upstream  
CCCACCGCGGCGCAAGCTACCGCCTAGGCGCTCGGAACTCCACCGCCACTATTGATCTCA  
GTTCCATATCCGCCCAACTAGTTTCCCAGGGAGCCCACTC

>RXN02922  
ATGATCTCACCGCAAACAATCATCGACAATCTTGCTCCAGTCCTCGCGGAGATCGCAGCA  
ACGGCTGCGCAGCGCGAACAGGATCGAGAATTCAGCCGTGATTTGGCAAAGCAGCTTAGT  
GCCGGTGGGTTCATAAATCCGCATTCCAGTTGAATTTGGCGGTTTGGGTTTTAGCCTT  
CCAGAAGCATTTGAGGTGCTGGTGGCAGCGGCCGCTGCAGATTCAAATATCGCGCAGGGA  
TTGCGGCCTCACTTCTTGCGAGTGGAGAGCTTATTGATCGCTCCTTATTTCAGAGCACCGC  
ACCAAGTGGCTGCGAAAAATCGCTGAGAAAGGCGTGGTCATTGGCAATGCGTTGACTGAA  
GTGGGAAACAAGCCAGGTGAGCTGAAAACCAAGATCCGAAAGGAAGGCGAGTCTTACGTT  
CTCAGCGACACCAAGTTCTATTCCACGGGCAGTCTTTACGCCGACTGGATTCAAGTACAT  
GCGAAAGATGAGGAAGATCAAGATGTTTTCGCCTTTGTTGATCGCGACGCATCAGGCGTT  
GTTTTGGTGGATTACTGGGACGAATTTGGGCAACAATTTTGCTCCGGAACCAGCTTC  
TTTGAAAAAGTCGTGGTAGATCCACTGGACATTGTACCCCGTGATTACACCGCACCCAGC  
GCTTTCCAGGCGCTGGCGCAGTCACATCATTTGTCTACGTTGACTGGTATTTTCGCAGGCA  
ATCACCCGTGACATTGTTACCTATGTACAAAACCGCACCCGTATTTTCAGCCACGGAAGT  
GGTGACCTTCCACGCTTTGATCCGCAGGTGCAACAGGTGGTGGGTGAGGTGAAAGCCAAG  
TCGTATGCAGTCGAGAAAATCTTTCAGGGTTTCGCACAAGAACTGGATCTTGTCGTCGAT  
AAGGCAAAAGCCGGCACTGCTACGGAGGTCGATCTGGCCGCTGTCGACCTGAGCGCCTAC  
CAAGCCCAGTTAGCGGTGGCACCTTTGGTGCTGAGCCAGGCCACCCAGGCCTTTGAGGTT  
GGCGCAGATGCCTTAAACGGCGGCCACGTGGCTGCCCAATACACGATCGGATCCTTGTCAT

>RXN02922-downstream  
TGAGCCAAGAAATTTTGAGCCAT

>RXN02923-upstream  
GCATCTACATTGAAGGAATCCACGGAGCGCGCATCGAAGACATCGTTGTGGTGAATGAAG  
ACGGTTGTGAAACCCTCAACAACCAGCCCAAGGAACTGCG

>RXN02923  
TTGAGCATTCTTCTCCTAGGCGGAACCTCTGACATTGCCGGTGAGATTGCCACGTTGACG  
TGTCACGGCGAAGACGTTGTTTTGGCTGCTCGTCGACCAGAGGCTGCACAGGGCTTAGCG  
GAAGATCTTCGACAGCGCGGTGCCACATCTGTTTCATGTTTTGAGCTTTGACGCCCAAGTA  
CTAGACACGCACCGAGAACTTGTGAAGAAAACACAAGAGCTAGCTGGCGAGATTTCCCTT  
GCCGTGGTTGCTTTTGGCATCTTGGGAGACCAAGAACGCGCAGAAACCGATGAGACCCAT  
GCGGTAGAGATCGCCACCGTGGATTACACCGCTCAGGTCTCCATGCTCACTGTGCTTGCT  
GATGAGCTCCGCGCACAACTACTCCAGCAGCGATCGTGGCGTTTTCTCTCGATTGCTGGG  
TGGCGGGCGCGCCGGCCTAACTATGTCTATGGATCCACCAAGGCTGGTCTCGATGCATTT  
TGCCAAGGGCTTGAGATAGCCTGCATGGGACACACGTGCGATTGATTATTGCGCGTCCT  
GGCTTTGTTATTGGTTCTATGACCACGGGGATGAAGCCTGCTCCGATGTGCGGTGTATCCA  
CGAGATGTTGCCGCAGCTGTTGTTAGTGCTTATACCTCTAAGAAGAGGAGCACGACCTTG  
TGATTCCGGGACGTCTGCGGGTTCTCGCCTGGATTATGCGGATGGTTCTCTCGTCCGGTG  
TGGCGGAAGATGCCACGC

>RXN02923-downstream  
TAGATACCCGTTTCAGCCCTCACA

>RXN02929-upstream  
CAGGTGGGGACCTCGCGTATCCCAGCTGGTGGAAAGAAATCGCAGCGCAGTTGAATCAGCT  
TGCTTCTTCTGAAGCTGTGCCGGCCGCTGCTTAAGTTTTT

>RXN02929  
GTGCTGAAGAGAATTTTCTCAACCCCTGGGTGGCTACCGCGTTGTCCGTTAGTCATTTTG  
GGGTTTGTGGTGCTGTTTTAGGTTTTCAGGTTTTCAGCGGTGTTATTGATTTAAGCCCCACAGCAGTG  
ATTAGACATTTGAGTGGGCAGGACACGCTCACCCCTCGAGATCAGGCCATCTTCTTTGAT  
ATCCGGCTGCCTCGAATTATCGCTGGTGTCATTGTGCGAGCAACGCTGGCTATTTCTGGT

GCTTCTTACCAAGCGGTATTTAGAAACCCGCTGGCTGATCCTTATTTGTTGGGTGTGTCC  
GCAGGTTCTGGCCTTGGTGTACGGCAGTGATTGTTGGCGGTACCGTGCTGGGATTTTCT  
GCACCGAGCATCGGCGTGATTGGTGCAGCATTGTAGGTGGTGTGGCCGAGTACTTGCC  
ACGCTGATGGTGAGTCGGGGAGTAGGACAGGGATCATCAACCACCGTGGTTATTTTGGCG  
GGCGTGGCGGTGCTGCTTTTGCCAGTTCCATCCAGACCTATATTCAGCAACGACACATC  
GATACGGTGGCGCGCGTATATGTGTGGATGTTGGGCAACCTCAATGTCACCAACTGGATG  
TCGATCTTCATCGTGGCTGTGGTGGCGGGACTATGCGCGGCCGTGATCATGTCCTGCGCC  
AGGTTGTTAGACGTGATGGCTGTTGGTGATGTGGAAGCCCGCACATTGGGCGTCGATCCA  
GGCCTCGTACGCATTGGCATTGTCATCGTGGCAACCCCTTGGTACAGCTGCAGTGGTATCC  
ATTTCCGGTCTCATCGGGTTTGTGGGCATCATTGTTCCGCACGCCCTGCGCCTAATTGTT  
GGCCCGGGGCATCGGATTTTACTGCCACTGTCTTTCGTATGGGGTGCCATTTTCCTCGTG  
TTGGCAGATACCGCAGGGCGAACATTGATGGCTCCTCAGGAACCTCCCGTGGGTGTGGTG  
ACAGCTGCACTCGGCGCACCGTTCTTCTTATTTATTTTGCAGACAACCAGCAGACAACGA  
GTTCCAAAAGGAGTGCT

>RXN02929-downstream  
TAAGTGGCGATCATTGAATGCGA

>RXN02933-upstream  
TGATCTGCTGTATCAGGTGGTTGATCCAAGAGTCGGTGCTGTTGGGGTTGCTAGCACTAA  
GGTTCCAGGGAGCGTGGCTTAAGTGACAACGATCAAAAAC

>RXN02933  
ATGCCCCCTTTCAGGGAAAATCGGCGGCTTCATCGTTGCCGTTGTATTTGTTCTTGCTGCG  
CTGTCTTTTCATTTGGACTCCGTTTGATCCAGTTCAAGCTTTCCACAGGAGCGCCTTGAG  
GGAAGTTCTTTGAGGCACCTGTTGGGAACGGATCGTTATGGTCGCGATGTTTTATCCCAG  
ATCATGGTTGGTTCCCGCGTCACGTTGTTGGTGGGCATCATTGCGGTGGCGATCGCAGCA  
TTAATCGGCACGCCACTGGGTATTGCTGCGGGAATGCGCCGTGGCATGGTGGAAACCTTT  
GTCATGCGTGGTGCCGATTTAATGTTGGCGTTCCCAGCACTGTTGTTGGCGATTATTTCC  
GGCGCCGTTTTTCGGCGCCTCCACGTGGTCCGCGATGGTCGCGATCGGCATCGCAGGCATC  
CCTAGTTTTGCCCCGCGTGGCTCGTGACGGCACATTGCAGGTGACCAGTCAGGATTTTCATC  
GCAGCTGCTCGGCTATCAAAAGTAAGTTCCGCCCGGATCGCGCTTCGCCATATTTTGCCC  
AACATCACCAGCATGTTGATCGTTCAGGCATCAGTAGCTTTTGCCCTGGCGATCCTGGCG  
GAAGCCGCATTGAGTTTCCTCGGTTTGGGCACCACTCCCCCGGATCCCAGCTGGGGTCGC  
ATGTTGCAAACCGCTCAAGCATCCATCGGCGTCACCCCATGTTGGCGGTGTGGCCCGGT  
GCTGCGATCGCTTTGACGGTCCTTGGTTTTAATCTTTTCGGTGATGGTTTACGCGATGCC  
ATCGATCCAAAGCGGGAGGTCGGCCGTGCT

>RXN02933-downstream  
TAAAGTTTCTGATTTAACGGTTG

>RXN02947-upstream  
GTATGTTACACAAGAACCCTGCACAACGCCTTCAAAGTACGTCGACCACGACCAAGCGC  
ATTATTCACTCTCACCCCTTCAGGATTTAGACTAAGAAACC

>RXN02947  
ATGACTGCAGCACAGACCAAACCTGACCTCACCACCACGGCTGGAAAGCTGTCCGATCTT  
CGCTCCCGTCTTGCAGAAGCTCAAGCTCCAATGGGCGAAGCAACTGTAGAAAAAGTGAC  
GCTGCTGGCAGGAAGACTGCCCCGGAACGTATCGAGTATTTGCTCGATGAGGGCTCTTTC  
GTAGAGATCGATGCTCTTGCTCGTCACCGTTCCAAGAACTTCGGCCTGGATGCCAAGCGT  
CCAGTTACTGACGGTGTGTGACTGGTTACGGCACCATCGATGGCCGTAAGGTCTGTGTG  
TTCTCCCAGGACGGCGCTGTATTCGGTGGCGCTTTGGGTGAAGTTTATGGTGAAAAGATC  
GTTAAGGTATGGATCTTGCGATCAAGACCGGTGTGCCTTTGATCGGAATCAATGAGGGT  
GCTGGTGC GCGTATCCAGGAAGGTGTTGTGTCTCTGGGTCTGTACTCACAGATCTTCTAC  
CGAACACCCAGGCGTCTGGCGTTATCCCACAGATCTCTTTGATCATGGGTGCCTGCGCT  
GGTGGTCACGTGTACTCCCCTGCTCTGACTGACTTCATCGTCATGGTGGATCAGACTTCC  
AAGATGTTTATCACCGGCCCTGATGTCATCAAGACTGTCACCGGTGAAGATGTCACCCAG  
GAGGAGCTCGGTGGCGCTCACACCCACATGGCTACCTCCGGTACCTCCCATTACTCTGCT  
TCTGATGATTCAGATGCTTTGGATTGGGTTTCGCGAGCTGACCTCTTATCTTCCATCCAAC  
AACCGTGCGGAACTCCTCGCCAGGAGGCCGACATCATGATCGGTTCCATCCAGGAAAC  
ATCAACGATGTGGATCTGGAATTGGACACCATCATCCCGGATCCCCGAACCAGCCTTAT

GACATGAAGGAAGTTATTTCCCGCATCGTCGACGACGCCGAGTTCTTCGAGATCCAGGAA  
 GACTACGCAGAGAACATCCTGTGTGGCTTCGCTCGCGTTGAGGTCCGTTCTGTTGGCATC  
 GTGGCTAACCAGCCAACCCAGTTCGCTGGCTGCTTGATATTAAGGCATCTGAGAAGGCT  
 GCCCGTTTCATCCGCACCTGCGATGCCTTCAACATCCCAATCCTTGAGTTCGTGGACGTT  
 CCAGGCTTCCTGCCTGGCACCAACCAGGAATTCGACGGCATCATCCGCCGCGGCGCAAAG  
 CTGCTTTACGCTTACGCTGAAGCAACCGTCGGCAAGATCACCGTCATCACCCGCAAGTCC  
 TACGGCGGAGCGTACTGCGTGATGGGTTCCAAGGATATGGGCGCTGGCCTGGTA

>RXN02955-upstream

ATGCACTGGCTCCCATCAAAGACGAATTCTTGACCTCAGAATTCCAGCGTGAACCTACG  
 AAGCAGTGC GCGCCGCTGATACTTCAGGAGGTGCGGCATC

>RXN02955

ATGATGAATTTTAAGTCCATCGTGTGCGTCACTGCCTGGCAGGTGTTTAGCCGCCAGGTG  
 CTGCACAGCCCATCAACGTGGTCTGAAGAACTATCCAAGCTGTTGTTTCGTGTGGCTATCT  
 TTCGCAGGTAGTGCCTTCCTCTTTGGAGAGCGTGGACATATTGCGGTTGATTTTCATCGCG  
 CGCAAACCTGCCTGTTTCTGCGCAGCGGGTCTGCAGGTCATTGTTTCAGTTGTTGATTGTT  
 GTTTTTTGCATCCTCGGCATGATCTGGGGTGGCTACTTGGCTGCATCAATCGCGTGGAAT  
 CAGCAGCTCACTGCGCTGCCACTTACCTTGGGATGGGTGTATGTTGTCATCCCGATCGCG  
 GGTGTGTTTCATCGCGTTGTTTCGCGATCATCGATCTCATCGAAGTGGCCACAGGCAAGGAA  
 GAGCCTTACCCCTTGTGATGAATCAGAAGAACCTCGAGATTGGACGAGCTAGAGGCC  
 CAAAGCGCTATAGATTCTGCAAGTTCAGCGGAAGGTAGGAAC

>RXN02955-downstream

TAATATGTTGTCGCCAGCAGCTG

>RXN02966-upstream

AAATATAACCCCCAGGGTATCTTGACAGATTAAAGCTCGATGTTTTAGGCTCTACATATA  
 CCCCCACGGGTATCCCCTCAACTTTGATCTAAGGTGTCAC

>RXN02966

ATGCTTTTTGAACGCATCTACGAAGAAGGCCTCGCCCAAGCCAGCTATTTTCATTGGCTGC  
 CAACCGCAAGGCAAAGCGATTGTTGTTGATGCTCGCCGAGATATCCAGACCTATCTGGAC  
 CTTGCAGCAAAAAACAACATGGTTCATTAGCGCCGTAACCGAAACCCATATTCATGCCGAT  
 TATCTCTCCGGTACTCGCGAACTTGCAGCTGCCACCGGCGCCGAGATTTTCCTCTCTGGC  
 GAAGGCGGAGCTGATTGGCAATATGGCTTTACAGGCACCACCTTGATGCACAATTCCACC  
 ATCAAGCTGGGAAATATCACCATCACAGCCAAGCACACTCCCGGACACACTCCAGAGCAC  
 CTGTCATTTTTGATTACTGATGGTGCGGTCTCAAAGGATCCCGGTTTTATGCTCAGCGGT  
 GACTTCGTCTTCGTAGGTGACGTGGGACGTCCAGATTTACTTGATGAGGCAGCTGGCGGC  
 GTGGACACCCGCTTCGCCGGAGCACAGCAACTCTTCCATAGCCTAAAAGAGCAGTTCCTT  
 GCACTCCCCGACCACATTCAGGTTTATCCAGGTCATGGTGCTGGCAGCCCTTGTGGCAAG  
 GCATTGGGCGCGATCCCTAGCACCAACCGTGGGATATGAAAAGGCTAATGCGTGGTGGGCT  
 CCATATCTGCGCAGTGATGATGAAGCCGGCTTTGTGGAAGAGCTTCTCGACGGCCAGCCA  
 GATGCCACGCTTACTTTGCTCGCATGAAAAAGCAGAACAAGCAGGGACCTGCAGTACTT  
 AGTACATTATCCCCGCTTGTGAAGCTAGAAGCCGAGGAAGTCGTCGAAAAGCTTGGTTCT  
 GAAGCAGTATTTGTGGATACCCGCGAGCAAAACCAAGTCCATCTCGGAACCGTTGTTGGG  
 GCATTGAATATTCCGCGCGGCGCCAAGGCGTCCAATTTTGCGGCGTGGGTATTGATCCT  
 CAAAAGGATGCTCAGGACCTTATTGTTTTGGCTCCGGACGCCAATACCGCTGCGGATTTC  
 CGCGACGCTTTGCTGCGGGTTGGCATCGACACTGTGCGTTATTTACCAACAGTATCGAT  
 GGATTGCCTACCTTTGTGCCAGAACTCATCTCCCCGCTGAGCTAGCTGAGACCAACTAT  
 GACGCACTGATTGATATCCGTGCAAAGTCCGAATTTGCCGCTGGCAGCATTCGCCGCGCG  
 CAGCAGCTTTCTGGAGGTTTCGGCCATGTGGCGCCTCAATGAGCTGCCTGCGGGTGGCACT  
 TTGGTAACCTTCTGCCAATCAGGAGCGCGAAATACCGTGGTAGCCAATGCTTTGCGACGC  
 GCCGATTACCGTTATCGAGCTCGAGGGCAGCTACGCCGCGTGGGAAAAATCAGCTGCC  
 AATCCTAAAAACTTGCAGACTGCCGTC

>RXN02966-downstream

TAGTTTTAGATCCGGCGCTGTAT

>RXN02979-upstream

CTAGGTCAAGGAACTTCACTCGGCTAGTCCTTAGACTCAAATGTGTTTCAGACAAACACTG  
GCACCGTAAGGCACGAAAGTTACCGAAAGGACTGGTTCCC

>RXN02979

ATGACCGCCCCAAACACTCTCAAGCAAACAACCTCTTCGCTCTGATGAGTTCTCTTGCCCA  
TCCTGTGTCTCCAAGATTGAAAACAAATTGAATGGATTGGATGGCGTCGACAATGCAGAG  
GTGAAGTTCTCCTCCGGAAGAATCCTTGTTGATCACGACCCCAGCAAGGTCTCTATCAAG  
GATCTAGTCGCTGCAGTCGCAGAGGTTGGCTACACCGCAAAGCCATCAGCAATC

>RXN02979-downstream

TAAAACTCTCAGTTAGACCATTA

>RXN02987-upstream

GTTGTTTGATCCAGGTCAAGGAATTAACCCGGAAAGGACCGTATCTTTAAAGGTGCAAGC  
ACAGGAACATGACGATAAAAGATGAAAGGACCTGGTTACG

>RXN02987

ATGACCGCCCCCGCCACGCTGAAGAACACCACCTTGCGCTCTGATGAGTTCACCTGTCCG  
AGCTGTGTGCGCAAGATCGAAAACAAGCTGAATGGTTTGGACGGCGTGGAGAATGCGGAG  
GTGAAGTTCTCCTCCGGACGCATCCTGATCACCCACGACCCACAGAAGGTCTCCGTACGT  
GACCTGGTCACCGCGGTAGCCGAGGTCGGTTACACCGCCAAGCCGTCGGCGATC

>RXN02987-downstream

TGACGCACTCCCGACCCCAAG

>RXN02991-upstream

TTGTCGTGTTTCGCGATCTTCGCCGTTGGCTTCATGATTCTGACCCTGCCTATGGGCCTTG  
GCTTGGGCAAACCTCTCTGAGCGTTTGGCGGTGAAGAAGTA

>RXN02991

ATGGCTAATACAGTTCGCGCAACAGTCCTCTACGATGCTCCTGGACCAAAGGGCCGTCGA  
TTCAACCTCATAATCACCATTCTCACGGTGSTTCTGGGATTGGCGCTCCTCTTCTGGATT  
GGCTCCATGCTTTCAGGCAACGGCCAACTCGATGCCAACAAATGGACTCCGTTTCATCAAT  
TCCCAAACCTGGACCACCTACATTCTTCCTGGTTTGTGGGGCACGCTGAAATCTGCCGTG  
TTCTCGGTGATCTTGGCTCTGGTCATGGGTACCGCACTGGGTCTTGGCCGTATCTCTGAA  
ATCAGGATTCTCCGCTGGTTCTGCGCCGTCATCATCGAGACTTCCGAGCCATTCCGGTT  
CTGATCCTCATGATTTTCGCCTACCAGATGTTTCGCCAGTACAACATCGTGCCGTCGAGC  
CAGCTCGCGTTTCGCCGCCGTGGTATTCGGTCTGACCATGTACAACGGTTCTGTGATCGCA  
GAGATTCTGCGTTCTGGTATCGCTTCCCTGCCTAAGGGGCAGAAGGAAGCAGCGATTGCG  
TTGGGTATGTCTTCTAGGCAAACACCTGGTCAATCTTGTTGCCTCAGGCCGTGGCTGCA  
ATGCTCCCAGCGTTG

>RXN02992

ATCGTCCCTTTGGGCAACACACTGATCGCACTGACTAAGAACACCACCATCGCCTCTGTC  
ATTGGAGTTGGCGAAGCCTCCCTGCTGATGAAAGCCACCATCGAAAATCACGCCAACATG  
CTATTTGTCGTGTTTCGCGATCTTCGCCGTTGGCTTCATGATTCTGACCCTGCCTATGGGC  
CTTGGCTTGGGCAAACCTCTCTGAGCGTTTGGCGGTGAAGAAG

>RXN02992-downstream

TAATGGCTAATACAGTTCGCGCA

>RXN02993

GTTGCTGAATACGTAGTCAACTCCATCGCTGATGACAAGGGCTGGGATCACCCCACCATC  
GAATGGCGTGAATCCCCTTCTGCGCAGCGTGAAACCCTCATTCAAACGGTGAGGTAGAC  
ATGATCGCAGCAACCTACTCCATCAACGCTGGCCGTTTCAGAGTCCGTCAACTTCGGTGGC  
CCATACCTGCTTACCCACCAGGCTCTGCTTGTTCGCCAAGATGACGATCGCATTGAAACC  
CTCGAGGACTTGGATAACGGTTTGATCCTGTGCTCCGTTTCCGGATCCACTCCAGCTCAG  
AAGGTCAAGGATGTCCTCCCAGGCGTTCAGCTCCAAGAATACGACACCTACTCTTCCTGT  
GTTGAGGCACTGTCCCAGGGCAACGTTGACGCCCTGACCACTGACGCCACCATCCTCTTC



GGCTACTCCCAGCAGTACGAAGGCGACTTCCGCGTTGTGGAAATGGAAAAGGACGGCGAG  
CCATTCACCGACGAGTACTACGGCATTGGCCTGAAGAAGGATGACCAGGAAGGCACCGAC  
GCTATCAACGCCGCACTTGAGCGCATGTACGCTGACGGCACCTTCCAGCGACTGCTCACC  
GAGAACCTCGGTGAAGACTCCGTGGTTGTTGAAGAAGGCACCCAGGTGACCTCTCCTTC  
CTCGACGCAAGC

>RXN02993-downstream  
TAGTGTGACGGCTTTTAAAGCC

>RXN02996-upstream  
TCCTGCCACAGAATCTGCCTGCTGCTCCATTAATAAAATTGCAGGCTAGAATAGAGGG  
TCGATTAGGAGTCGATGAAAAAGTCGGCGCCAACGAGGAG

>RXN02996  
ATGAACAACAACGTGAGTGATCAAAAGCTAAGTGGTAAAGAGCTTGCGGCACTAGAGAAA  
CAAGCCGCAAAAACCTCTCGAACTTGGTGATAAGAAGTGGTATCTCATCGCGGGAGTCGTG  
CTTTTCGCCATCGCACTCGTCCTCCACATATCCGTGGAGTGATGGGCTGGCAGGTTCTG  
ACGCTGTCGAATGTCGCGGAGGATGCCGGCATTACCTTGGTGAGTACGGTTTCTACTGG  
TTGGGCACCATCGGTGTATTCTGCTTTCTTTGGGCACTGTCGTGTTAAGCGCACGTGG  
ATGGCGTGGATTTTCATGGATTTTCTCCTGCGTCACTCTTGTGTTGCTGTGTTTGCCATC  
TGATGCGCCAAACAACCACAGCACCCAAAGTGAATTTTCGTCAACATTGGCATGATGCTT  
GCTGTGATTGCAGCGATCCTTGCTGTGTGGGGTCTATCTTCGGTGATTTTGGCCCGCAGT  
GATCGCCAAATGGAGATCGCTGAAATGCGCGCCGAGAACCAGACCTTGATGGTGTTGCA  
GCTACCCAGCGCGCACTTCTTGAGCAGCAGCAAAGCAACCAGAGATAATCCTTTGCTT  
GTCGACGATCGTCGCGCCCGCATCGCCCGCCGCGCGAGCGTGAACAGGATGCACAAGGG  
GAGCAGGCT

>RXN02996-downstream  
TAAGTTCTAGTTCAAGCGGTGA

>RXN03060-upstream  
TATGTCCTTTGGCTCCGGTACCCTGGCAGGAGTACCTGGGCTGTTTTTCTAAAATGGCCT  
GACGTTTTCAAGATTGAATTTAAGGAAAGCATCGTAGTTC

>RXN03060  
ATGAGTAACCCTGCCGCGAGCACACCTGCCAACAATTCCGACGATGTTGCGAAGGAGAAT  
TGGGACTCTTCTTTTACGCCGAAGACTGACATTGACTCTTCCCAGCCTGTCAATAACTCG  
ACTGGTGAAGCCGCTGCGCGCGCAGTGAACCTGTACAAGGCGTATGGCCAGGGTGATACC  
ACTGTCACCGCGTTGGATCACGTCAACGTGGAGTTTGAGAAGAACAAGTTCACTGCCATC  
ATGGGTCCTTCTGGCTCGGGTAAGTCCACGTTGATGCACTGCATGGCTGGTCTGGATGCT  
GCGACTGGTGGTTCGGCATTCAATTGGTGATACGGATCTGTGCGGGTTGAAGGACAAAGAG  
ATGACCTCTTTGCGTCGTGATCGTTTGGGATTCATTTTCCAGTCGTTCAACTTGGTTCCT  
ACTCTGACGGCGTCGGAGAACATTACGCTGCCTACCGATATCGCGGGCCGCAAGATTGAT  
CAGTCGTGGTTCGATGAGATTACCTCTCGTCTGGGTCTGACTGAGCGCCTTAAGCACCGT  
CCTGCAGAGCTCTCTGGTGGTCAGCAGCAGCGTGTGGCGTGTGCTCGTGGTGGTGTCT  
CGTCCGGAGATCATTTTTCGGCGACGAGCCAACCGGTAACCTTGGATTTCGAACTCTTCTAGG  
GAAGTGCTGGATATCCTGCGCACCGCAGTTGATCAGGATGATCAGACCGTTGTGATCGTT  
ACCCACGATGCCAAGGCGGCGTCCTATGCAGATCGTGTCAATTTTCTTGGCGGACGGTCGT  
ATCGTGAACCAGTTGTTTGATCCCACCATCGAGGAAATCTTGGCCACGATGAACGGAATT  
GAGGATATTGCC

>RXN03060-downstream  
TAATGAATTCCGGTTCACAATG

>RXN03065-upstream  
GACGGCGCCAACTCTGCATTCTTCGCCTCAGCGTGCGTGGCAGTGTTTGCACTGATCGTG  
GGCTTCTTTGTAAAGAGGCCAGCCCGCTAAGCTAGGTTCGC

>RXN03065  
ATGATCAGCATTGGAACCGACCTCGTTTACATTTTCGGCGTTTCGCAGAGCAGCTTGACACAG  
CCGGGAAGTTCTTTCATGGAGGTGTTTTCCGCAGGGGAGCGTCGTAAAGCAAATGAACGC

CAGGCAAGCCGCTACGCCGAGCATTGCGGGGGCGGTGGGCGGCAAAAGAATCCTTTATT  
AAGGCCTGGTCACAGGCCATTTATGGCCAGCCACCCGTGATCGCCGAAGAAGCCGTGGTG  
TGGCGGGACATCGAAGTTCGCGCAGACGCGTGGGGGCGCGTCGCGATCGAATTGGCGCCC  
GAATTGGCCGAGTGGTCCGGGAATCCATCGGGGAGTTTTCCAGCAGCTTGAGCATCAGC  
CACGACGGCGACTACGCGGTGGAACGTGCGTGT

>RXN03065-downstream  
TGACTATCCAGTAGCCACGGAGA

>RXN03079-upstream  
GAGCGGGGTGCTATCGGCCGAAAGTTTAGGGTTTTGTTCAATCTGTTGGTTAGTATTGC  
TTGGGTAAACAAGTCATAACAATTTTCATTAAGGGTCGTT

>RXN03079  
TTGTCGCGCACAGGTGTTTCGAAAAAACCAGCTCACCGCTCCTGTTGTCATCATCGGC  
ACCCTCGTCTTGTTGATCATCGCCTTCACCGCTTCCTCATGCTGGGTCCCGTGACGGTT  
CCATTGAATGAGCTTGCAACCAACCCCGTTGTCACCGATATCCGTGCACCACGCATTATC  
ATCGCAGCATTGGTGGGTGCGGCGCTGGCTGTCTCCGGTGCGATCATGCAGACGGTGT  
CACAAACCCGTTGGCGGATCCCGGCATTGTGGGTGTGTCCTCCGGTGCAGCTGTTGCAGCT  
GTCCTTGGCGATTGTACCGGTGCGAGTTTCTTTGGCCAATGGACCGTTCCTTTTGGCGCC  
TTCGTGGGCGCATTTGGTCACGGTGGCTGTGGTATATTTGATCGCTAGTTCCCGCGCGATG  
GATGGCCGTGGCGCAGATCCGGCCACGTTGGTACTGGTCGGCATGGCTATCACTGCCTTT  
TTGGGTGCTGTTATTTCCAGCGCCACTGCGAACGCACCACAAGATTCTGAGCTTCGATCC  
GTGACGTTTTGGCTCAACGGCGATCTGGTATCTCGGACGTGGGAACATGTGGGCGTTGCA  
ATAATCCCCATTATCGTTGGGTGATTCTAGCTATCGGCGGTTCGCGCATCTGAACTTG  
TTGCTGCTGGGTGATTCCACAGCGCAAACATCTGGACTCAACGTCAACCGCGCACGCATC  
ATTTTGCTAGCACTTGCGGCACTGCTCACCGCCACAGCTGTTGCGGTCTCCGGCACCAT  
ACGTTTGTGATTGGTAGTACCCACCTGGTGCGCATTGTTTTAGGTGCCGATCACCGA  
GCGTTACTCCCGGCCGCGCGATTTTGGGCGCCACGTTTGTATCGTTTCCGACACTGTT  
GCCCCGATGATCTTCTCCCCCATCGTCTTGCAAACAGGCGTGGTGGTGGCGTTTATTGGC  
TCACCAATTTTCCTTTATTTACTGCTCAGCATGCGCAAGCGACGCGGATTGGGGCTG

>RXN03079-downstream  
TAAAAACTCATGCCTCAATTAGT

>RXN03080-upstream  
CTTGCAAACAGGCGTGGTGGTGGCGTTCATTGGCTCACCAATTTTCCTTTATTTACTGCT  
CAGCATGCGCAAGCGACGCGGATTGGGGCTGTAAAACTC

>RXN03080  
ATGCTCAATTAGTTGAAATTCGTGATCTCAACGTTGAATTCCCCTCTCGCCATGCAGTG  
AAAAACGTGTCTTTTTCTGCACCTGCTGGAAAAGTCACCGCACTGATTGGCCCAAATGGT  
GCTGGTAAAAGTACTGCCCTTTCGGCGATTGCAGGATTGGTTGAATCCACCGGCGAGGTA  
ATGGTTGGTGGGAGTGGGGTTGCGTCGAAAAGCGCTAAAGCCCGAGCCCGCCTGCTCTCA  
CTCGTGCCGCAAAACACCGAGTTGCGCATTGGTTTTAGTGCACGCGACGTTGTGCGGATG  
GGCCGCTACCCGCATCGTGGCCGCTTCGCCGTGGAGACCGACGACGATCGACGCGCCACC  
GATGACGCCCTGCGCGCCATCAACGCGCTCGACATCGCCGAGCAGCCCGTCAACGAATTA  
TCGGGCGGCCAGCAGCAGCTCATCCACATCGGCCGAGCGCTCGCCCAAGACACCGCCGTC  
GTGCTTCTCGACGAGCCCGTCTCCGCCCTTGATCTACGGCACCAAGTTGAAGTCCTTCAA  
CTCCTGCGCGCCCGAGCTAATTCCGGCACCAACCGTGATCGTCGTCCTTCACGATCTCAAC  
CACGTTGCCCGTTGGTGGGACCATGCAGTGTGATGGCCGACGGCGAAGTTGTCTCCCAA  
GGTGACATCCGCGAGGTGCTCGAACCTGCCACACTGTCCACCGTGTACGGACTGCCCAT  
GCGGTGCGCGATGATCCCGAAACCAGCTCACTTCGCGTGATCCCGCATCAAATCCCTTT

>RXN03080-downstream  
TGATTGAAAGTTTGAATTAAAAA

>RXN03081-upstream  
ACGGACTGCCCATTTGCGGTGCGCGATGATCCCGAAACCAGCTCACTTCGCGTGATCCCGC  
ATCCAAATCCCTTTTGATTGAAAGTTTGAATTAAAAACC

>RXN03081

ATGAAAAAATCACTCATCGCCATTGTTGCCAGTGCGCTCGTGTTAAGCGGCTGCACCTCT  
GATTCTTCTGACTCTTCCGGCACTTCCGGAAGTGTGGAAACCACTTCGATTACAACCAGC  
GTTGCCGCAGCTGACGGCGCATTCACACGCACCGTCACACTCGACGATTCTCCATCACC  
TTAGAATCCAAACCAGAGCGCATCGCCGTACTCACCCAGAGGCAGCATCCTTGGTTCTC  
CCCATCACAGGCGCCGACCGCGTCGTGATGACCGCCGAAATGGACACCGCTGACGAAGAA  
ACCGCAGCTCTGGCCTCCCAAGTGGAATACCAAGTCAAAAACGGTGGCAGGCTCGACCCC  
GAACAAGTTGTGCGCCGGCGACCCAGATTTGGTGATCGTCAGTGCGCGTTTCGATACCGAA  
CAAGGCACCATCGACATTTTGAAGGCCTCAACGTCCCG

>RXN03081-downstream

TAGTTAACTTCGATTCAGACGCT

>RXN03082-upstream

CAGAAGCAATCGCAGAAATCGATGCAAACCGCATTCGACATTCGACAAGCCTGCCACCTC  
CCCCACTGTGCTCACTTTGATGCAACGCGGACCACGCCAA

>RXN03082

ATGGTCATGCCAGAATCTGCCATGCTCACCGGCCTGATCCGCGAAGCCGGCGGCACTCCA  
GTGGTAGATTCTCTCGGCGCGGTAGGCACCATCACTGCAGACCCAGAACAAGTTGTTGCG  
ATGGCACCTGAGATCATCATCATTCAGGACTTCCAAGGTAAAGGCCGAGAGAACTTCGCT  
AATTTCTCTCCAACCCAGCGCTAGCCAACGTTCCCGCCATTGAAAACGACAAGATTTTC  
TACGCCGACACTGTCACCACTGGAGTTACTGCAGGTACCGATATCACCACTGGTCTGCAG  
CAAGTGGCAGAAATGCTGAGC

>RXN03082-downstream

TAGTTTTGAGATGTTGAAACTAG

>RXN03084-upstream

CCACCCCCACGTCTAAGTTTTCCCCTATTTACACACACCTGACCGAAGCTGTAAGGTTTG  
CCTAATCTTTTTCAATCTAAAGTCAGGATATTCACAGCCC

>RXN03084

ATGTCATCTCGCAGAAAATCTCCTCCGCACTGATCGTGCTTCTCGCAGCAGCACTACCT  
CTTACTGCTTGTTCCTCCAGCTCAGAAGAGGAAGCATCCACCAGCTCTGCGACTCGCGAA  
TTCACAGACGCTCACGGAACAACCGAAGTTCCCGAAAATCCTCAGCGCGTCGTTGTCCTC  
GAGCCACTTGAGCTAGACACCGCAATCGCCCTCGGAATCACCCAGTGGGTGCAGCTGTC  
GCCAACAACGTCACCTGGTATTCCTGCATATCTCGGCGTCGATGGAATCGAGCCTGTCGGC  
ACCGTTTCTGAGCCAAATATCGAAGCGATCGCTGCTCTCGAGCCCGACCTGATCCTGGGC  
ACCGATTCCCGCCACGCCGAAATCTACGACCGCCTCGAATCCATCGCCCCAACCGTGTTT  
ATGACAACCCATGTTGATCCGTGGAAAGACAATGTCGTCTTCATCGGCGATGCATTGGGC  
AAGAAGCAGGAATCCGAGGATCTCATCCAAGGCTTTAATGACAAGTGCGAAGAGATCAAG  
TCCGAGCATGATGTCGAAGGTAAGACCGTCAACATGATTCGTCCCCGCGACGAGCAAACC  
ATGAGCCTATACGGCCCGACCTCATTTGCCGGCAGCTCTTTGGAGTGCGCAGGACTCACC  
ATTCCTGATCAGGAATGGAAGGATGACCTCCAGGCCGACATCGCTCCTGAGAACTTCATG  
CTCGCCACCGCCGACTACGTCTTTGTACCGCAACTGATGTCACCGATGAAAATGAGCTC  
CCCGAAGTAATCCGAGAAAACCGCGAACAGTTCCCATCACTACCCCTTGTCGATACCAGC  
TACTGGGTATCTGGCGTCGGTCCACTTGGCGGCAGCAAAGTCTTGGAAGACATCGATGCC  
TTCCTCGACGCACAGCAA

>RXN03084-downstream

TAATGTCCACAGCTCTCCCCGAT

>RXN03095-upstream

AACGCCTCAATTAGTGCCAGACCTTGCCGACCGCAGACCAAACCTTCACCATTTCAAACCA  
TCCCTAGCCACAACAACGGCAGTTGTGCAATGATCTGCGT

>RXN03095

ATGAATGCAGATAAGAAAATGTGCGGAATGAACCCGGATAGCCAATACGTCGAACTTGCC  
GTCGAAGTTTTCGGACTCCTCGCGGACGCCACTCGAGTTCGCATCATCTTGGCACTTCGA  
AACAGTGGTGAACCTTCCGTAAACACCTCGCGGACATCGTCGATAAATCCCCCGCAGCA

GTTTCCCAACACCTCGCCCGGCTGCGCATGGCCCGAATCGTGTCCACCCGTCAAGAAGGT  
CAACGAGTTTTCTACAACTCACCAATGAACACGCATCACAGCTAGTCTCCGACGCTATT  
TTTCAGGCGGAACACACCATTGCGGACGGCCAGACTCCCCACACCACCACCGAGAACGA  
GAACAATCA

>RXN03095-downstream  
TGACCACCCACAGTCACCAAGAA

>RXN03097  
ATTTTCAGCCAGTGCAGGTGCTATAGGTTGGTTAATTTTAGAATATATTTTTTAAAAAGACG  
ACAAGTTTACTTGGACTTTTACTCGGTGCATTAGCAGGATTAGTTGTTATTACTCCTGCA  
GCAGGATATGTAACATATCTTAGTGCAACAATAATGGCTTTAATAGGAGGTATCTGTTGT  
TATATTGTCATTAATTACATCAAGGTAAAATAAATATCATGATGCATTAGATGCATTT  
GGTATTCATGGTGTGGTGGTATTATTGGTGTGTTTTAACAGCAGTTTTCCAAAGTAAA  
AAAGCCAATCCTGACATTGAGAATGGCTTTATTTATACTGGTGACATACATATTATACTT  
GTACAAATATTATGTGTAAACAGCAGTTGTAATTTTATAGTATCGTCATGACGTTTATTATT  
GCGAAAGTAATTAAATTAATTACACCATTATCTGTTACGGAACAAGAAACGAATATAGGA  
TTAGACAAGATTGTTACGGTGAACATGCTTACTTTGAAGGTGAGCTAAATAGATTCAAT  
AAACATATTGATAT

>RXN03097-downstream  
TAGAATATATTTACATAGAATAT

>RXN03103-upstream  
ATCTTCAGAGTCACTTCTTTCAGTGTCAATTTTCTCGGCCCTAATCCCCCGCTGGAGTTC  
AATCAGCGATTGCAACCTTTTAGATATATAAGGAGACAAC

>RXN03103  
ATGTCTGCAAAGCGTACTTTTACCCGTATCGGTGCGATTCTTGGAGCAACTGCACTTGCC  
GGAGTTACCCTCACCGCCTGTGGTGATTCAAGCGGTGGCGACGGATTCTCGCAGCCATT  
GAAAATGGTTCTGTCAATGTGCGGCACCAATACGATCAGCCTGGTCTTGGCCTCCGCAAC  
CCAGACAACCTCCATGAGCGGTCTCGACGTGGATGTTGCTGAATACGTAATTCAACTCCAT  
CGC

>RXN03103-downstream  
TGATGACAAG

>RXN03109-upstream  
ACTGGCGCTTCCCGATGGTCAATCATTTGGCCTTTGGTGCCCAAACCTGGCGAGTTGTTGCT  
CCGCGCATCCCGCGAACTGTATGTGCAGGGCGGCGAGTAG

>RXN03109  
ATGGTTGTGAAGGAGGTTGACGTCGAAAAGCAAAAAGCTGGCCGGGTGCCTGGTGCTATA  
GCTAAGCGTCGGACCGTGCGGATTGTGCTGTTTGTGCGCTGGGCGCGATCGTGATTGCG  
GCGTCGCTGTGGTCGATTCTGGTTCGGCCAATACACCATCCCGATTGCGGATCTACCTGCG  
ATTTTAGCCTCCGGTCCGACCGGTGCGCAGACGATGGCGGAACAAGTCGTGTGGCAAATC  
CGCATGCCGCGCATCGTGCTGGGACTGCTCGTGGGTGCCGCTTTGGGCGTGGCCGGCGCG  
CTGTTGCAGGCGGTGTTTTCCAACCCGCTGGCGGAACCGTCGATCATCGGCGTGACCTCC  
GGCGCGGGCGTGGGTGCTGCTGCGGTGATCGTGTTAACCTGACATTTTTGGGCACATCC  
ACCGTCGCAGTCGGCGCGTTTATTACCGCGGTGATCACCACGATTTTGGTATATCAGCTG  
GCCAGAAGCCGTGGACGTGTGCAAGTGATCAACCTGATCCTGACAGGCATAGCCATTAAT  
GCAGTATCCGGCGCGCTGACCTCAGTTCTTGATCTACATCGCGCCGACGAGCTCCCGCGA  
AGAAATATTTTCTGCAGATGGGTTCTCACGGCTCGCATGGCGCACGTCAACGT

>RXN03110-upstream  
AATGAGTGAACCTGCGCTTGAACCTATACCCCTGGGGTATTACTGTAGATTCTCAATACC  
CCGAGGGGTATCTAGTTTTTACGTTGAGAAGGAGAGCTCA

>RXN03110  
GTGCTTATTGAACGCATCTACGACGAAGACCTTGCGCAGGCCAGCTATTTTATTGGCTGC  
CAAGCCCAACACCGCAGTCGTGGTTGATCCGCGTCGCGATATTGCCGTCTATCTGGAC



ATGGCCAAGAAAAACGGAATGGAGATTGTTGGAGTTACCGAAACCCATATCCATGCGGAC  
TATTTGTCAGGAACCCGTGAGTTAGCTGCTGCAACTAATGCCACCATGTACGTCTCAGGG  
GAGGGCGGCGCCGATTGGCAGTATGAATTCGACGCCGAGCGAATATGCGACGGCAGCGAG  
ATTCGCCTGGGAAATCTGGTGCTCACAGCTGTTACACCCCAGGCCATACCCCGGAACAC  
TTATCGTTCCTGCTGAAGGACGGCGCGTTTCGCAGATGAGCCAGGATTCATGCTCACTGGC  
GATTTTCGTTTTTCGCGGGTGATCTTGGCCGACCAGATTTGCTCGATGAAGCAGCTGGGGGA  
GTGGACACTCGTTTTGAGGGGGCTCGCCAAATGTTCAAGAGCTTGAAGGAAAAATTCCTG  
ACATTGCCTGATCACATCCAGATCTTCCCTGGTCATGGTTCCGGTTCCGCGTGTGGCAA  
GCCTTGGGTTCCGGTTCCTTCAACAACACTTGGATATGAACGTCAATTTGCGTGGTGGGGA  
AAGTATCTGGAGGCAGATGATGAACAAGGATTCATTGATGAGCTTCTGGAAGGCCAACCT  
GATGCACCTGCATACTTCGGCAGGATGAAGAGGCCAAAATAGGCAAGGGCCCGCAATTATG  
GGCGCTCGCGAGCTGTTGCCACAGCTGGAAGCTTCTGATCTGCACGACGTCATTGTTGTT  
GATACCCGCTCAGCCGATGAAGTTCACCAGGGCACTGTAGCTGGTGCAGTGAATATTCCT  
GCGGGCAATTCGATGGCGAAATTTGGCTCGTGGACCGTTGATCCCGAGAAGGATTCCCGA  
GCTTTGGTTCTGCTCGCGGCAAGCCAAATTTGGTGCCATGGAGATGTGGGACCACATGGTT  
CGCGTGGGAATCGATAATGTTGCTGGTTTTATCACCAACTTTGATGGGGTGGACCTAGTT  
GCACCGCAAACCTGTGTCCCCAGATCAGCTGGATGAATTGGAATACGATCTACTTCTTGAT  
GTCCGCAACCGCAGTGAAGTCGAAGAAGGCTACATCCAGGAGCACTCCATATTAATGGT  
GCATCCGTGCTGTGGAATCTGGAGAACTGCCACGTGACGGAAAGATCGTGAGCTACTGC  
AAGAGTGGAACACGCAGCTCAATCGCCGCAAGCACCTGCGTAATGCTGGTTTTGATGTG  
GTGGAACCTCAAGGATCCTATGACAACTGGGTCCGGCACAAC

>RXN03111-upstream

CGTGACCGAATTGAGCAGGAACTTCGGGGCCAGCCGACTGATTAACCGCTTTGGCCAGGA  
GCCTTTTGCCTTCGCTTTCGCGCGGCCAAGGATATGACTGG

>RXN03111

TTGAAGACCCTTCGTGCCGCGGTTGCCGCAGGTGCAGGCACCAATGTTAGTGACATCGTC  
GAGCGCGCAAATGCGCTGCTTGCACTAGTTGCAGATGATCTCATTGGCACCTTCCATTT  
GGTTTCGATCCAGTGGCTTGGGCTAACAACCTCCGAAGATCCAGCTTTCGATACTGCACAA  
TCTGCAGTGAGCGTGCCGGGTATCTTTGTCTCCAGATCGCAACCCTGGATTCCCTTGAG  
GCGCAGCGCCTTGATGTGGATCAGGCTGTGTCCAGCATTGGTCATTCCCAGGGCGTATTG  
GGCGTGCACCTGCTCAATGATGCGACTCGTGCTGATGAACTCGTTGCCATTGCGCAGTTG  
ATCGGTGCAGCGATCACCCGCACCGCACGCATGACGGGCCTGATCGCGCAGGGCGACAAC  
ATGCCGATGCTGTGATCGCCGGAATTTCCCGCGAACAGCTTCAGCAAGCTATCGACGCG  
GCCTGCGCCGAAGTCCCTGCGGAGATCCGCCCGGTTATCGGTCTGCGCAACTCACGCGAT  
TCTTATGTTTTGGTTGGCCGCCCAGACGACAACGCTCGCGTTGTTAAGGTCATTGAGGCA  
ATGGCTGCCAAGGATAAGAAGGCCATTGAAGATAAGCTGCGCGGCGGTTCCGCGTTCAGC  
CCCCGTATTACTCCGCTGAAGGTGCAGGCTGCTTTCCATCACCCAGCTATGAACATGGCT  
GTGGAGCAGACCGTGGCGTGGGCAACCACTGCTGGTTTGGATGTGGAACCTCACCCGCGAG  
ATCGCCGCTGATGTTTTGGTTAACCTGTCGATTGGGTAGCACGCGTCAACGAAGCGTAT  
GAGGCTGGCGCTCGCTGGTTCCCTCGACGTTGGACCAGATGGTGGCATCGTTAAGCTGACT  
GCCAACATCCTTGAGGGCCGCGGCGCGGATTCCCTTCTATGTTGGTGACGCGCAGGCCAG  
GCCAAGATATTTGATGCTGGCATGGCACCTGAACTTCAGTGGATTACCAGGAGTTCGCA  
CCACGCGTTGAGCACGTTGATGGAACCCACGCCTGGTTACCAAGTTCACTGAGCTGACC  
GGCCGCACCCCAATGATGCTGGCTGGCATGACCCCAACCACCGTTGACCCTGCCATTGTT  
GCAGCCGCTGCAAACGGTGGACACTGGGCTGAGCTCGCTGGTGGCGGACAGGTTACCCCA  
GAGCTGCTGGAAACCCACATCGCACAGCTCACCGACATGCTTGAGCCAGGTATCAACGCC  
CAGTTCAACTCCATGTTCTTGGATCCATACCTGTGGAAGATGCAGATTGGTGGCAAGCGC  
CTTGTTCCCTAAGGCCCGCGCTAATGGTGCATCCATCGACGGCATCGTCATCACCGCCGGC  
ATTCCTGAAAAGGATGAAGCTGTTGCATTGGTCAAGGAACTGATGCGTGATGGTTTTCCCT  
TGGATCGCATTCAAGCCAGGTGCCATCAAGCAGGTTAACTCTGTGTTGGCTATCGCTAAG  
GAAGTTCCAGAACTCCCCATCATCATTAGATTGAGGGTGGCGTTGCAGGTGGACACCAC  
TCTTGGGAAGACCTCGATGAGCTGCTGATCGCCACCTACGGCAAGGTCCGCGCACTGGAT  
AACGTGGTGCTGTGTGTCGGCGGTGGCATTGGCTCACCTGAGCGCGCTGCTGATTACGTC  
ACCGGTTCCCTGGTCCACTTCCTACGGCCTGCCAGCTATGCCTGTTGATGGCATCTTGGTG  
GGTACCGCTGCGATGGCAACCAAGGAAGCAACCACCTCCCAGGCCGTCAAGGAACTTCTT  
GTTTCCACCCAGGGCTCTGATGAATGGGTTCCCTGCTGGTGGCGCAAAGAACGGAATGGCA  
TCTGGCCGTTCCAGCTTGGCGCAGACATCCACGAGATCGACAACCTCTTTGCTAAGGCT  
GGACGCCTTCTTGATGAGGTTGCAGGCGATGAGACGGCTGTGCAGGCGCGCCGGGATGAG  
ATCATTGAAGCGATTGGCAAGACCGCCAAGGTGTACTTCGGTGACATCGGATCCATGACT

TACGAGCAGTGGCTCAACCGCTACCTCGAGCTGTCTGGCCCTGTTGATGGTCAGTGGATT  
GATGCTTCCTGGGCTGCACGTTTTTGCCAGATGCTGGAGCGTGCCGAGGCGCGTTTGATC  
GAGCAGGATCATGGCCAATTTGAGCCAAGCCTGACGGTGGAGGATGGCGTCGACAAGCTT  
GTTGCTGCTTACCCGCATGCCGCAACCGACCTGCTCACCCCGGCTGATGTCGCCTGGTTC  
TTGGGCCCTGTGCCGCACGCCGGGCAAGCCTGTGAACCTTTGTGCCCGTCATTGATAAGGAC  
GTGCGTCGCTGGTGGCGCTCGGACTCCCTGTGGCAGTCCCACGATGATCGCTACACCGCT  
GATCAGGTGGCTATTATCCCTGGTGTCTGTCGCCGTTGCTGGCATCACCAAGGCCAACGAA  
CCTGTCGCTGACCTGCTTGATCGCTTTGTGCGACGCCACCATCGAGCGCATCGATGAGCAC  
GATTCCCGCTCCCGCGACATCATGGGCAAAGTGCTTTCTCACCTGGCACATTCTGGGCT  
GGCCGCAACATCCCATCGGTGATCCACAGCCTTGGGCATGCTGACAAGTGGTCCCGCTCC  
GAATTCGAAGCATTCATAGCCCAACCGGCGCCAACTTGGTGTACGAAGACGCCGAGCAC  
GCGATGCTGACTGTGCCTTTGGCGGGTTCCACCGCATTCGGCACCAACCGCTGAGCTGAAA  
ATCCGTTTTCACCAGCCCCATCGACGCTCTGCCAAGCGCTGTCCCACTGGTCACCCAGGAA  
GACGCTGAAGCCGCGATGGGTGAACTGACCCGCATCGCAGCTGGCGGCACCTGGCAACT  
GTGAACAATGGCACCGCTACCTGGGAAACCTCCGTGATGCCGGCGTCATCGCTGACTAC  
AACACGTCACCGCAGGCTACCTGCCAGCATCCGTTGTTCTGACACACCGCACCTGAC  
GTGCTGGTTGGCCGCGCATGGCCAGCAGTTTTCGCTGCCGTAAAGTCCGCAGTCATCCCA  
GGCACCGATTCCGCATCCGTTGTGGAAGGCATGCTGTCCCTGGTTCACCTGGAGCACCA  
ATTGTGCTCAAGTCCGATGTCCCAACCGACGGCGCGCTGAAGGTTTCCGCGACTGCCGAT  
GAGGTAGTCGATACCGACCTGGGTGCGCTCGTGATCGTGCGCGCAGAAATCGCCGACGCA  
GAAGGCAACCTGATTGCTACGTTGGCTGAGCGTTTCGCGATCCGCGGACGCAAGGGCAAC  
GCTGTGCGACGCAACACCTCCGCACTGCCAACCACCGTGGACACCCACGCTCAGCT  
CGCGCAGTGGCAACCGTTGTTGCACCTGAATCCATGCGCCCATTCGCTGTGATCTCCGGT  
GACCGCAACCCAATTCAGTCTCTGATGTTGCGGCTTCCCTGGCTGGTCTGCCAGGTGTG  
ATCGTGCACGGCATGTGGACCTCTGCCATCGGTGAACTGATCGCCGGTGCAGCATTCAAC  
GATGAGCAGATCCAAACTCCCGCAGCCAAGGTGCTGGAATACACCGCAACCATGCTGGCA  
CCAGTTCTTCCAGGTGAAGAAATTGAGTTCAGCGTTGAGCGCTCCGCAGTGGACAACCGC  
CCAGGAATGGGAGAGGTCCGCACCGTTACCGCAACCGTCAACGGCAACTTAGTGCTTACC  
GCCACCGCTGTTGTGGCAGCTCCATCTACTTTCTACGCATTCACAGGCCAGGGCATTACG  
TCCAGGGCATGGGTATGGAAGCACGCCGTAACCTCTCAGGCAGCTCGCGCTATCTGGGAC  
CGCGCCGATGCACACACCCGCAATAAGCTGGGCTTCTCCATCGTGGAATCGTGGAACAC  
AACCCACGCGAAGTAACCGTGGCAGGGGAGAAGTTCTTCCACCCAGACGGCGTTTTGTAC  
CTCACCCAGTTCACCCAGGTGGGCATGGCAACTCTGGGCGTTGCTCAGATCGCTGAAATG  
CGTGAAGCACATGCCTTGAACCAGCGTGCATACTTTGCTGGACACTCCGTTGGTGAGTAC  
AACGCGCTTGCTGCATATGCTGGTGTGCTGTCCCTGGAATCCGTTCTGGAGATCGTTTAC  
CGTCGTGGCTTGACCATGCACCGCTTGGTGGATCGCGATGAAAACGGTCTGTCCAACCTAC  
GCGCTCGCAGCTCTTCGCCCCAACAAAGATGGGTCTGACCGCAGACAACGTTTTTCGATTAC  
GTTGCGTCTGTTTCCGAAGCTTCCGGTGAATTCCTGGAGATCGTTAACTACAACCTTGGCT  
GGCCTGCAGTACGCAGTTGCTGGAACCCAGGCTGGTCTTGCCGCCCTTCGTGCCGATGTT  
GAGAACCGTGCACCAAGGTGACGCTGCCTTCATTTTGATCCCTGGCATTGACGTGCCATT  
CACTCCTCCAAGCTGCGCGACGGTGTGGGCGCGTTCCGTGAGCACCTTGATTCCCTGATC  
CCAGCTGAGCTGGATCTGGATGTGCTGGTTGGCCGCTACATTCCAAACTTGGTGGCTCGC  
CCATTGCAACTCACTGAAGAGTTCGTGGCATCCATGGCAGAAGTGGTGGAGTCCACCTAT  
GTCAATGAGATCTTGGCTGATTTCAAGGCTGCTTCCGCCGATAAGCAGAAGCTTGCCCGC  
ACGTTGCTTATTGAGCTGCTTGCATGGCAGTTCGCATCACCTGTGCGCTGGATCGAGACT  
CAGGATCTGTTGATCAAGGGCCTTCAAGCTGAGCGTTTCGTGGAGGTCCGTGTTGGCTCT  
GCTCCAACGCTTGCCAACATGATGGGCCAGACCTGCGCCTTCCTCAGTACGCGGACGCC  
ACCATTGAGGTGTTAAACATTGAGCGCGATCGCCAGTTGTGTTTCGCTACCGATGAGGTT  
GTGCGTGAAGTGGCGGTGGAAGAGACCCAGCAGCTCCTGCAGAAACCACTGAAACCCCA  
GCAACCCAGCAACCCAGCCCTGTTGCAGCTGCAGCCCTGCCACCGGGCGGCCCTCGC  
CCAGATGACATCAGCTTCACTCCTTCTGATGCCACTGAAATGCTCATCGCTATCTGGACC  
AAGGTTGCCCCAGATCAGATGGGTGCCACTGATTCCATCGAGACCCTGGTTGAGGGCGTG  
TCCTCTCGCCGTAACCAGCTCCTGCTGGATCTTGGTGTGGAGTTCGGCCTCGGCGCAATT  
GACGGAGCAGCCGATGCTGAGCTCGGTGATCTAAAGGTCACCGTGTCCAAGATGGCTAAG  
GGCTACAAGGCGTTTGGCCCTGTGCTCTCCGATGCTGCAGCTGATGCCCTGCGTCGCCTC  
ACTGGTCTTACCGGTAAGCGCCCGGATAACATCGCAGAGCGCGTCACCGGCACGTGGGAA  
TTGGGCCAGGGCTGGGCTGACCACGTGGTCTGCTGAAGTTGTGATCGGCGCCCGCGAAGGC  
GCATCCCTGCGCGGCGGCGACCTGGCGTCACTGTCTCCTGCAAGCCCAGCGTCTGCATCA  
GATCTTGATTGCTTATCGACGCGACCGTCCAGGCCGTAGCCTCCCGCCGCGGCGTTGCG  
GTCTCCCTGCCTTCAGCAGGCGGCGCTGCCGGTGGCGTGGTTGATTCCGCAGCTCTTGGC  
GAGTTTGCAGAGCAGGTACCCGGACACGATGGTGTGCTTGTGCTCAGGCAGCCCGCACCATC

TTGACCCAGTTGGGTCTTGATAAGCCAGCAACCGTTTCCGTGGAAGACACCGCAGAGGAA  
GACCTCTACGAGTTGGTCTCCAAGGAACCTCGGTTCTGATTGGCCACGTCAGGTTGCACCA  
AGCTTCGATGAAGAAAAGGTTGTTCTGCTTGATGACCGTTGGGCTTCTGCGCGTGAGGAT  
CTCTCCGCGTTGCTCTTGGCGAAGCTCGCAGCAACTGATATCGATGTACAGGCGCAGGCG  
AAGCTGTTGCAGCACAAAGCTGAATTCTTTGGACTTGATGATCTCGCAGCTAGGCTCGCGA  
ACAAAGCTTCTTGGACTACGCCGACAATGTTGCGGC

>RXN03126-upstream

TCTTGGACAACATTACCCACACACGGGACACTCAAACGTGCATGAATTCACCTGTCTGC  
GATACCCAAAAATCACTCCACCACCACTAGGGTGTCTTAT

>RXN03126

GTGCAGGAACAATCGAAGCAGAAAGACCTCCAGGCTGATATCGCCAGAATCACTGCCGTG  
AAATCGGACACAGTTCCGAATTCCAGTCAATGACCTTTGGCGCTGCCTGGAACGATATC  
GTCCGCGGATTCAAGCAACATGAGTTGTGGCTGCAACTCGGCTGGCAAGACATTAAGCAA  
CGCTACCGGCGATCCGTCCTTGGGCCCCCTGTGGATCACCATCGCCACCGGTGTCATGGCG  
CTCGCCCTCGGCTTGCTGTACTCCGTGCTGTTCAAAATCCCCATCGCGGAATTTCTGCCC  
CACGTCACCGTCGGCCTGATCATTTGGAACCTTCATCTCCGGATGCATCAAAGAAGGCTCC  
GACATCTTCATAGATAACGAGGGACTCATCAAACAGCTCCCCCTCGGCGCTGTCCGTCCAC  
GTGTACAGACTCGTGTGGAAACAAGCCCTCTTCCTCGCCACAACCTGGTCATCTGGGTC  
ATTCTCATGATGATCTTCCCCCGACCCCTCGGCTGGGACGTCTCCTGATCATCCCCGCA  
ATGTTCTCCTGGTGATCAACGGCGTGTGGGTAGTCATGTTCTTCGGCATCATCGCCACC  
CGCTACCGCGACGTCTCCCCGTTGCTAGAAGCCGGAACCCAACTCCTCTTCTACGTCACC  
CCCATCGTCTGGATGACTTCCACCCTGCAATCCCAGAGCGCAGAAATCGGCAACCGCGCA  
CGCCTCGCCGAAGTCAACCCGCTCTACCACTACCTCGAAATTGTCCGCGCCCCCATGGTC  
GGCGCCGACCTCCCCGCTACCACTGGTGGATCGTCTCGCCTTCACATTCGTCGGCCTT  
GGCCTTGCTCTCCTCGCGATGAAGCAATGGCGATTCCGCGTCAGCTACTGGGTA

>RXN03126-downstream

TAAGGAGCACCACATGGTATCCA

>RXN03132-upstream

TAACTTATTTATACATAAAAACACAATAAAAACCGCACACGCGGCGAACTTCAATAAAT  
CCCTAGACTGCAAAAAATGGTTAGGCTAACCTTATTTCCA

>RXN03132

ATGAATGTGAATCAACAGTTGGGAGCCCGCACCGCCATGAACCACCCTGAGACCGCAACC  
GTCCTTCGCTCCATCTCTGACATGGTTAGCACCGAAACCAATCCGCGCCGTAAAAGCCGC  
CTCGAGCAGCTCATTTACGCCACCGCCAGCGCCTGGCCCCACTACCCCATTTGCCACGCA  
GCCCAGGCCGCGGTGCAATTAGCCAGGCCAATGCGGGTTTTTGAGCTCCAGAGCTTTGAA  
GGCGTCAAGCACGCACTCCACCACATCGATCTTCGCCCCGCCCTCGAATGGGACATCATG  
GGATTTCCCGAATCCCCCGACACGCTGCCCATTTTGCTCAGTGACCTGCGCGACCCCCCT  
TACGCCACCACTGCTGTGCCACCTCAATCCACGCCACGCTCCGCTCACCGATCCACACAT

>RXN03132-downstream

TGACGCTTCCAGGCGCCACCGCG

>RXN03157

GGCCACCTCGACATCGTGACCCGCGCCGCGCGCAATTTAGCGAAGTCACCATCTTGGTC  
ACCGCCAACCCCAACAAAACTCAGGACTGTTACCGTCGCAGAACGCATGGATCTCATC  
CGCGAATCCACCGCACACCTGGACAACGTAAAAGTAGACACTTGGGCCTCACTGCTCGTG  
GATTACACCACCGAACATGGCATCGGCGCCCTAGTCAAAGGCCTGCGAAGCTCCCTCGAC  
TACGAATACGAGCTCCCCATGGCACAGATGAACAGGCGACTCACGGGCGTAGACACCTTC  
TTCCTCCTCACCGACGAGAAATACGGCTACGTACGCTCCACACTGTGCAAAGAAGTTGCC  
CGCTTCGGTGGCGATGTCTCCGGCCTCCTACCTGAGGTAGTGGCAAAGCCGTGACAGAA  
AAATACAGCAACCAGCAC

>RXN03157-downstream

TAGTTTCTTTTGCATCAAGCGTC

>RXN03160-upstream



GAGCATATGGTGC GCGCGGCCGATATGCTGATCAATTCCAACCCCGATCCGCACGCTTAA  
CTTCTGCCAAAAGTCGTTTTGACCATAAGCTAAGCGATT

>RXN03160

GTGAATCGAATTGCAGAAATCGCACGCAGTTTCGGCGTGCTGGGCTTCAGCGCTTTCGGC  
GGCCCCACCGCGCACCTCGGATATTTCCGCACGGAATTCGTGGAGCGGCGGCGCTGGCTG  
GATGATCGCCAATATTCCGAGATCGTAGCGCTCAGCCAACTACTTCCCGGACCTGGATCG  
TCGCAGGTCGGTATGATGCTGGGCTACCACCGCGCCGGTTTTTCCGGCATGGCGATCGCC  
TGGCTCATGTTTACCTGGCCCTCATTTGGCGCTCATGGCGGCGTTTCGCCCTGCTTTTTGAT  
GCGACCTCCGCCAGCTGGACGCTCGGCCTGCTCGCCGCAGCGGTTCGCCGTCGTTTTCAAA  
CGCAGTCACCGGGCATGGCGCGGTTCAATGGCTTCCACGCCGGGGCGCCGGCCACCATCG  
GGGGTCGGCCTCGGGGCATCGCGGGTGCTCGGCCCTCCCCAACGGGGT

>RXN03160-downstream

TAACACACCTTGGGGTTCAATCA

>RXN03164-upstream

CTTTTTTGCATCCAGATGCACAAAGCCGTGGCACAACGAGACAAACTGAGCACAATGGC  
TGTCATGGCATATCAACCAGCAGACAATCGCTATGACGAC

>RXN03164

ATGATCTACCGCAGGGTGGGAAATTCTGGGCTGAAGCTTCCGGCAATTTTCGCTTGGGCTG  
TGGCACAACCTTCGGTGATGACAAGCCGCTTTCAACGCAGCGCAGCATTATTCACCGCGCG  
TTTGATAGGGGAGTCACTCACTTCGATTTGGCTAATAACTATGGACCTCCAGCAGGTTC  
GCAGAGACCAACTTTGGCAGGATTTTGGCTGAGGATCTCAAAGCCACCGCGATGAGTTG  
ATCATTTCTTCCAAGGCGGGTTGGGATATGTGGCCTGGACCTTATGGTTTTGGTGGTTCC  
CGAAAGTATCTAGTGAGTTCCTTGATCAGTCCCTGACTCGCCTCGGCTTGGATTACGTG  
GATATTTTCTATCATCACCGCCCGGATCCAGATACTCCTTTGGAAGAAACCATGTACGCA  
TTGCGTGACATTGTTGCGTCTGGAAAGGCTCTTTACGTGGGTATTTCTTCCTACGGTCCA  
GAGCTCACAGCGGAGGCGGCTGAGTTCATGGCGGAGGAGGGCTGCCCGCTTCTGATTCAT  
CAGCCAAGCTATTCCATCATTAATCGTTGGGTGGAGGAACCGGGCGATGACGGTGAGAAC  
TTGTTGCAGTCAGCTGCCAACAATGGTCTTGGCGTCATTGCTTTCTCACCCTTGCGCAG  
GGCCTGCTCACGGACAAATATCTCGATGGAATTCCAGAGGGTTCCCGCGCCAGCCAGGGT  
AAGTCCCTGTCTGAGGGCATGTTGAACGTGAACAATATTGATATGGTCCGCAAGCTCAAT  
GACATCGCCCAGGAACGCGGGCAGTCACTTGCGCAGATGGCGCTTGATGGGTGCTGCGC  
GAGCAAAGAGAGTACGGCGCCGGATTACCG

>RXN03164-downstream

TGACCAGTGCATTGATTGGTGCT

>RXN03183

GAAGCCGAAGCAACCGCAGGCAAATTCGAAGTACAGCCCCTCGTAGGTAAAGACGGCGTC  
GGCGTATCCACCCTTGGTGGCTACAACAACGGCATCAACGTCAACTCCGAAAACAAGGCA  
ACCGCCCGCGACTTCATCGAATTCATCATCAACGAAGAGAACCACCTGGTTTCGCGGAC  
AACTCCTTCCCACAGTTCTGGCATCCATCTACGATGATGAGTCCCTTGTGAGCAGTAC  
CCATACCTGCCAGCACTGAAGGAATCCCTGGAAAACGCAGCACCACGCCAGTGTCTCCT  
TTCTACCCAGCCATCTCCAAGGCAATCCAGGACAACGCCTACGCAGCGCTTAACGGCAAC  
GTCGACGTTGACCAGGCAACCACCGATATGAAGGCAGCGATCGAAAACGCTTCCAGC

>RXN03183-downstream

TAGTTCGGTAATTTAGTTCATTC

RXC00354 - 5'-Region

GGCTTGTCGGTAAGGCTGCAGGGTAGCGGGAGTTTCCTTCAGATTGGAAGTTCTTTAATTTTCTCGATT  
ATGTACCTCATTTACGCGTAAAGTTTGGGGC

RXC00354 - coding Region

ATGGGAAAGTTACTTTTCGTAGACATCGGTGGCACACTGCTGGATTACTCAAATGAAGTTCCGCGTTTCG  
GCCGTTGACGCGATCCGTAAGGCACGCGCCAAAGGACACCGCGTGACTTGAGCTCTGGTTCGAAGCAGC  
GCTGAGGTGACTTCTCAGTTGTGGGATATCGGAGTGGATGGCCTCATTTGGCGCAAATGGTGGATATGTG  
GAAAGCGCACAGGAGTCTGTGTTCCACCGCCGTTTGTCGGGTGAGGAGACCCGCCACATTGTGGAGTGG



CTCTACAACCGTGGTTTGGAGTTTTATCTCGAGTCCAACAACGGTTTGTATGCAAGCCGTGGTTTCCGT  
GAGGCTTCTAAGCCAGTGCTGTCTCGCCTTTCGGAGAAGACCGACGTGACAGTCGATAGCATGTACCCG  
GATATGTTCTGGGGCGCGAGCCTTGATCGTGACGATGTGAACAAGATCAGTTACATCTTCAATTCTCAG  
GAAGATTTGGACGCAGCGCGTGAGGCGTTCCTAACCTGGAGCACACCACGTGGGGTGGTCAGACGGGT  
GCGTTGTTTCGGCACGATCGGTGTGTCTGTCAACAAGAAGATCGGCGTGATCGCCTGCTGAAGTACCTG  
AACGCAGATCGCGCAAACACCATTTGCGTTCGGCGACAGCGATGAGGATCTCTCCCTATTTGAGGCGAGC  
GCTTACGGCGTCGCGATGGGCGAGGCCACCGAATCGCTCAAGGCTGCTGCTGACCTGGTCACGGATGCT  
GTTGGGCAGGACGGCTTGCGCAATGCGTTTTTAAAGCTTGAGCTTATCGACGCC

RXC00354 - 3'-Region  
TGACCCCATCAAAGAACTTCCCA

RXC01748 - 5'-Region  
ATCACCAAATGTGGCGGTTTTGCGTCGAAAAGCGTGCTCTTTCTACACCTCTTTGAGGTTCATTTTTCGC  
GGTTTCCTCACAATCGCCTATTGTTAAGTAC

RXC01748 - coding Region  
ATGGCAGACGCGAAAAAGCAGGCGGATAAAGCCGCCAAGAAGCAGGTAAGAGCAGCCAAGAAGGCACAG  
CGCAAGGAGACTCGCTCACAATGTGGCAGGTCTTCAACATGCAACGCAAGCAGGATAAGGCTCTTATT  
CCGCTTCTGTTGCTCGCTATTCTTGGTATCCCGCTGGTCCTTTTCCTCATCGGTTTGATTTGGGGTGGT  
CAGTGGTGGATGCTTCCGATCGGCATTGCTGCAGGTGTTGTAGCTGCAATGTTTATTTTCACCCGTCGC  
GTTGAGCGTGACGTGTACAAGCGCGCCGAAGGTCAGCAGGGTGCTGCTGGTTGGGCTGTGGAGAACCTC  
CGCTCTGGCGTGGGCATGACCTGGCGCACCAAGACCGCTGTTGCAGTGACCACTCAGATGGATGCAGTG  
CACCGCGTCATTGGTCTGTGTGGTGTGTGCTGGTCGGCGAGGGCTCCCCTCACCGCCTGAAGCCAATG  
CTTGCGCAGCAAAAGAAGCGCCTGAACCGCGTGCGCACCTGGTGTTCCAGTGTATGAAATCATCACGGGC  
AACGGCGAAGGCCAGACCCCTATCGCGAAGCTGCAGCGTGAAGTGGTCAAGCTGCCTCGCAACTACAAG  
AAGAACGACGTCGCTGCCCTGGCCGCTCGCATTGAGGCTATGGACAATGTCGGAAACGCTCCTGGCGGA  
TCTTTGCCTAAGGGTCCATTGCCAAAGGGCGCAAGCATGTCCGGTATGAACCGCCGCGCTCGCCGACAG  
GCTGAACGCAAGGGCGAGGCT

RXC01748 - 3'-Region  
TAAAGCCTTTTCGCTTTCGCGTC

RXC01749 - 5'-Region  
GGTTTTTTCGCTGCTCTGGTTTAGGGACTGGTTTTGGGAACGTGCCAGTTCCACATCAAATAACGCTGA  
GGTCGTACTTAATCCATGAGATCATGAATGG

RXC01749 - coding Region  
GTGAGCTTCCTTGTAGAAAATCAATTACTCGCGTTGGTTGTATCATGACGGTCGGACTATTGCTCGGC  
CGCATCAAAATTTTCGGGTTCCGTCTCGGCGTCGCCGCTGTACTGTTTGTAGGTCTAGCGCTATCCACC  
ATTGAGCCGGATATTTCCGTCCCATCCCTCATTTACGTGGTTGGACTGTGCTTTTTGTCTACACGATC  
GGTCTGGAAGCCGGCCCTGGATTCTTCACCTCCATGAAAACCACTGGTCTGCGCAACAACGCACTGACC  
TTGGGCGCCATCATCGCCACCACGGCACTCGCATGGGCACTCATCACAGTTTTGAACATCGATGCCGCC  
TCCGGCGCCGGCATGCTCACCGGCGCGCTCACCAACACCCAGCCATGGCCGCGAGTTGTTGACGCACTT  
CCTTCGCTTATCGACGACACCGGCCAGCTTCACCTCATCGCCGAGCTGCCCGTCGTCGCATATTCTTG  
GCATACCCCTCGGTGTGCTCATCGTTATTCTCTCCATCGCCATCTTCAGCTCTGTGTTCAAAGTCGAC  
CACAACAAAGAAGCCGAAGAAGCGGGCGTTGCGGTCCAGGAACCTCAAAGGCCGTGCGATCCGCGTCACC  
GTCGCTGATCTTCCAGCCCTGGAGAACATCCCAGAGCTGCTCAACCTCCACGTCATTGTGTCCCGAGTG  
GAACGAGACGGTGAGCAATTCATCCCGCTTTATGGCGAACACGCAACGATCGGCGATGTCTTAACAGTG  
GTGGGTGCCGATGAAGAACTCAACCGCGCGGAAAAAGCCATCGGTGAAGTCAATTGACGGCGACCCCTAC  
AGCAATGTGGAACCTTGATTACCGACGCATCTTCGTCTCAAACACAGCAGTCGTGGGCACTCCCCTATCC  
AAGCTCCAGCCACTGTTTAAAGACATGCTGATCACCCGCATCAGGCGCGGCGACACAGATTTGGTGCC  
TCCTCCGACATGACTTTGCAGCTCGGTGACCGTGTCGCGTTGTGCGACCAGCAGAAAACTCCGCGAA  
GCAACCAATTGCTCGGCGATTCTTACAAGAACTCTCCGATTTCAACCTGCTCCCACTCGCTGCCGGC  
CTCATGATCGGTGTGCTTGTGCGCATGGTGAGTTCCCACTACCAGGTGGAAGCTCCCTGAAACTGGGT  
AACGCAGGTGGACCGCTAGTTGTTGCGCTGCTGCTCGGCATGATCAATCGCACAGGCAAGTTCGTCTGG  
CAAATCCCCTACGGAGCAAACCTTGCCCTTCGCCAACTGGGCATCACACTATTTTTGGCTGCCATCGGT  
ACCTCAGCGGGCGCAGGATTTTCGATCAGCGATCAGCGACCCCAATCACTACCATCATCGGCTTCGGT  
GCGCTGCTCACTTTGTTTCATCTCCATCACGGTGCTGTTTCGTTGGCCACAACTGATGAAAATCCCCTTC  
GGTGAAACCGCTGGCATCCTCGCCGGTACGCAAAACCCACCCTGCTGTGCTGAGTTATGTGTCAGATGCC

TCCCGCAACGAGCTCCCTGCCATGGGTTATACCTCTGTGTATCCGCTGGCGATGATCGCAAAGATCCTG  
GCCGCCCAAACGTTGTTGTTCTACTTATC

RXC01749 - 3'-Region  
TAGCATTGACCCCTTAAGCGCAG

RXC01971 - 5'-Region  
AGGTCTTGTTTATTTTCGGCTACTGATTCAGTAGCTGCGCTCCGATAGGATTCTTAGTTTTTCAGTTCAGT  
ATCTTTGAGCCACGGCTAGAATGTGAATCCT

RXC01971 - coding Region  
ATGTCTAAGAAGAAGCCTCGCCCCATTCCGGTTCCTGCCCAATTTATCCCTGGTCTCATTGATGCGCAT  
ACACATTTGGCATCGTGTGGAGGAGATCTTGCAGGGTTGGTGGAAAGGGCCAAGGAGGCGGGCGTCGAA  
AAGCTTTGTACCGTCGGTGATGGTTTGGCTGAGGCCGAGCTTGCCTGGAGGCCGCGCAACAGTTTGGC  
AATGTGTTTGTGCTGCGTGTGCGATTTCATCCGACGAAGGCTGATCAGTTGGATGGGGCTGCGCGTGCGCGG  
CTGACGCAGATGGCGGCGGATCCGAATTGTGTGGCCATTGGTGAGACTGGTTTGGATTTCGTATTGGATC  
AAGCACGATCCAGAGGACACGGCGGCGTTGGATGTGCAAGAGGAGGCGCTGCGCTGGCATATTGATTTG  
GCAATTAGTGCGGATAAGCCGTTGATGATTACCAATCGTGAGGCGGATGCTGATTTGATGCGAGTGTG  
GCGGATGCTCCACCTCCAAAAGATACGATTCTGCATTGTTTTCTTCGCCGTTGGACGTGGCGAAGGAA  
GCGTTGGATCGTGGATATGTGTTGAGTTTTGCGGGCAATGTGACGTTTAAGCGTAATGAGGAGTTGCGG  
GAGGCTGCTCGTATTGCGCCGATTTCCAGATTTTGATTGAAACCGATGCGCCGTATATGACGCCGGAG  
CCGTTTCGGGGGAGTAGGAATGAGCCGTCGTTGATTGGTCATACGGCGCTATGCATTGCGGAGGTTGCGG  
GGGATGGCTGTGGAGGATGTTGCGGCGGCTTTGAATGAGAATTTTGATCGCGTTTATGGGGTCACAAAT  
CTA

RXC01971 - 3'-Region  
TAACGTGAGGTAGCTCACAGTCA

RXC02697 - 5'-Region  
TTTGGCTCACCTCGATGATGTAGACATCCCCGATGAGGTGCGCGCACAGTTGCGGGCACTGGCTATCCG  
CTCAACCGAACGTCGGATGTAGTAGACGCGT

RXC02697 - coding Region  
ATGACACTTTTTCAACGTTTAAACCAACCCTGTAGTGCTCGGCGGCCTAGCAGGTGTTTTGCTTCTGCTC  
GGCTCTTTCGGTGGCGGTGCCATTCCGGTACCGTGGCGGAGTGCTCGATGCGTTGGGGCTTAACTTCCTT  
GCTTTTGGCCACGCGCAGGGTATTTCCAATACCGTGTGTGGGTTGGGCAGCTGCTGCTGATTGGCGCG  
TGGGTTACCTTGGACGTCGGTTGTTCAAGAAAAAGTCGCTGATGACACCGCAGACGCTGCTGACTTA  
GGTCTTGTAAGCGCACGTTGTATGCCATGGTGGTGGCCCTCATTTTTGCGGCACCAATGATGTCGCGT  
GATGTTTATTCCTATCTCATGCAGGGCGCGATGCTGCGTGATGGCTTCGATCCCTACACTGAGGGCGCT  
GCGGTAAACCCTGGCCCCATGTTGCTTGAGGTCTCTCATGATTGGCGCAACACCACGACGCCGTATGGT  
CCACTACACCTGTGGATTGGAGACATGATCACCACGGTTGTGGGCGATAATGTCACCTTGGGCGTCGTC  
GCTTACAAGATCTTGTGATCATTTGGCCTTGCTGTGACAGGCTGGAGCATTGTCCGCATTGCACAACAT  
TTTGGAGCCAACCCAGCAATTGCATTGTGGATTGGTGTGGCCAATCCTGTGATGATCATCCACATGATC  
GGCGGCATGCACAATGAATCCCTCATGGTGGGATTGGTCAGCGTCGGCTTGTTGCTAGCACTGAAGAAG  
CGTTTCGTGGCAGGTGTGGCACTCATTGCAGTGGCTGTGTGCTGAAAGCTACAGCGGCGATTGCACTT  
CCTTTTGTGGTGTGGATCGGCATGCATCATTTTCGAGGATTCTTAGCCACCAAAAAGGGCAAAGACTCC  
CCTACCCTTAAGCAACAGGTCCCCGCGTTCTTTGCCACTGGAGCTGCAGGTGTTGCTGTCACTGGTGT  
GTTGTGAGTGCATCACTTGGGCGTCTGGCGCTTCGTGGGGCTGGATCAGTGAGATCAGTGGCAACAGC  
AAGGTAATCAACCCGCTGGCTTTCCCTTCTTTGGTGGCCAGTGTGATCACCATGGTGGCTGAAGTGTT  
GTTGACGATTTGACTACAACGCAGTGGTTAATGTTGTGCGCTCAATCTCCATGCTGATCATGCTTGGC  
GGGTTGGTCGTATGTTGGTGGCTGTTCCGCCAGAACGAACGCAGGGCGGTCAGTGGTACAGCAGCGGCT  
TATGCCGTGGCTTTTGTGTTCAATTCTGTGACCTTGCCGTGGTACTACGCCAGCTTGATCTCTTTGCTC  
GGCACATTTAAACCACCGATGTGGTTGATTCGCTTCGCAGCGGGTGCTTCGGTGTGTTATCGCGCTGATG  
TTTACCGGAAGTGGAACACCAGCTGTACAACATCGTTACGGTGATCATCGCAGCAATTATCGCGTGG  
CTTGCCACCGTGGTGTGATCTTTGATGACACTGACCCTGCAACAACGGCCACGGAGAAACCCTCCCCGAT  
ACCGTTTCC

RXC02697 - 3'-Region  
TAGTTGCATAAGGTAAACCGCCA

RXS00148 - 5'-Region

CTTTGAGGGCAGCGCGCATGCGCCCGATGGTTATTTGAACATGACAATTGATGCCGCGGCGACGCTGGC  
TGACCTGCTAGATGCTTTGGGAGCTTAAATC

RXS00148 - coding Region

ATGACGTCGATCCCTAATTTTTTCAGACATCCCATTGACTGCTGAGACACGTGCATCGGAGTCACACAAC  
GTTGACGCCGGCAAGGTGTGGAACACTCCCGAAGGCATTGATGTCAAGCGCGTATTCACGCAGGCTGAC  
CGCGACGAGGCGCAAGCGGCGGGACATCCGGTGGATTCTTTGCCAGGTCAAAGCCATTTATGCGCGGG  
CCGTACCCAACTATGTACACCAATCAGCCGTGGACGATTTCGCCAGTACGCAGGCTTTTCAACCGCCGCG  
GAATCCAATGCGTTTTATCGGAGGAACCTTGCTGCGGGTCAAAAAGGTTTGTGCGTTGCGTTCGATCTA  
GCGACCCACCGCGGTATGACTCGGATAATGAGCGCGTGGTCCGCGATGTGGGTATGGCCGGCGTGGCG  
ATTGATTCGATTTTGGATATGCGTCAGCTGTTTGATGGCATTGATTTGTCCAGCGTGTGCGTGTGATG  
ACCATGAATGGCGCTGTGCTGCCGATTCTTGCGTTCCTATATCGTGGCGGCTGAGGAACAAGGTGTGGGT  
CCGGAGCAGCTTGCGGGCACGATCCAGAATGACATCTTGAAAGAATTTATGGTGCGCAACACCTATATT  
TATCCGCCGAAGCCGTGCGATGCGCATCATTTCCAACATCTTTGAGTACACCTCCTTGAAGATGCCACGT  
TTTAACTCCATTTTCGATTTCTGGCTATCACATCCAGGAAGCGGGAGCGACTGCCGATTTGGAGCTGGCC  
TACACTCTGGCGGATGGTATTGAATACATCCGTGCAGGTAAAGAGGTAGGCCTTGACGTGGATAAGTTC  
GCGCCTCGTCTGCTCTTCTTCTGGGGTATTTCTATGTACACCTTCATGGAGATCGCAAAGCTGCGTGCG  
GGACGACTGCTGTGGAGCGAGTTGGTGGCAAAATTCGATCCGAAAACGCCAAGTCCCAGTCGCTGCGC  
ACGCACTCGCAGACCTCTGGTTGGTCGTTGACCGCGCAGGATGTGTACAACAACGTCGCCCCGACCGCG  
ATTGAGGCGATGGCTGCAACCCAGGGCCACACCCAGTCGCTGCACACCAATGCACTTGATGAGGCGTTG  
GCGCTGCCACCGATTTCTCTGCTCGTATCGCCCCGAAACACCCAGCTGTTGCTGCAGCAGGAATCTGGC  
ACGGTGCCTCAGTTGATCCATGGGCGGGCTCCTATTACGTGGAGTGGTTGACCAATGAGCTGGCTAAC  
CGCGCGCGCAAGCACATCGATGAGGTGGAGGAAGCCGGCGGAATGGCGCAGGCCACCGCGCAGGGAATT  
CCTAAGCTGCGCATTGAGGAATCAGCGGCACGCACCCAGGCTCGCATTGATTCCGGCCGCCAGGCGCTG  
ATCGGCGTGAATCGCTACGTGGCGGAAGAAGATGAGGAAATTGAAGTCTCAAGGTTGACAACACCAAG  
GTTTCGCGCAGAACAGTTGGCTAAACTCGCGCAACTGAAAGCAGAGCGCAACGATGCGGAAGTCAAGGCT  
GCGCTGGATGCGTTGACAGCTGCTGCCCCGCAACGAGCATAAAGAGCCAGGGGATTTGGATCAGAACCTG  
CTCAAACCTTGCCGTCGATGCTGCGCGCGCAAAAGCTACCATTTGGAGAGATCTCCGATGCTTTGGAAGTT  
GTCTTTGGCCGCCACGAAGCAGAAATCAGGACGCTGTCTGGCGTGTACAAGGATGAGGTTGGAAAGGAA  
GGCACAGTGAGCAACGTCGAACGCGCGATCGCCCTGGCTGACGCCTTTGAGGCTGAGGAAGGCCGCCGC  
CCACGTATCTTTATTGCCAAGATGGGCCAGGATGGACATGACCGTGGACAGAAGGTTGTGCGCTCTGCC  
TATGCTGACCTGGGCATGGACGTGGATGTTGGACCGCTGTTTCAAACCTCCAGCCGAAGCTGCCCGCGCC  
GCCGTGGACGCCGATGTTACGTGGTGGGTATGTCTTCGCTGGCAGCAGGCCACCTCACCTTGCTGCCC  
GAGCTGAAGAAAGAACTTGACGCTCTTGCCCGCGATGACATTCTGGTCACCGTGGGCGGCGTCATTCCG  
CCGGGCGATTTCCAGGATCTCTACGATATGGGTGCCGCCGCGATTTACCCTTCAGGAACCGTCATCGCG  
GAGTCGGCGATCGATCTGATCACCCGACTCGCCGCACACCTGGGCTTTGACCTGGATGTGGATGTGAAT  
GAA

RXS00148 - 3'-Region

TGATCACGGTTTCCTAGAAGACA

RXS00149 - 5'-Region

TTTTCGTAGGTAAACACAGGTGAAGGCTTTACAAGCTTGTGAACTCCCTACACAAAAGCAATCCAATAG  
CTATCCATAAGCAAGAGAAAGTAAGTCTACG

RXS00149 - coding Region

TTGACTGATCTCACAAAGACTGCGGTGCCCGAGGAACTTTTCAGAGAACCTCGAAACTTGGTACAAGGCT  
GTGGCCGGTGTTCGCGCGCACACAGAAAAAGACATCGGCGACATTGCCGTAGATGTGTGGAAGAAA  
CTCATCGTCACTACACCGGATGGTGTGATATCAATCCGCTGTACACCAGAGCAGATGAGTCCCAGAGG  
AAATTCAGTGAGGTTCCCTGGTGAAGTTTCCCTTCACTAGGGGAACCACTGTTGATGGTGAACGCGTTGGT  
TGGGGTGTACTGAGACTTTCGGACATGACAGCCCGAAGAATATCAACGCTGCGGTGCTGAATGCTCTG  
AATTCTGGCACCACCACATTGGGTTTTGAGTTCTCTGAGGAATTCACGGCAGCTGATCTTAAAGTTGCT  
CTCGAAGGCGTGTATCTCAACATGGCTCCGTTGCTGATTCATGCGGGTGGATCCACGTCAGAGGTTGCA  
GCGGCGTTGTATACGTTGGCGGAGGAAGCCGGAACGTTTTTTGCTGCGTTGACCTTGGGTTCTCGTCCT  
TTGACGGCGCAGGTTGATGGTTCGCACAGTGACACCATTTGAAGAAGCAGTTTCAAGTTGGCAGTGAATGCT  
TCCAAGCGTGCGAATGTGCGCGCTATCTTGGTGGATGGTTCCAGTTTTTCCAACCCAGGGCGCGTCCGAT  
GCTCAAGAAATTGGTCTAAGTATCGCCGCCGGTGTGGATTATGTCCGTGCTTGGTTCGATGCAGGCCTT  
TCCACGGAAGCTGCACTTAAGCAGGTGGCGTTCCGTTTTGCGGTCACCGATGAGCAGTTCGCGCAGATT  
TCTAAGCTGCGTGTGGCTCGACGTCTGTGGGCCAGGGTGTGTGAGGTGCTTGGTTTTCCAGAGCTGGCC  
GTAGCACACAGCATGCGGTGACTGCACGAGCGATGTTTAGCCAGCGTGATCCGTGGGTGAATATGCTG  
CGCAGTACTGTTGCAGCTTTCGCTGCAGGCGTCGGTGGAGCAACCGATGTGGAGGTTTCGTAATTTTATG



GATGCGATCCCAGATGGAGTTCCTGGAGTGTGCGAGGAATTTGCTCACCGCATCGCGCGCAATACTAAT  
TTGTTGTTGCTAGAAGAGTCACATCTTGGTCACGTGGTTGATCCTGCTGGTGGATCATATTTCTGTTGAG  
AGCTTCACCGATGATCTAGCGGAGAAGGCGTGGGCTGTGTTTCAGTGGCATCGAAGCTGAGGGCGGATAC  
AGTGCAGCTTGTGCATCCGGCACGGTGAAGTGCATGCTTGATCAGACGTGGGAGCAGACTCGCGCTGAT  
GTGGCGTTCGAGAAAGAAGCTCACTGGAATTAATGAGTTCCTGAACTTGGCGGAGTCTCCGCTGCCA  
GCTGATCGTCGGGTAGAACCTGCAGGTGTGCGTCGATGGGCAGCGGATTTTGAAGCGCTGCGCAATCGT  
TCGGATGCTTTCTTGGAAAAGAACGGCGCGAGGCCACAGATCACGATGATTCCTCTGGGACCGTTGTCC  
AAGCACAATATTCGCACTGGTTTTACTTCCAACCTGTTGGCTTCCGGTGGCATTGAAGCAATCAACCCG  
GGTCAACTTGTTCCTGGCACTGACGCTTTTGCAGAAGCTGCACAGGCCGAGGCATTGTAGTGGTGTGT  
GGAACGGACCAAGAGTATGCCGAAACGGGGGAGGGAGCCGTCGAAAAGCTCCGCGAAGCGGGCGTTGAG  
CGCATCCTGCTTGTGCGCGCCGAAGAGCTTTGAGGGCAGCGCGCATGCGCCCGATGGTTATTTGAAC  
ATGACAATTGATGCCGCGGCGACGCTGGCTGACCTGCTAGATGCTTTGGGAGCT

RXS00149 - 3'-Region  
TAAATCATGACGTCGATCCCTAA

RXS00948 - 5'-Region  
ACACCCTCCAAATGATCTCGTAAAACAGTATTGAATTTAGGTACGACTCTAATCGTACCTTGCCCTCAA  
GCCAAGCTAGTTGTACGATCAAACCTCGTTGT

RXS00948 - coding Region  
ATGGCAAACGTCGTACTAGTCGATCGAATGGAGCCTTTGGTGTCCAAGCTGTTTACCCCAATTCAAATC  
CGCGACATCACCATCCCCAACCGCGTGTGGATGTCACCGATGTGCACCTACTCTGCAGCCACCGGTTCA  
GGTCTTCCACCGATTTTACACAGGCTCATTACGCAGCTCGCGCAGCAGGTGGTGTGCGATTAGTCATG  
GTTGAAGCAACTGGAGTGAACCCCGTAGCTCCCATCTCCCCAGTCGACCTTGGACTTTGGAGCCATGAC  
CAAATTGAACCATTTCTCCCGAGTGACAGCAGCTATTCGCGCCGGTGGGGCAGTACCGGCCGTTCAATTA  
GCCCATGCTGGCCGCAAGGCATCCACCGATGCTCCGTGGAATGGTGGCGGATATGTTGGACCAGAAACC  
AATGGATGGGAGACTGTGCGCCCCAGCCCTCTGGCATTCCCAGGTTTGCCTGCTCCGCGCGAGCTGACG  
GTTTCAGAAATCCAAGAGGTTGTGCAGCAGTTCGCTGGCGCCGCGGTTTCGTGCCGATCAGGCTGGTTTT  
GATGTCGTGGAAATTCACGCAGCACACGGCTACCTTTTGCATAACTTCCTTTCTCCGATCTCCAACAAG  
CGCACCGATTATACGCGGATCTTTAGAAAACCGCGCTCGCATCGTGCTCGAAGTCATTGATGCAATC  
CGCGCAGTGTGGCCAGAGGAAAAGCCTGTATTATGCGCATTTCCACCACCGACTGGGTGGAGGAAAAC  
CCACAGGATGATCGCGAGTCTTGGACGCTGAGCCAAAGCAGGAGCTGGCTTTGTGGGCATCCGAGCAC  
GGAGTTGATTTGATCGATGCCTCTTCTGGTGGCCTCGACATCGTCCCCATTCCGCATGACCGCGATTAC  
CAAACCGCGAAGGCCGAGATCTTACGCAAGTACCGGAGTGACAGTCGCTGCTGTGGGGCGCATTTGAT  
GACGCCCCAACTGCGCACAAATTTGGTTGATTCTGGCGATGTCAATGCAGTTTTCTCGGCCGTCCACTG  
CTCAAGGATCCTTCTGGGCAAACCAAGCAGCCCTCGCACTAGGTGCGGAACCCAGGTATGTTACCAA  
TACGACTACGTA

RXS00948 - 3'-Region  
TAAAGGAGAGTTGACATGAAGGT

RXS01166 - 5'-Region  
ACCGTACCCACAGACACACCAGAATTAACAGAAACAGACTGAAAAACAACATCGCTCGACATGCGCGTA  
ATCCTAACCCGCGCACACTAATGTGGCCGAT

RXS01166 - coding Region  
ATGGGCTACACCAACCTCAACGACACACGGGTCTTGCAGCGCCGGGTCATGTGATGCCTGGTGGCGCACG  
ATGTCTCCGCTAGTGCAGCAGGGAAGTGAGGCAGTCTTTCGGCGCATCATGGGTCTCTCGCGGCGTCCT  
GATCGGAAACCTGGCTTTGACGATGTCCACATTTCCGGCGCAGCTGTTTCGAGTTCCCGGTCTAAAACAC  
GGCACGTTGGTCAATGCTGCACCTTGAAAGTTTTGGGCGCACGGGGCGAGCCCAACCCCGCGAGTTTCG  
TACCGTTTTGAATACATCACCGGTGATTCCGCGAGGTCGAGCCATCACTGCGACCGGCGCTGTCTCTTT  
TCCACACGCCCCCTGGACAACCGGCCCGCGTCCCGCGATCGCCATGGCTCCATCCACCCAAGGCGTCGCA  
CAGCACTGCGATCCCTCCACACCTGCGCCATCGGACTCAACGCATTCTATGACAAACCTTTCGACGCA  
ATCATTGCTTACGAACCTCCCGTCATCCTCTGGTTTCTAGCTCACGGACTTGACGTTGTGTTTCATCGAT  
TACCCCGCGACCCCGCAACCGGCGTCCAATACTATTGCGATTCCATCGCTGCAGCTAAATCGCTTCTC  
GACGCCGTCTCGCCTCCAGACAACTCGGCCTTTACCGGAAGCACCGCTTGGCCTGTGGGGATTCTCC  
CAAGGAGGCGGCGCCACTGGCTGGGCTGCACAATTGCAGGATTACGCACCTGATGTCCGCCCAAAGGCA  
GCGGTGCTGGGCGCTCCACAGTGGATCTTTCGCGCTTGGACACTGTGACGGCGGATTGCTCACC  
GGAGTGATTGCCATCGCGGAGCTTGAGTGAAGTCTTTCAGAGATGTTTGAAGGAAATCATGTCG  
GTGTTAAATGAACGCGGAGTCAGTGATGTGCTGAAAAATATCACAGCTGCGCGGGAGGTTCTTGTG



GCCAGTGGCTACTCGTCTTCCCGCGGGTGGACACATCAGGGCACGCCGCTGGCAGACATTCTGGACGAT  
CTGCCACTTGTTCGCTGAGTTTGGGAAGCAAAGCTGGGTCTGTGGCGCCAGAAATCCCAGTGCTG  
TTGTGGGGCTCTAAAAATGATGATGTCATTCCCATTTAGGGAATTGCGTGATAGCTGGGCG  
GACAAGGGTACGCCATTGACCTGGCATGAATCCCAAGCGCCGCGTGTGCCAGGACGCACAGGTCTCAAC  
CATTTCCGGGCCCTATTTTAGAAACCTGGAAAAGTACTCGGGATGGCTCATAGATCATCTTGTC

RXS01166 - 3'-Region  
TGAGTGCCGTTTTAAAGGCTCGG

RXS01746 - 5'-Region  
AAACCGCCACTCCCCCTTCACTGGGGAGTGGCGGTTTTGTGCTTTCATGCATGCAGTGTGTGACTTATC  
AACCTTGTTAGGGCTAGGGTGGATATCTATC

RXS01746 - coding Region  
ATGACTGCACCAAGAGATCCTTTTTTCCCGCAGATCTTCTATCCGCGCGTCTGCAGAGCCCATTTGAA  
ATTCAGCGGTGGGTTTGATCGATTATCAAGAGGCCTGGGATTATCAAGCAGAGCTTGCTACCCGTAGG  
GCTAATGATGAAATCCCTGATCAGCTGCTTATTTTGGAGCACCCGTCGGTGTATACCGCAGGTAAGCGC  
ACCCAGCCGGAAGATCTTCCCACCAACGGACTGCCGGTGATCAATGCTGATCGTGGTGGTCGCATCACG  
TGGCATGGTCCTGGCCAATTGGTGATCTATCCGATCATCAAATTAGCCGATCCGATCGATGTGGTTGAT  
TACGTAAGACGCCTCGAGGAAGCGCTCATCCAAGTTGTCGGCGATATGGGTGTTGCCGGCGCTGGGCGC  
ATTGATGGGCGTTCGGGTGTGTGGGTGCCAGCTCATGATGGTTGGGTGGACAGCAAGGTTGCGGCCATC  
GGCATTCGAATAACTCGTGGTGTGCAATGCACGGTGTGGCCATCAACTGCAACAACACGTTGGATTTT  
TATGAGCACATCATTCCTGTGGCATTGCTGATGCAGGCTTGAGCACACTCTCGAGGGAAGTGAAGAGG  
GACGTTTCAGTTGAGGAATTAGTCGAGCCATCGATCCGCGCATTTGGATGATGCTTTGGCTGGTCGGCTG  
GTTGTTTCTGATCATTTCTTTCGGCAGCGCGCCCGACCCAATAAGAATCTCCCTAAACGGGGG

RXS01746 - 3'-Region  
TAGTACGAGGAATTTTGTGCGTG

RXS01747 - 5'-Region  
CGAAGTAGAGCCGATTGCAGAATCGGCGGAATGAGACGTCGAAAAGCGTTTAAGCTTTCCTAAAAATA  
TCACTAACTCGAAAGATGTAAGGTTGCATTT

RXS01747 - coding Region  
GTGACTATCGCACCTGAAGGACGACGACTGCTACGCGTCGAAGCTCGAAACTCAGAAACCCCGATTGAG  
ACGAAGCCTCGATGGATTAGAAACCAGGTCAAAAACGGACCTGAGTATCAGGATATGAAGGAACGTGTC  
GCTGGCGCATCACTACACACTGTGTGTCAGGAGGCTGGCTGTCCTAATATCCATGAGTGTTGGGAATCC  
CGTGAGGCAACCTTCCTCATTGGTGGCGCCAACCTGCTCTCGCCGCTGTGATTTCTGCATGATCAACTCG  
GCTCGCCCTGAGCCACTCGACCGCGGTGAGCCACTGCGTGTGCTGAGTCTGTTGCTGAGATGCAGCTG  
AATTACTCCACCATCACCGGTGTTACCCGTGATGATCTGGATGATGAAGGCGCATGGCTGTACTCAGAA  
GTGGTTCGTAAGATCCACGAGCTGAACCCACACACCGGTGTGGAAAACCTGGTGCCTGATTTCTCCGGC  
AAGAAGGATCTGCTGCAGGAAGTTTTTGAATCCCGCCAGAGGTTTTCGCTCACAACGTGGAAACTGTG  
CCACGTATTTTCAAGCGCATTCGCCCAGCATTCCGCTACGAGCGTTCACTTGATGTGATCCGTCAGGCT  
CGCGATTTTCGGTCTGGTGACCAAGTCCAACCTGATTTTGGGCATGGGTGAAACCAAGGAAGAAATCACC  
GAGGCGCTGCAGGATCTGCACGACGCTGGCTGTGACATCATCACCATCACCAGTACCTGCGTCCTGGT  
CCTTTGTTCCACCCCATCGAGCGTTGGGTGAAGCCTGAGGAGTTCTCGAGCACGCTGATGCTGCAAAG  
GAAATGGGCTTCGCTGCTGTTATGTCCGGCCCATTTGGTTCGTTCTTACCGTGCAGGCCGTCTGTAC  
GCGCAGGCCATGGAGTTCCGTGGCGAGGAAATCCCAGCACACCTCGCGCACCTGAAGGATACTTCCGGA  
GGATCCACCGCCAGGAAGCATCTACACTTCTGGAGCGTTACGGTGCTTCCGAAGACACCCAGTGGTG  
TCCTTCAAC

RXS01747 - 3'-Region  
TAAGCCCGAAGTTTTTTAACCGC

RXS01879 - 5'-Region  
CTTTGCGGGCCGCTGATATTGATCCAACGCTTCGTGGCGAAAAGCTTGATGTCACTGACTATGTGCGCC  
TAGCTGGGGTGTTCAGCAAAAGGATGAGAA

RXS01879 - coding Region  
GTGAAAATTACCGCTAAGGCGTGGGCGAAAACCAACCTGCATTTAGGTGTGGGACCGGCTCACGACGAT  
GGATTTACAGAGCTCATGACGGTGTTCAAACCATGATCTGTTTGACACCGTCACCTTAACCACCTC

GATGAGGAGTTGGTGGAGGAGGGGAGCGTCGTCAAGCAATTATCTGTGACCGGTGCCCCGTGGCGTGCCT  
GAGGACGCCAGCAATCTTGCGTGGCGCGCTGTGGATGCGTTGGTTAAGCGGCGCGGAAAAGACGCCG  
CTGTCTGCAGTTTCGCTGCATATTTCCAAGGGGATTCCGGTGGCTGGCGGCATGGCTGGCGGCTCTGCG  
GATGCGGCTGCGACACTGCGCGCAGTGGATGCCTGGATTGGGCCTTTCGGCGAGGACACATTGCTGGAG  
GTTGCCGCGGAGCTCGGCTCAGATGTGCCGTTTTTGCTGCTTGGTGGCACCATGCGCGGTACCGGTGCG  
GGCGAGCAGCTGGTAGATATGTTGACGCGCGGCAAGCTACATTGGGTGGTGGCCGCGATGGCGCATGGC  
CTGTCCACGCCTGAGGTATTCAAAAAGCATGATGAGCTGAATCCGGAATCGCATATGGATATCAGCGAC  
CTCAGCGCCGCACTTCTCACCGGCAACACCGCCGAGGTGGGGCAGTGGCTGCACAATGATCTGACCAGC  
GCCGCACTCAGTTTGCGCCCTGAACTGCGCAGCGTCCTCCAAGAAGGCATCCGCTCCGGCGCGCATGCA  
GGAATTGTCTCCGGCTCCGGCCCCGACCACGGTATTCTTGTGCGAATCGGAGCACAAAGCGCAAGACGTT  
AAAGAGGCGCTAATCGACGCCGCGCAGGTGTACGCTGCTTACACCGCCACCGGCCCTGCGGCCTCAACC  
GCCGACCAGCGCGGCGCACACATTTTACTGTTTCA

RXS01879 - 3'-Region  
TAATAAAGACAACTTAAGTATC

RXS02023 - 5'-Region  
GATGTGGCAGCAATTTTGAAGCAGTACCTGAGCGAGTAACCGCATTCGGGGTTATCGTGGGACTTCCGA  
AATGTAAGTAGAGACTAGAGGAGGAAACACG

RXS02023 - coding Region  
ATGGCTCCTAAACAACTCCCAGCCCAGAGAAGAATCGAAACCTGGTGGGACCAGTTCTGCAACGTCGG  
CAGACAGAGGGTACTTTTGATCAACGCTTGCTAGAAATGCGCGCTGATCACAATTGGAAGCACGCCGAT  
CCATGGCGTGTACTGCGTATTCAGTCTGAGTTTGTGGCGGGTTTTGATGCCCTCCACGAGATGCCAAAG  
GCCGTAACCGTCTTTGGTTCCGCACGCATTAAAGAGGATCACCCGTAACAAGGCGGGTGTAGAACTT  
GGTGAAGAGCTCGTTGCAGCGGACTACGCAGTTGTACCGGTGGCGGTCCAGGTCTGATGGAAGCCCC  
AATAAGGGGGCAAGCGAGGCCAATGGTTTATCAGTTGGTCTGGGCATTGAGTTGCCACATGAACAGCAT  
CTGAACCTTATGTGGATTTGGGTCTGAACCTCCGGTACTTCTTCGCACGCAAGACCATGTTCTGAAA  
TACTCCAGGCTTTTGTGTGTCTGCCTGGTGGTTTCGGCACGCTCGATGAGCTTTTCGAGGTCTCTGC  
ATGGTACAAACCGGCAAGGTACCCAACCTTTCCCATCGTGCTGATCGGCACTGAGTTCTGGGCAGGTTTG  
GTGGATTGGATCCGTCACCGCCTGGTAGAGGAAGGCATGATCGATGAGAAGGATGTTGACCGGATGTTG  
GTCATGATGACCTGGATCAGGCCGTCAAATTCATCGTCGATGCACACGCTGGATTGGACGTAGCGCGT  
CTCCACAAT

RXS02023 - 3'-Region  
TAAGCAGTGGCTACATTAGGTGT

RXS02106 - 5'-Region  
GGTCGCCGCTTTTCGACGCCCGCCTGCGGCGGGATGACTGTGATGGAGGGGCGCGTCGACAAGCAAAT  
CTCTTTAGCAAATTCGGTTACTGTGGGGCGC

RXS02106 - coding Region  
ATGAATAACCATTTTGAGCTCAAAGTACCTGGTGGAAAGCTTGTCGTCGTTGATGTGACCACCGATCTG  
GATTCATTTGCTGACGTGAAGATTTCCGGCGATTTCTTCCCTCGAACCCGATGAGGCATTCTTCGCCCTT  
GGCCGGGCGCTGCAGGGGGCGTCGGTGGGTGATAACACTGATCGTTTGCAGGCAAAGTTGGATGCAGCG  
TTGGCGGAATATGATGACGTTGAGCTACACGGCTTTAGCACTGCGGATATTGCTTTAGCTGTGCGTCGG  
GCAGTCACCGGCGCGCAAGATTTACCGGATTATGAATGGGAAATCCTGCACCCAGGGGTGCTTCCTACC  
CCACTTAACGTTGCGTTGGATGAGCTCCTTTTGGACCAAGTTGCCAGTGGTCAGCGTGGCCCGACGATG  
CGCATTTGGGATTGGGATGATCGCGCCACAGTGATCGGTAGTTTCCAGTCATATGTCAATGAAATCAAC  
CAAGAAGGCGTTAATGAACATGGTGTGACCGTGGTACGACGCATGTCTGGTGGCGGTGCAATGTTTATG  
GAGGGCGGCAACTGCATCACCTATTCCTGTATGCACCGGAATCTCTCGTTGCTGGTTTGGAGCTATGAG  
CAGTCCTATGAATATTTGGATCGTTGGGTGATTGCTGCGCTGAAGACACACGATGTTGACGCTTGGTAC  
GTGCCTATCAATGACATCACCTCCACCGGCGGAAAAATCGGTGGCGCTGCACAGAAACGTCGCAGTGGC  
GCAGTCCTCCACCACGTGACCATGTCCTATGACATCGATGCGGACATGATGACCCAGGTGTTGCGCATT  
GGAAAGGTGAAGATTTCCGACAAGGGTCTTCGCAGCGCAAAGAAGCGCGTTGATCCTCTGCGCCGCCAA  
ACAGGTGCATCACGTGAGCAAATCATCGACACCCTAAAGTCCACATTCAGTGCTAGGTACGGCGCGCAA  
GAAGTAGAGCTCAGCGATGAAGATTTTCGCGGCAGGCCACGACCTAGTAAAAACCAAATACGCCACCGAG  
GAGTGGACTAAGCGAGTTCAA

RXS02106 - 3'-Region  
TAGTTTCTATGGATCTGCACAAG

RXS02228 - 5'-Region

ACAGAAGCGTCAACTGCTCAACTTCTCGACAGCGACACACACGGCGTGGGACGCTACGTTGCTCGC  
TGGACTTTTAACTTAAGGGAGATCTAGATC

RXS02228 - coding Region

GTGGTAACACCGATCGCAGTGGTTGGACCCACTGCATCTGGAAAATCAGCTTTGGGAATTGCTCTAGCC  
CACAAGCTTGACGGTGAAGTAGTCAATGTGGATTCCATGCAGCTGTACAAAGGCATGGACATCGGCACG  
GCAAAGCTGACTGTGGAAGAACGCGAAGGCATTGCGCATCATCAGCTCGATGTCTGGGACGTTACCGAA  
ACTGCGTCAGTGGCGAGGTTTCAATCCGACGCCGTTGCCGATGTGGAAGATATTATGTCCCGTGGCAAA  
ACCCCATCTTGGTTGGCGGCTCCATGTTGTACGTCCAATCTTTGGTCGATGATTGGCAATTCCCACCT  
ACCGACAGCGCTGTTGCGGCACGCTTTGAGGCCCGCTTGGCAGACATCGGTGTGGAAGCACTACACGCT  
GAACTTACTCAGCTTGACCCAGAAGCAGCAGCCGTCATCGAAAGCAATGATCCCCGACGCACCGTCCGA  
GCATTAGAAGTCATTGAACTAACCGGCCAGCCCTTCCAAGCAAGCCAACCGCCCAAAGACGCGCCACCT  
CGCTGGGGAACTCGAATCATTGGCCTGAAAACCACTCCAGAATGGCTAAATCCACGCATCGAGCAGCGC  
ACCGCCAGGATGTTTGAACAAGGCTTTGTGCGCCGAAGTGGAAACACCTTGTGCAGCAAGGACTCATCGCT  
GACTCCACCGCGGGACGAGCAATCGGCTACTCCCAAGTACTGGCAGCCATGGCAGGGGAGATGACCTGG  
GAAGACGCCTTCGAACGCACGGTCACCGGAACCAGACGCTATGTCAGGCGCCAACGCAGCTGGTTCAAC  
AGAGACCACCGCGTGTCTGGGTCGACGCCTCTGGCGATCCCACCGCACAAGCCTTGGAGATTTTGGGT  
CTACAA

RXS02228 - 3'-Region

TAGCGAGGGTGAATTTGACCATC

RXS03212 - coding Region

GCCTCACTTAACTGGTCAGTCATCGTTCCAGCCCTAGTCATTGTCCTAGCGACAGTGGTGTGGGGTATC  
GGATTCAAAGATAGCTTTACCAACTTTGCTAGTTCTGCGTTGTCAGCAGTAGTTGACAATCTCGGCTGG  
GCCTTCATTTTGTGGTGGCACAGTCTTTGTATTTTTTATCGTTGTTATCGCCGCTAGTAAATTCGGCACG  
ATTCGCTTAGGCCGCATTGATGAAGCACCAGAGTTTCGCACGGTGTGATGGATTTCCATGATGTTTGCT  
GCAGGTATGGGTATTGGTTTGATGTTCTACGGAACCACAGAACCTTTAACCTTCTACCGCAATGGTGTA  
CCTGGACATGATGAACACAATGTTGGCGTTGCTATGTCCACGACAATGTTCCACTGGACCTTGCATCCA  
TGGGCTATCTACGCAATTGTGGGCTAGCCATTGCCTATTTCGACCTTCCGAGTGGGCGGTAAACAGCTT  
CTAAGCTCTGCATTTCGTGCCACTCATTGGTGAAAAGGTGCAGAAGGATGGTTGGGCAAGCTCATCGAC  
ATCCTGGCGATTATCGCCACCGTATTCCGGCACGGCATGTTCCCTTGGCCTTGGTGGCCTGCAGATTGGT  
GCAGGCCTGTCCGCAGCAAACATCATTGAAGATCCAAGCGATTGGACCATCGTTGGCATTGTTTCTGTT  
TTGACCCTGGCATTATCTTCTCCGCTATTTCTGGTGTGGGCAAGGGAATCCAGTACCTCTCCAACGCC  
AACATGGTTCTGGCAGCTCTGCTCGCGATTTTCGTGTTGTTGTCGGACCAACCGTGTGATTTTGAAC  
CTGCTGCCAGGTTCTATTGGCAACTACCTGTCCAACCTTCTTTCAAATGGCAGGCCGCACTGCCATGAGT  
GCCGACGGCACAGCAGGTGAGTGGCTAGGTAGCTGGACCATCTTCTACTGGGCATGGTGGATCTCTTGG  
TCACCATTCGTAGGAATGTTCTTGGCACGTATTTCCCGTGGCCGCTCCATCCGTGAGTTCATCCTGGGC  
GTGTTGCTCGTCCCAGCAGGTGTGTCCACCGTATGGTTCTCCATTTTGGTGGCACTGCGATTGTCTTC  
GAACAAAATGGGGAATCCATTTGGGGTGATGGTGCAGCAGAAGAGCAGCTTTTGGATTGCTTCATGCA  
CTTCCAGGTGGGCAAATCATGGGCATCATCGCCATGATTTTGCTGGGTACTTTCTTCATTACCTCTGCT  
GACTCTGCTTCCACCGTCATGGGCACCATGAGTCAGCACGGCCAGCTGGAAGCCAACAAGTGGGTGACA  
GCTGCCTGGGGTGTGCTACCGCAGCTATTGGACTAACGCTATTGCTTTCTGGTGGTGACAATGCCTTG  
AGCAACTTGCAAACGTCACCATCGTGGCTGCAACACCATCTTGTTTGTGGTTATTGGATTGATGTTT  
GCG

RXS03220 - coding Region

ATGGGCTTAAGGGAAATTTTGTCCAGCAAGTGGCTTGTGCGCATCCTCCTGGTAGGTATCGGATTGGGT  
GTCGCACAGCAGCTGACCGGCATCAACTCCATCATGTACTACGGCCAGGTTGTTCTCATTGAGGCTGGT  
TTCTCCGAGAATGCAGCTCTGATCGCCAACGTGGCGCCAGGAGTGATCGCAGTTGTCGGTGCATTCATC  
GCACTGTGGATGATGGATGGTATCAACCGCCGTACCACCTCATTACCGGTTATTCTCTCACCACCAT  
AGCCACGTATTGATCGGTATCGCATCCGTAGCATTTCCAGTCGGCGATCCTCTTCGCCCCCTACGTTATC  
TTGACTCTGGTTGTGGTCTTCGTGGGATCCATGCAGACCTTCTCAACGTAGCTACCTGGGTATGCTC  
TCTGAGCTCTTCCCGCTGGCAATGCGCGGTTTCGCAATCGGTATCTCAGTGTTCTTCTCTGGATCGCA  
AACGCGTTCTCGGATTGTTCTTCCCAACCATCATGGAAGCAGTAGGACTAACCGGAACCTTCTTCATG  
TTCGCCGGAATCGGTGTGGTTGCCTTGATCTTCATCTACACCCAGGTTCTTGAAACTCGTGGACGTACC  
TTGGAGGAGATTGATGAGGATGTTACTTCCGGTGTGATTTTCAACAAGGACATCCGAAAAGGAAAGGTG  
CAC

RXS03220 - 3'-Region  
TAAAAACCCAGACACTGCATAGATAACACG



## APPENDIX B: AMINO ACID SEQUENCES

> RXA00051 (1-1404, translated) 468 residues  
 MNASPAPTRS FKGLRARHIH FIALGSAIGT GLFYGSAGAI QAAGPSVLLV YLLGGAVVYF  
 MLRALGEMAV HHPVRGSFAV YTRAHLGGWA GYITGWMFAF EMLIVCLADL TAIGIYMNEF  
 FPGTPQWTWV VATLLIVGGA NLASVRWFGE LEFIFTIIVK TAVVAMIVGG AAILAFGLGA  
 NAEVAGVSNL WEHGGFFPNG VEGMIAAFIL VLFAFGGTEI IGvagSEAED PEKSIPKAVN  
 TVPVRILLFY VGAILVILAL NPWPSITGEE SPFVQIFDTL GVNWAAGLLN AVVITAALSA  
 INADLFGAGR VLTGLAKENL APKAMGKIAK NGVPVMTTII MIIVLIVGVI LNAVLPERVF  
 EIVASLATFA TVYVWLMILL AQVGSRRNMP ADEVKSLKFP VPFYFPGQYF AILFIAFTFG  
 IMVWYDNYHL PLAVGVGFLV LMTILYYATG RPKAIAPIDY EELDPRRD

> RXA00091 (1-753, translated) 251 residues  
 VITLTNVRKE YSSDVAIGPV NLEIPAGGIT ALVGPNGAGK STLLTMIGRL LGIDEGNITV  
 ASYDVTSTAS KDLAKIISIL RQENHFVTKL TVRQLVGFR FPYSGRLTE EDEGIISRYI  
 DFFNLTELED RYLDQLSGGQ RQRAYVAMVL CQETDYVLLD EPLNNLDIAH SVEMMKHLEN  
 AAAQFGRITII VVLHDINFAA RYADYIVAVK HGMIEKEGTP EQIMKNEILS EIFNTEIEVI  
 EGPHGKIACY H

> RXA00092 (1-204, translated) 68 residues  
 IARALIGPRK ILLADEPTGA LDTSTGDAVL RVLQRIDSG AAGLLVTHEP RFAAWADRTI  
 MLRDGEIQ

> RXA00104 (1-756, translated) 252 residues  
 MTAQIDDSIL THRLAQGTGE ILKGVNRVGV LRGRNLGDAG DELAQSWIAR VLEQHRPNDG  
 FLSEEAADNP DRLSKDRWI IDPLDGTKEF ATGRQDWAVH IALVENGVPPT HAAVGLPDLG  
 VVFHSADARA VTGPYSKVIA ISHNRPPKVA LSCAEQLGFE TKALGSAGAK AMHVLLGDYD  
 AYIHAGGQYE WDSAAPVGVC KAAGLHCSRL DGSELTYNK DTYMPDILIC RPELADELLE  
 MCAKFYEENG TY

> RXA00113 (1-3294, translated) 1098 residues  
 ASGGGVVDSA ALDAYASTVT GEEGVLANVA RGILSQLGLD TKDEVEGA EI DTelyDAVEA  
 ELGTGWLKLV TPVFSADRAI LFDDRWARAS EDLARLANGE DIAVERFAGT GETVVKQAAW  
 WAEHVEDTAL AATLKQVSEV AAKPANEPHI DDVALVTGAA PESIAGAVAA RLISQGATVI  
 LTASNVSQAR KEYARKLYAA NATPNAKLWI VPANMSSYRD VDAVIDWIGN EQRVTVGSTV  
 TVTKPALPT LAYPFAAPSV SGTLDAGPQ AENQARLLW SVERTIAGLA DLASRGVDGR  
 VHVVLPGSPN RGMFGGDGAY GEVKAADFAD LAKWGSETGW PQFVSLAQAR IGWVAGTGLM  
 GRNDVLIPAA EKLGIHVYTP EEISSELLGL ASAESREKAL EAPIDYDLTG GLSGGVSTIAA  
 LAASLESDAV ETTSAAEDTI KALPSPKHPE QPVGTPVGEV KTDLEDMMVM VGVGEVSSWG  
 SGRTRFEAEY GIQRDGSVDL TAAGVLELAW MMGLISWSED PKPAWYDADG TEVPEEEIYE  
 RFRDEVIARC GVRELVDADF LVDGGSLDAA EVFLDRDISF SVTSAAEEAQA YVDADASVTV  
 EEADGEWIVT KKKGSTSFVP RKATLTRSVA GQLPTDFDPA KWGIPAS MID ALDNIAAWN  
 VTAVDAFLSS GFSPAELLQS IHPADVSTQ GTGIGGMQSL RKL FVNRF LG QDRPSDILQE  
 TLPNVVAAHT MQSYVGGYGQ MIHPVAACAT AAVSVEEGVD KIRLNKADFV VAGGIDDIQV  
 ESLTGFGDMN ATADTQAMLD KGIDPRFISR ANDRRRAGFL EAAGGGTVLL ARASVAAELG  
 LPVLAVVAHA QSYADGAHTS IPAPGLGALG AARGGKKS VL ARELNKLGLT PDDVRVSKH  
 DTSTNANDPN ESELHNLLWK TIGREADNPM FVVSQKSLTG HSKGGAALFQ IGGLVSILET  
 GKLPQNASLD CVDPEMEAKG ENFVWLKPL DLGAGSIKAG VLTSLGFGHV AAVVVLATSG  
 IFEQAMRNAG LDVEAWRARA TQRLRTGANR LEAGMVGRAP LFEQVDGRRL PEHGAHQAEI  
 NLLIDADARL GADGIYQG

> RXA00158 (1-2085, translated) 695 residues  
 VTELSRNFGA SRLINRFGQE PFAFAFAGQG YDWLKT LRAA VAAGAGTNVS DIVERANALL  
 ALVADDLIGT LPFGFDPVAW ANNSDPADF TAQSAVSVPG IFVSQIATLD SLEAQRDLVD  
 QAVSSIGHSQ GVLGVHLLND ATRADELVAI AQLIGAAITR TARMTGLIAQ GDNMPMLSIA  
 GISREQLOQA IDAACAEVPA EIRPVIGLRN SRDSYVLVGR PDDNARVVKV IEAMAAKDKK  
 AIEDKLRGGS AFSPRITPLK VQAAFHHPAM NMAVEQTVAW ATTAGLDVEL TREIAADV LV  
 NPVDWVARVN EAYEAGARWF LDVGPDGGIV KLTANILEGR GADSFYVGDA AGQAKIFDAG  
 MAPELPVDYQ EFAPRVEHVD GTPRLVTKFT ELTGRTPMML AGMTPTTVDP AIVAAAANGG  
 HWAELAGGGQ VTPELLETHI AQLTDMLEPG INAQFNSMFL DPYLWKMQIG GKRLVPKARA  
 NGASIDGIVI TAGIPEKDEA VALVKELMRD GFPWIAFKPG AIKQVNSVLA IAKEVPELPI

IIQIEGGVAG GHHSWEDLDE LLIATYGKVR ALDNVVLVCG GGIGSPERAA DYVTGSWSTS  
 YGLPAMPVDG ILVGTAAMAT KEATTSQAVK ELLVSTQGS D EWVPAGGAKN GMAYGRSQLG  
 ADIHEIDNSF AKAGRLLDEV AGHETDLQAR PDEII

> RXA00164 (1-1689, translated) 563 residues

VGRIPRAKWW FLGALVLLSA GAYASVLVPQ VLGRIVDLVS DGAQMRDFVE LSVILIAVAI  
 AGAVLSACGF YVVSRISEKI IANLREDMVG TALGLPTHQV EDAGSGDLVS RSTDDVSELS  
 AAVTETVPIL SSSLEFTIAAT IIALFSLDWQ FVLIPVVVAP VYFASKHYL SKAPDRYAAE  
 RAAMAERARK VLEAIRGRAT VRAYSMEDAM HNQIDQASWS VVVKGIRART TMLILNMWML  
 FAEFLMLAVA LVIGYKLVID NALTIGAVTG AVLMIIRLRG PMNMFMRVLD TIQSGYASLA  
 RIVGVVADPP IPVPDSGVKA PQGKVELRNV SFSYGD SWAV KDIDITINS G ETVALVGASG  
 AGKTTVAALL AGLRVPDQGO VLVDDEFVSH LSDRERIARL AMVSQEVHVF SGTLRQDLTL  
 AKPDASDEEL AHALGQVNAL DWLESLPEGL DTVVGARGIQ LEPVVAQQLA LARVLLLNPA  
 IVIMDEATAE AGSAGASALE EAADAVSKNR SALVVAHRLD QASRADQILV MDKGEVVESG  
 THQELLDHGG IYQRLWTAWS VGR

> RXA00181 (1-1572, translated) 524 residues

MSDNTWFIIA IVIYMLVMVL IGYWSYRKTE KYDDYMLAGR GLNPFVAAMS AGASDMSGWL  
 LMGLPGALFV TGMSELWIAV GLTIGAWANW MWVAPRLRSY SEISANSITL PSFFENRLRD  
 KSRALRIIAA LIIIVFFTFY ISSGMVAGGV YWESTFGGDY LLGMAIVAGV TVLYTFIGGF  
 LAVSYTDAVQ GTIMFFSLII VPMAYFALA NPMDIWSFAN SNDYGPHTDG IGNPTYFSMI  
 SGISAAAIIG NLGWGLGYFG QPHIVVRFMA LRTPAEAKQG RRIGISWMII CLIGATFTAI  
 ISTVFFAQNP DANITDTRAY ESIFLDLARM LFHPLIAGLI LTAVLAAIMS TMSSQLLVTA  
 SSLIEDLLKV VKKDSLERT LIMLSRATVI ILAIIAAAMA INPSDSILGL VGFAGWAGFGS  
 AFGPIILASL YWKRLNAAGA ISGMITGAIV SIAWGMSPLS DTLYEIIIPGF ALATIVMVVV  
 SLLTKEPSEE ILNEFETAKD LAAAVESNED VDFADAAQKL SKES

> RXA00186 (1-747, translated) 249 residues

MGEKTSVAYV HDVLIKGVPV RIYNPHNDG PLPVFIYFHG GGWVLGDLES VDSTVRDIAV  
 ASGALCISVD YRRAPHPFL AALDDCQVVT EAVLNGELAS ANQHLVAVGG DSAGGNIAAV  
 IAQQLRDQIT HQVLVYPVMD VILLVICSII TTGFALLMHP KSKDKTETIS DEFLAEIQAG  
 SEKISILRST PAEKANASRW IMYFVGIGL LYSVFSLWTG GVTGLTLNSF NFLFLSLGMV  
 LTANYGPEY

> RXA00187 (1-351, translated) 117 residues

VISGFFTSIS TATTWPVIAF LYSGLLNIAV PSGGSKFIE APYIIPTPVD LGADMGLVLQ  
 AYQMSDGATN LLIPFFALPY LANFKIKFSQ VVG YTVPPVL VVIAVICIYL FLRASII

> RXA00201 (1-186, translated) 62 residues

VADCGLPIPE HVEIIDLALV FGIPTFEQVL NALKPEVVVE GAVIAEGAPQ RIREMVDTDV  
 EV

> RXA00228 (1-591, translated) 197 residues

MRDLRSMIGV SSSALGNRIP SEEKVSDLVI SAGYAILGRW REDYDEMDFG QATEILEQVG  
 AMHLADRTWG TLSEGERKRV LVARALMTNP ELLILDEPTA GMDLGGREDL VG YLGELAMD  
 PDAPAIVMIT HHVEEIPAGF THAMLLDEGE IVAQGLINTV MTNENLSKAF HQPIQVDRIG  
 ERYFARRVRT ARSHRAQ

> RXA00243 (1-927, translated) 309 residues

VTSEQALDPI HPGQFRLSRI QLINWGTFHG TVDIPVTREG ILVTGGSGSG KSTLIDAITA  
 VLLPQGKLRN NSAAQANTPR NKGRSLVTYI RGAWRAQEDP LQDQIVSTYL RPRATYSLVG  
 LTYSNNEGVE HTLVAIIFYLK SGHNLTSDIS SYYGVPVVDQ DINALLDFLK EGIDKRQIRA  
 AFKEAIFSEQ HSVFSGRFRS RLGISSEEL LLLHRAQSAK DLQSLDDLER DYMLVEPDTE  
 SIAKTAVEQF QDLEGAYEQV EDIKRQIHTL DPLVQLKNRR EKAQQSKDHA NALKKALPTV  
 GNRIKKEEQ

> RXA00259 (1-2202, translated) 734 residues

MSGLFTPFSD AAKNNTVKTD GDSVSGRDL P ITKISEDRE RSAYSAQLAN IICDVAPWGA  
 STVFSLTGQW GSGKTSLVNL IRSEESLSNE KWTIVDFNPW VASDPQSLIE EFYRVIVGTV  
 PDDKTGQKIK TVLQKTFTI GSIAGGVGGF GVLEALALSK GVDAANAVYK TWKQEQDSWP  
 TLYTRAANHF KDLNKRILIV VDDIDRLHTD ELALLMKVIR LLGRFPQVNY LLVYEEESLL

TTLARSTAVG GSEDDALRFM EKIVQYPFDV PPLTSFQIEK ELSALFDKLF QGVSLSGDPE  
 DFALVKSRMF DVWEKTLVTP RLLHRFAALL TNWTRIYGSG EVNGVDLTIL ATIRIVFPSV  
 YKRLSRAKEV LLQGGRTTGS QKPGWEKQLC EGMNNEQMDL LKTMLLFLFP RLSDHPSTRM  
 HRERGISTEV YFDTYLMFQR PGHVISDEQL DKYLSNADDA MGFVDLINS DNDMVASVMK  
 KLPLAIDRLD GEGVRHMAVE VLFTAANGMH DKGRQVRMSG IFSDLYSHAC SILGALPQLP  
 VEQLYEKFFS EMTLNEAAFW LNQVGERARA CGNDVSGLEL FRKVNIKTEA RILSVLKNQD  
 PSDWDLGPYS LGILAKSSNF SSVLKSLSQG IEEHQFDVID IGVLFLLTVY SSRQGPPSGGA  
 WIDSFQHSLE SRYVPDSLRA ITKSEVDVEL GKIQFTDFSW EGKRKVVAYA LETGRSDFTR  
 ERLGGYSIAD SIVD

> RXA00269 (1-789, translated) 263 residues  
 MLSINGISKT FFPGTVNERR ALQQLKLDMA EGDFVTVIGS NGAGKSTLLN AVSGRLLVDS  
 GEISIDGNKV NKMSEHKRAR YIGRVFQDPL AGTAPNLTIE ENLAIALLRG KRRGLGFALT  
 SKRREQFKQE LERLELLEN RLTAKVGLLS GGQRQALSLL MAGFTQPKIM LLDEHTAALD  
 PQRAELVTTL TEKIVADGNL TTLMVTHNME QAIRLGNRLI MMHEGQIVYQ ADQATKSKLT  
 VRDLLQEFAN IKGATLSDKA FLG

> RXA00281 (1-684, translated) 228 residues  
 MINVEGLTKQ YGQVRAVDDL SFEVKPGIIVT GFLGPNAGAK STTMRLILGL DNPTAGHATI  
 EGQPYRSLKN PLTKVGALLD AKATHPNRTA ENHLKWIARA NGLSTKRVDE VLTLVGLTGV  
 GSKKTGGFSL GMGQRLGLAA ALLGDPEYLI LDEPVNGLDP EGIHWVRTLL QNIAKQGRTV  
 LVSSHLLSEM AQTAEHLIVI GRGKLVADMP MHEFVRSHSA STVVVRAA

> RXA00298 (1-1845, translated) 863 residues  
 MSSNIAITTE PEGKNKKGLK SDPFIFSISV GFIVVFVIAT IALGEKARTT FSAIAGWLLLE  
 NLGWMYIGGV SLVFIFLMGI FASRYGRVKL GDDDDDEPEHT LIVWFCMLFA GGVGAVLMFW  
 GVAEPINHAF NVPMANEESM SEAAIVQAFY YTFYHFGIHM WVIMALPGLS LGYFIYKRKL  
 PPRLSSVFSP ILGKHIYSTP GKLIDVLAIV GTTFGIAVSV GLGVLQINAG MNKLWSTPQV  
 SWVQLLIILI ITAVACISVA SGLDKGIKLL SNINIAMAVA LMFFILFTGP TLTLRLFLVE  
 SFGIYASWMP NLMFWTDSFQ DNPGWQGWKT VFYAWTICW SPYVGMFVAR ISRGRTVREF  
 IGGVLALPAI FGVVWFSIFG RAGIEVELSN PGFLTQPTVV EGDVPAALFN VLQEYPLTGI  
 VSAFALVIIV IFFITSIDSA ALVNDMFATG AENQTPTSIR VMWACTIGAV AGSLLIISPS  
 SGIATLQEVV IIVAFPPFLV QFVMMFSLK GMSDAAAVR RVQTRQWEKT DTPEKLEEHS  
 SQPAPGYDDE GNPLPMPALE HDEDGNIVIP GNVVIEGDLG VVGDVVDDPE EAQEMGSRFK  
 IVEQTRPQSR DEYDI

> RXA00346 (1-690, translated) 230 residues  
 MLLTFNDAV DPLWRGLNLE LRQGEFLAVL GPNGVGKSTL IGTLGTRKL THGSVKTDAR  
 VGYIPQQRIF DVPLRARDMV SLSAAHGVVS KRGPAGKGDV KLLARVGASG IADRRVGELS  
 GGQQQLVRQA QALATRPQLL LADEPLLSLD PGVAQRTVSL FGELKAEGVG VVVVTHDVNP  
 LMGLVDRIY LAPNGHTIGT VGDVMQSEKL SELYNAPVTV ARINDRIVVV

> RXA00368 (1-579, translated) 193 residues  
 SLMLSLGAAL ICGVLGWLIG VLITRTQHFA NVPLTLTVLL PTALPGMIIG VGWLILGRYT  
 GIYNTWPVIL GAYVCAFTAL VVQAVRGPLS QAPEAIEEAA RISGAGRLRS IMDTTGAMAI  
 PAAFAGAVLV AVTAVRELTV SILLIAPGTT TLGVQVFNLQ QAGNYNQASA LSLMFAIIGI  
 VALALTQRSQ KEF

> RXA00369 (1-717, translated) 239 residues  
 VSSIKLRDLS VSFRDGTGFL QDINLKIEPE EFVVLIGPSG SGKTTMLGTI AGFVEPSSGS  
 VLIAGEEMTH VPPERRRMGM VFQQHAVWPH MSVAKNVGYP LARSGQKGAS ISKRVERTLA  
 LVGLEGFGRS RPASLSGGQR QRVALARAI ADPTVLLLDE ALSALDEPLR DALRRELVS  
 TRREGLTTVH VTHDRAEAS IADRIVVLGN GRIQQVATPT ELLSAPATAD VARFIVDAT

> RXA00370 (1-798, translated) 266 residues  
 GKALWNSAYT TVLSAVGATI IGTIMALTLD RTDVFGRTAL RLFLLSPLLI PPFIGAIAWL  
 QLFGKNQGIN RFFGTEVWDI YGADGVTFLL IVHSYPTVYI IVSAAALRQLP SDLEQAARIA  
 GADTFTVLRT ITLPLLKPAL LSAFTLTVA NLADFGIPAL LGSPARFETL ATMIYRFMES  
 GTVSNPLQVV STIGIVLLFL GIAAVTADYL VSLYAASKLQ DAGTPHRETL NKSRIPVSVI  
 TWIIALIITA APLLGLAYRA LLPAPG

> RXA00410 (1-666, translated) 222 residues  
MMIYGKGSTE VRALDGISVQ IQSDKWTSIM GQSGSGKTTL LQCLSGLAQP TSGRVTLNKN  
NITLSSLSEN KRAKLRRTHI SMVFQDFNLV PILSVKDNIL LPLRLAHRV DKQWFEHITS  
VLKIDNMRH LPGELSGGQQ QRAAIARALM SRPDIVIADE PTGSLDSVTS DAVLNLFRSI  
VDDFGQSLVF VTHDKDAAHR GDVLITMRDG KIIDTADLRV GR

> RXA00419 (1-462, translated) 154 residues  
DNEAQWRDQA LAVEATTVNY TAGVSVGVLL GQKFEQQGHG TIVALSSVAG QRVRRSNFVY  
GSAKAGFDGF YTQLGEALRG SGANVLVVRP GQVRTKMSAD GGEAPLTVNR EDVADAVYDA  
VVNKKDIIFFV HPLFQYVSFA FQFIPRAIFR KLPF

> RXA00421 (1-159, translated) 53 residues  
MLNAVGAQN ILLGGTSEI GISIVSRFLK QGPSHVTLAA RKDSPRVDA VAE

> RXA00432 (1-891, translated) 297 residues  
LSALVIFGGV QRIANVTQWM VPFMAGAYII VGVVVIVINI QQVPTMINDI IAGAFGFRPV  
ATASVWGAFF LAFMNGMRRG LFSNEAGEGS VPNAATATV SHPVKQGLVQ TLGVYFDTL  
VCSITAFVIL LSGVEYATGD IQSSSLTQSA LASVVGWGT HFITVVMFFL AFSSVLGNY  
LAQANIQYFT DSKTVMTVFR LLVLLSVFSG AVASVPLIWA LGDTFAGIMV LINLAAIPL  
GGVAVKLLKN YTIQKKAGLD PVFHRDMMPE VRNIACWNGK DAATSNYHEA MEVIKKS

> RXA00436 (1-525, translated) 175 residues  
MELLETFITD VINDNLWMIL PFLVAAGLY FGGRTLLVQI RMIPEMFKAV VEKPAKDGEF  
ADKQDISAFK AFTISAASRV GTANVAGVAL AITLGGPGAV FWMWIIALVG GATSFIESTL  
GQLWKVKDGD SYRGGPAYYM TLGLNARWLA VVFGVAITLT FGFVYNALQS NAVVE

> RXA00449 (1-1005, translated) 335 residues  
LALTAETVGG MKNQKKFATG LMLSIAYSAS IGSLGTLIGT PPNALLAAYM SESHDIHIGF  
GQWMILGVPI AVVFTIIAWL VLTTFVKPEM KEIPGGRELI KREIAEMGPW TAPQVTVGVI  
FAAAALAWVF IPLTLDWTGS QLSINDSLIG IAAGLLMFIV PANFKTGERI LDWRTAGELP  
WDVLLLFGGG LSLSAMFTST GLSLWIGELA KGLDALPIFI LIFAI AVLVL FLTEFTSNTA  
TAATFLPIMG GVAVGIGLTA GGEQNVLLLT IPVALSATCA FMLPVATPPN AIAFGSGYIK  
IGEMVKGGLW LNIIAVILIT IFTYFVAIPL FGIML

> RXA00456 (1-312, translated) 104 residues  
VLQALLAIMV SLSVAAILLEG NRALVGLLLA TTLGLGVAQW IQKVVAEDLG QHYVHEVRRE  
LVGAALVPGN TASLGVTVTR ASNDLTAVRN WVALGIVPMV TGLP

> RXA00459 (1-987, translated) 329 residues  
VCTRAAGGGA VTLKRARELR KKRGRMAARI ADSVMAGELL HATGAIDREL NAVTRDSDRV  
VIAAVRRSWA TGFSRALMAM AASLGTVSIV ISGHLEVSEV AGIMMLLGVL ATPVAELGRV  
VEYRQNYKAA TRILIPLLQR GSEFKHSQOK LPGLQATEGI PGVYVKGISA LPERIYLHG  
SADATRKWVT SLSAMEEGTD VIVNGQRLSQ LPLKQRRALI GIASAHHLS RGSVSRVLGL  
RVPDATVEEI EQALEQVGLN NTGKQRLKNG GHPWSTSQIN KLKIASATLR TPPLLVLEGI  
TPENLLNYPG VIISTVQENP SETWRQVNI

> RXA00477 (1-1644, translated) 548 residues  
MKVSTKTPRS SGTAVVIGAG VAGLATSALL ARDGWQVTVL EKNTDVGGRA GSLEISGFPG  
FRWDTGPSWY LMPEAFDHFF ALFGACTSDY LDLVELTPGY RVFSGTHDAV DVPTGREEAI  
ALFESIEPGA GAKLGNLYDS AADAYDIAID RFLYNNFSTL GPLLHRDVL T RAGRLFSLLT  
RSLQKYVNSQ FSSPVLRQIL TYPVFLSSR PTTTPSMYHL MSHTDLVQGV KYPIGGFTAV  
VNALHQLALE NGVEFQLDSE VISINTASSR GNTSATGVSL LHNKRVQNL ADLVVSAGDL  
HHTENLLPR ELRTYPERYW SNRNP GIGAV LILLGVKGEL PQLDHNNLFF SEDWTDDFAV  
VFDGPQLTRP HNASNSIYVS KPSTSEDGVA PAGYENLFVL IPTKASSSIG HGDAYMQSAS  
ASVETIASHA INQIATQAGI PDLTDRI VVK RTIGPADFEH RYHSWVGSAL GPAHTLRQSA  
FLRGRNSSRK VNNLFYSGAT TVPGVGIPMC LISAENIIKR LHADTSAGPL PEPLPKTTP  
SQKTSYDH

> RXA00478 (1-831, translated) 277 residues  
VIEEYSTSFS LSTWLLSPRI RNDIRNLYAV VRIADEIVDG TAHAAGCSTA KIEEILDAYE  
IAVLAAPQQR FNTDLVLQAY GETARRCDFE QEHVIAFFAS MRKDLKANTH DPDSFTTYVY



GSAEVIGLLC LSVFNQGRIT SKKRLEIMQN GARSLGAAFO KINFLRDLAE DQONLGRFYF  
PKTSQGTLTK EQKEDLIADI RQDLAIAHDA FPEIPVQARI GVISAYLLFQ KLTDRIEATP  
TADLLRERIR VPLHIKLSL ARATMKGLSM SIYRKNS

> RXA00480 (1-1116, translated) 372 residues  
MDNGMTITTE HSTHPDLDFN DEIYRELNRI CASLSQQCST YQPEFRTCLD AAFQALRGGK  
LIRPRMLLGL YNTLVDDIE VKLNTVLQVA VALELLHFSL LVHDDVIDGD LYRRGKLNFI  
GQILMHRTP E SFAQIQRDPE HLDWAQSNGL LMGNLFLAAT HQIFARLDLP HHQVRLLDL  
LNHTINDTIV GEFLDVGLSS KAISPNDIA LEMSRLKTAT YTFELPMRAA AILAEPLQEI  
ETKIGEIGTN LGIAYQLQDD YLSTFGDAE HGKDAFSDLR EGKETTIIAF ARDTAKWTDI  
QDNFGSADLS TSQAERIQHL LIQCGAKNHS LNAISDHLNI CRSMIKTLSP QVDPKAQNLL  
LKQVEQLASR KS

> RXA00524 (1-333, translated) 111 residues  
VTTNHQLSAE EISLAYGERT IIDSLSDIV PGKITSIVGP NGCGKSTLLR AFARLLKPSA  
GQALIDAHPL PSLPGKELAR MLGLLPQSPT GPEGIVVADL VGRGRHPHQG L

> RXA00526 (1-690, translated) 230 residues  
MSLIEMRNIV KTYNIGSEGE LTVLHGVDFH VDRGEFVSFV GTSGSGKSTM MNIIGLLDKP  
TDGTYTLDGV DVLDISDDAL ASHRAKSIGF VFQNFNLIGR IDALKNVEMP MMYAGIPAKQ  
RRSRVELLE MVGMGERLNH EPNELSGGQK QRVAIARALA NDPEIILADE PTGALDSATG  
RMVMDIFHQL NKEQGKTIVF ITHNPELADE SDRVVTMVDG RIIGSEVKHS

> RXA00559 (1-213, translated) 71 residues  
MSDNPHENPR ENPHRSPEVV LRFMAAPT DV LMAGSHGVGG GRVLEWIDKA AYACATHGSG  
TYCVTAYVGH I

> RXA00570 (1-498, translated) 166 residues  
PTIVMAMVAG IFLRFGLDLI DASVTDPLIA LPMVIVFVAL SMSPRLASIA PPVAVAAVVG  
TIVAIASGKL ASGILDNGII SRPVFTAPEF SFAAIMELVV PLAITVVIVQ NGQGVAVLKA  
AGHRPGVNLA AAASGLWSLP MALIGNITTC LTGPTNALIV AGAKSH

> RXA00571 (1-1185, translated) 395 residues  
QIGALSPAVA GTLGSIAMIG VMIGALSAGA VGDRLGRRKV MLTAIVWFSV GMALTAFASS  
IALFGFLRFL TGLGVGMIVA TGGAIIEAFA PANRRNLFNA IVYSGVPAGG VLASILALLE  
EDVIGWRGLF LIGGSPLLFL LPLAYFFLPE SPRWLTSRGR AADAKALCAR YGLPTEEFV  
EKQQETKGTG FAGIFSSKYL MGTLIGAMS FIGLLSTYGL NTWLPKIMES NGATSHDSL  
SLLFLNGGAV FGGLIASWFA DRIGAKTVIT STFALAAICL GVLPNISSWP MMYTAIAFAG  
VGVLTQVLT YGLTSNFFGT ECRAAGVAWC AGFGRLGGIV GPAIGGLIIG AGFGPSSAFL  
IFAAAAAIGA VCTLLIPRSP AEVEVKVAQE PLARV

> RXA00572 (1-3831, translated) 1277 residues  
QWLNRYLELS GPVDGQWIDA SWAARFAQML ERAEARLIEQ DHGQFEPSLT VEDGVDKLVA  
AYPHAATDLL TPADVAVFLG LCRTPGKPVN FVPVIDKDVR RWRSDSLWQ SHDDRYTADQ  
VAIIPGVVAV AGITKANEPV ADLLDRFVDA TIERIDEHDS RSRDIMGKVL SSPGTFWAGR  
NIPSVIHSLG HADKWSRSEF EAFHSPTGAN LVEYDAEHAM LTVPLAGSTA FGTTAELKIR  
FTSPIDALPS AVPLVTQEDA EAAMGELTRI AAGGTLATVN NGTATWETSV DAGVIADYNN  
VTAGYLPASV VPAHTAPDVL VGRAWPAVFA AVKSAVIPGT DSASVVEGML SLVHLEHHIV  
LKSDVPTDGA LKVSATADEV VDTDGLRLVI VRAEIADAEG NLIATLAERF AIRGRKGNV  
ARTNTSALPT TVDTPRSARA VATVVAPESM RPFAVISGDR NPIHVSDVAA SLAGLPGVIV  
HGMWTSAGE LIAGAAFNDE QIQTPAAKVV EYTATMLAPV LPGEEIEFSV ERSVNDNRPG  
MGEVRTVTAT VNGNLVLTAT AVVAAPSTFY AFPQGQIQSQ GMGMEARRNS QAARAIWDRA  
DAHTRNKLGF SIVEIVENNP REVTVAGEKF FHPDGVLYLT QFTQVGMATL GVAQIAEMRE  
AHALNQRAYF AGHSVGEYNA LAAYAGVLSL ESLEIVYRR GLTMHRLVDR DENGLSNYAL  
AALRPKNMGL TADNVFDYVA SVSEASGEFL EIVNYNLAGL QYAVAGTQAG LAALRADVEN  
RAPGQRAFIL IPGIDVPFHS SKLRDGVGAF REHLDSLIPA ELDLDVLVGR YIPNLVARPF  
ELTEEFVASM AEVESTYVN EILADFKAAS ADKQKLARTL LIELLAWQFA SPVRWIETQD  
LLIKGLQAER FVEVGVSAP TLANMMGQTL RLPQYADATI EVLNIERDRP VVFATDEVVR  
EVAVEETPAA PAETTETPAT PATPAPVAAA APATGGPRPD DISFTPSDAT EMLIAIWKV  
RPDQMGATDS IETLVEGVSS RRNQLLLDLG VEFGLGAIDG AADAELGDLK VTVSKMAKGY  
KAFGPVLSDA AADALRRLTG PTGKRPGYIA ERVTGTWELG QGWADHVVAE VVIGAREGAS

LRGGDLASLS PASPASASDL DSLIDAAVQA VASRRGVAVS LPSAGGAAGG VVDSAALGEF  
 AEQVTGHDGV LAQAARTILT QLGLDKPATV SVEDTAEEDL YELVSKELGS DWPRQVAPSF  
 DEEKVVLLDD RWASARE

> RXA00590 (1-387, translated) 129 residues  
 MRVVLFLAVL GVVAGGVTLT TTGNPAAEAF QHAAGDIGLR IFGAVLWAAS ISSVIGASYT  
 SATFLVENKP EKKRLQNWVT IIFILISCSV FIMLGTAPAI LLVFAGAFNG LVLPGVFTLM  
 IYVAIFRQK

> RXA00591 (1-1353, translated) 451 residues  
 MTTSSSTASPI AELQNLSPKQ RKSESRRRAII SSYLGSTIEF YDFLLYAAAS ATVFPVFFFT  
 NLDPLAGTIA AYGTFAGGYL ARPLGGAIFG HFGDRLGRKK MLVLSMLIMG VASTCIGLVP  
 SAEMIGSMGA VILIMLRICQ GIAVGGGEWGG AALMALEHSD SKKRGFAASF TNAGAPTGAA  
 LGTFALGTAS AVLTQEQFLS WGWRIPELLS FVLLIVGLVI RAKVSESPLE AAAAAAEKAK  
 PTERKVPLLQ VLRRPKALIL TMLGGASGFG LQVLLSTFSI SYATQSGIER SSVLYAFAVA  
 SVFSVFFVIL FGRVSDLFGR RPYMIIALVL FVAYLPAFFR MLTSDNWFIL LSAFTIALAL  
 HAMLYGPLAA FISEQFGTSA RYTGASLGYQ LATLIGAGFT PTILASLYAG PGGGTSVTPV  
 IVFLATMSLV SIIAIAITRE SKDHDLSTYE H

> RXA00596 (1-453, translated) 151 residues  
 MLNALKFIPW LIGQIFLSGF SVITAAVKKD TGFNPVVIRY PLRVTTDFQI AALSTCITAT  
 PSTLSLGLRE PRKPGDPTIL LIQAVFGSDP VEVFESIADM EQRLVPSVAS IDHGVPGQGP  
 YKEIRPSDAE WPSREIADTA QNTVSQDKRE F

> RXA00607 (1-381, translated) 127 residues  
 MILALTVAAIL FGGGVYLIQQ RGMVRIVFGM SLIGHAANLT ILYAGVPTWR GEAFPDRTPL  
 TDAADPLPQA FVLTAIVIAM ATTTIMLALA ALGRSDDTRS IEPDDDQSPL TTSARSVTNP  
 TDQEDKA

> RXA00623 (1-1338, translated) 446 residues  
 MDSNTESSSV EVKNEHIKQV KPPKKDRTHW LYIAVIIALI GGITLGLISP ELGKEFKILG  
 TMFVSLIKMI IAPVIFCTIV IGIGSVKAAA TVGRAGGIAL AYFITMSTFA LAVGLLVGNF  
 IQPGSGLNIS VDEESSFAST ESSPEGLLGF IHSIIPETFF SAFTDGSVLQ VLFIAILVGF  
 AAQSMGEKGQ PILDFVSHLQ KLIFKILNWI LWLAPVGAFG AMAGVVGETG FDAVVQLGIL  
 ILAFYVTCVI FIFGVLGAVL KVFTGVNIFK LVKYLAKLEFL LIFATSSSES ALPNLMRKME  
 HIGVAKPTVG IVVPTGYSFN LDGTAIYLTM ASIFIADAMN MPMSLGEQVG LLVFMIIASK  
 GAAGVSGAGI ATLAAGLSSH RPELLHGVDV IVGIDKFMSE ARALTNFAGN SVATLLVGKW  
 TGTVDNMNVH DVLNGKSPFV ELEEDH

> RXA00660 (1-1023, translated) 341 residues  
 PGHTPEHLSF LLKDGAFAHE PGFMLTGDFV FAGDLGRPDL LDEAAGGVDT RFEGARQMFK  
 SLKEKFLTLP DHIQIFPGHG SGSACGKALG SVPSTTLGYE RQFAWWGKYL EADDEQGFID  
 ELLEGQPDAP AYFGRMKRQN RQGPALMGAR ELLPQLEASD LHDVIVVDTR SADEVHQGT  
 AGAVNIPAGN SMAKFGSWTV DPEKDSRALV LLAASQIGAM EMWDHMRVVG IDNVAGFITN  
 FDGVDLVAPQ TVSPDQLDEL EYDLLLDVRN RSEVEEGYIP GALHINGASV LWNLEKLPRD  
 GKIVSYCKSG TRSSIAASTL RNAGFDVVEL QGSYDNWVRH N

> RXA00681 (1-744, translated) 248 residues  
 MPSPRTVLIT GAAGGLGRAE AEGFAAQGDR IAVADINLDG AQETVDKLKA LGADAAAFEV  
 DVTSLESTEA LAAGAAEFGG GRIDVLINNA AIYATVTRSP FEDIDPAEWD LVMGVNLKGP  
 WLVTSSVSPF LSDNARVVNL SSATVFSGSA HWAHYVASKG GVIALTRVLA KELGGRGIVT  
 NAVAPGFTLT EASLGLMDSA ETYGVDRGSI KRASQPKDIV GTTMFLASPE AEYITGQTLI  
 VDGGRQFI

> RXA00690 (1-1146, translated) 382 residues  
 VKWIERVLS RRMVHPWAWW VWALGIAGCA SMTNNPYILA LTFATLCFVV FNRRGSSPWS  
 RAFPIYLMIA GWLVVYRLVM HIVVGAKIGT IELFRIPPVQ LPEWAAGIHV FGTVYLEGLI  
 IATTQGLTLG TMIVAVGAAN SLADPKKLLK SLPGALGELG TAVVIGISIA PQMAESAERI  
 NRARTLRGDD AKGVRGFARI LMPVFQDTLD RSLALANSMD ARGYGRQAHV SKFQQRVTSI  
 FGAFGILGVT VGLFVVLDAS SPMFVAVPVF ITGVGFLIIS LVVASHRKTS TTFDQLPWGA  
 AEWLVCITGV IPLLMAALTR YLDPGSMITT WVPLHMPDTV PLLVVAGLVV ATMPGFLTPT

LPKNKVRVKR RKAINSPERA EV

> RXA00733 (1-408, translated) 136 residues  
MSNTAGPRGR SHQADAAPNQ KAQNFGPSAK RLEFGILGHDR NTLIFVIFLA VLSVGLTVLG  
PWLLGKATNV VFEGFLSKRM PAGASKEDII AQLQAAGKHN QASMMEDMNL VPGSGIDFEK  
LAMILGLVIG AYLIRS

> RXA00735 (1-669, translated) 223 residues  
GPTGAGKTTL VNLIMRFYDI NSGSITLGET AQDAVDIRTM AREDLRSRTG MVLQDTWLFA  
GTIRDNIYLG RPEATEEEML AASKAAYVDR FVRSLEPGYD TVLDDEAMNL SVGERQLITI  
ARAFLANPRL LILDEATSSV DTRTELLIQR AMSKLRQDRT AFVIAHRLST IRDANLILMM  
KDGEIVEQGN HRELMALEGA YWELYSQFN APAKEELQAD GDH

> RXA00796 (1-198, translated) 66 residues  
MSKIAIITGS TRPGRVNIDV ANWVLERAQE RNDAQYELVD IADFNFPVLD EAMPAGYGQY  
ANEHTK

> RXA00801 (1-633, translated) 211 residues  
MAHDGLRVEN IVTSGIFALD GGEWEVDNNI WVGNDDEVF IIDAHAHTAAP IIEAVGGRAV  
KGILCTHAHN DHITVAPELS KEFDAPIFVH PGDQMLWEET HGNIETHEDLA DQOKFQIAGT  
ELIVLNTPGH SPGSSCFYLP EANELFSGDT LFQGGPGATG RKYSSFDTII ESLKTSILDL  
PAETTVRTGH GDHTSVGAEA PHLEEWIKRG H

> RXA00802 (1-714, translated) 238 residues  
MDLKLGGQVI LVVGGAGTIG SEVVKLLTEE GATAVAASRS TPLSIDASDE ASVRAGIDQV  
IAEHGRDLGL VVSSAPAAQT LSAETADDPD TVLAAIEGKA ITFMKAATVA LEKMREAGHG  
RIVALSGMNS YKTLSTTASA RNAALNVVVK NLADRHAGTG ITVNAISPFG VVAEPDAEVN  
RANGDTTWR RRRSRFCCR RAPHQFLERL FRWDIRRRAS SFLSSRELPK RKHPRVRA

> RXA00819 (1-990, translated) 330 residues  
MVGGSPQEQ RLDAQIKSGE VKGVFALTEP DHGSDIAGGL ATTATKDADT GEWIINGEKR  
WIGGASTADL IATFARDTAD NQVKCFLVAP QAEGVSMEII DRKASLRIMQ NAHITYNNVR  
VSGDARLHNI NSFKDVSECL RMRSDVAVM AVGAQAGAYE AAVKYVRSRE QFGRPIAGFQ  
LIQEKALML GNLTA SLGMM VKLTDQQQAG IFKEENSALA KMFTSLKLRE TASWAREICG  
GNGIILDNDV ARFHADA EAV YSYEGTHEIN ALIVXXXILX XXFFLYYXXF EEDLHDYFHH  
PKPSFLSKTH QPSPARTWAF RSGALSPRRW

> RXA00821 (1-843, translated) 281 residues  
VTKLERMEHP AYSQLRPVTP SASVVLCPNP GYSSLEG TNS WVIRAPEDPR SIVIDPGPED  
EGHLNVLHSH AEEVGLILLT HRHYDHADGA QRFRQLTNAP VRAMDPSYCA GAEEIHDGEI  
ITIDGVTPQI EVVATPGHTR DSVSYFIWSG VPHESTLEGI VSGDTIAGR H TTMISSETDGD  
LGEYLNLA I LEERGKDIPL LPGHGPDGQD VSSFARKYIE RRELRLNQIR EVWETRGRDV  
SMKDLIDAIY DDVDPVLRGA AEQSTHVAIR YLQAQEASAS N

> RXA00827 (1-753, translated) 251 residues  
VNLLIKINPV TRIIALMVLT TPLLLSLDVM SAAIALVATI ILAPFAGVTW KMLLKRGWML  
FLMAPVAALS MALYGRPDGK EYFSELLIHV TDNSLALAAA IGLRVLAIGL PVVVL IARID  
PTDLGDGLAQ LLKLPERFVI GAVAGSRLMT LFREDWYSMS RARRARGIAD QGKIKHFFTM  
TFGLLVLSLR RGSKLATAME ARGFGRTTGR TWARESTVGA RDLVLILVCA AISAIALTVS  
IQTGF FFLG T

> RXA00842 (1-1200, translated) 400 residues  
MIIQILRVAF AFVGIIVGAG FASGQEV MQY FVAFGIDGIW GVIVSAVIMS VMALIILQLG  
SYFNAGEHGE VFRRVSHPVF SKILDIGVVV TLFSTGFVMF AGAGSNLNQQ WGLPLWIGSV  
IMVLLVLAAG MLDVDKVT TV IGAITPFIII FITAASIYTL VGNFSSVEQL DSAALEV GTT  
LPHWAVAAVN YVGFNLMVAV SMAVVIGGSM FNPRVAGRGG LLGGLILGFL IIISALT LFA  
TVEEVGQDDM PMLTIINNLN PLAGQVMAVV IYGMIFNTAL GMFYALGRRL TAKNPQRFRP  
VYVVTVLIGF VLSFVGFKNL VGYVYPVLGY IGLLLIAVMM VAWVRGRVRI YKESERRMRI  
ADLLQIGHDG ALSGAELAVL NQEIQDSNLD EEQIKAAVRK

> RXA00847 (1-1449, translated) 483 residues

VACQANPGPA PVEEPTTATA TTTATETTTV ETEAPKQDRE TISIGIDPIR NGFNPHLLSD  
 DSPLVRDTAS LVLPSAFEGN QLNTDLLDNV EQVDETTVRY TIAQEAQWSD GTPITGSDFE  
 YLRRSIVAGT GTLNDSAYSA ISEIRTSGGG KTVDVIFEHP VADWHLLFNN LLPSHLITGN  
 STFQTAFYDS IPASAGRYMV RSIDRQRGVI TLSRNDRFWG ANPAHVEVLQ FNTVASASRA  
 GEYLRTGQSS FMNLSPQETL VDTLNLVPDT EVRVSDTTRT LELVFNAEAL APAQRAYLTS  
 LIDVPLTAKL AGGRSANLGV PQTVEASVDK QEIPALRLAA DPADDAGLAA ARGIVDMLAA  
 DGIKAQVVT DLNSAIAGNF DAIVAWTRTA TDSIALADRV GCGVNLAKEW AEGTTEYING  
 VLAGIDFDP AWEQQFNTEN HLRVPILRET RVEAKNNGIL GAADGWPGGI SSAASWRKND  
 VEE

> RXA00851 (1-609, translated) 203 residues

MNSIPLGFYV DKQSVVHSFP ALWKFPLLLFIIGGSIAAS TPVHGLILVG IAVVFYVLAK  
 IPLKVAWEQL WPVLPILIML GAFQWWQRGF DFAATTVLTL FSAVMAAML TLTRLEALM  
 NAVERMLQPF ARFGLPVETI TLAISLTIRL IPLQLATVKE VLDARKARGA GFSIAAFGTP  
 VIIRSIKRAR NIGDALLARG AGD

> RXA00852 (1-690, translated) 230 residues

MPEIIFDNT VRYDDSLILE PLSLKLTEQR IGIIGANGGG KSTLIRMING LGEPTTGRVL  
 VDGLDVSHSG REVRKKVGFV FSDAENQIVM PTVREDIAFS LRRHKMPRAE KAQRVDEMMA  
 RFNLSEHADQ SPHTLSGGQK QLLALAAVLI LEPEVIIADE PTTLLDLNR LMIKDVFNKL  
 EQQLIVVSHD LDFLSDFERV ICINDHKIAA DGPPQKSIDL YVSLMAEPAK

> RXA00856 (1-537, translated) 179 residues

VSDVSAGVNG AQDPSNQAVK PSNWNLPNFL TSLRIIVIP FAWLTLKGET ENNAFAWWAL  
 VVFILLMITD KLDGDIARAR GLVTDFGKIA DPIADKALMT TAFVCFNIIG ILPWWVTALI  
 VLREFGITIW RFFQLRAGNV VPASKGGKLG TALQTVAVAL YLCPFPSWMD IPSQIVMYA

> RXA00870 (1-1512, translated) 504 residues

MSEPQTISHW IDGAISPSTS GKTAPVYNPA TGQVTANVAL ASQEEIDATI ASATKAAKTW  
 GNLSIAKRQA VLFNFRELLN ARKGELAEII TAEHGKVLSD AMGEILRGQE VVELATGFPH  
 LLKGAFNENV STGIDVYSLK QPLGVVGIIS PFNFPAMVPM WFFPIAIAAG NAVILKPSEK  
 DPSAALWMAQ IWKEAGLPDG VFNVLQGDKL AVDGLLNSPD VSAISFVGST PIAKYIYETS  
 AKNGKRVQAL GGAKNHMLVL PDADLDLVD QAINAGYGAA GERCMASVV LAIESVADEL  
 IEKIKERIDT LRIGNGAGDE QGEPHGLPLI TDVHRDKVAS YVDIAEADGA KIIVDGRNCA  
 VDGHEEGFFF GPTLIDDIPL TFRAYTEEIF GPVLSVVRVA SFDEAIELIN SGEFGNGTAI  
 FTNDGGAARR FQHEIEVGMI GINVPPIVPV AYHSFGGWKN SLFGDAKAYG TQGFDFFTRE  
 KAITSRWLDP ATHGGINLGF PQND

> RXA00875 (1-567, translated) 189 residues

MTTEVELVVL ADSEGNPIGT APKATVHTKD TPLHFAFSTY ILNPRGELLV TRRALSKKTW  
 PGVWTNSMCG HPGPDETND AIRRGRVDEL GLEVDSFLDI QEILPDYQYR AVDASGIVEW  
 ELCPVHLVRL AVGEFVEPLD DEVVEFEWAE PQKLEDAVDA TPFVFSPLV DQLSAPELRQ  
 AILEAFDAE

> RXA00878 (1-1863, translated) 621 residues

MRLLGRIKLT TSALWPYYLG IIVVSIVIAA LSLSPFILR EATDSIVSAV TGSNTVDAVT  
 RTIIFLALAL FVASFLNTVM TNIGGYIGDV MASRMQILA TRYAKLLAL PQKYFDNQVT  
 GTIARLDRS INGITQFMQS FSNFFPMLI TMVAVLIISA IFYWPLAILL AMLFPIYMWL  
 TALTSKRWQK YEGEKNHEID VANGRF AEV GQVKVKS FV AETRELADFG GRYGKTVAIT  
 RPQSGWWHRM DTLRGAALNI IFLAIHLLIF YRTLHGHTI GDMVMLIQLV TMAQQPVYMM  
 SYIVDSAQRA IAGSRDYFEV MAQQVEPTAN KELVDATLAS DTPRISVGTP AALPAGEPAM  
 EFKNVTFAYE EGKPVISDVS ITARHGERIA LVGESGGGKS TLVNLLGLY KPNSGSLAVC  
 GVDVKDLTSE ELRASVG VV QDASLFSGSI AENIAYGRPG ATREEIIEVA KKANAEFIS  
 AFPEGYETVV GERGLKLSGG QKQRVSVARA MLKDAPLLVL DEATSALDTK SEQAVQAGLE  
 QLMENRTTLM IAHRLSTIAG VDTIVTIQNG RVEEVGSPTL LAVSGGIYSE LLRLTNSTAE  
 ADRERLRAFG FTGDAPAEED

> RXA00880 (1-1845, translated) 615 residues

MTSPNTLQEY TEPAKYTIGE SETCLTALLD QIKTRPYGVL FSKPANYEWV NVTAKEFQDE  
 VFAVAKGIIS VGVEQGDRVA LLSNTRYEWA VLDFAIWAAG AVSVPIYSSS SLSQIEWIIE  
 DSGAVLAITE TPDHTDLMKN LVIGEDGTPA IKGSPSKLRR ILEINSSALE TLKFEGRELS



DELVWERIHA TKAADLASLV YTSGETTGRPK GCELSHYHWL AEVRALITND IGAIAMPGSR  
 LLTFLPLAHV LARAVHLAFA VTGATQSHWS DFSTLTLELQ RSRPNLILGV PRVFEKVRNA  
 AAANAADGGA IKRIMFERAE KAAIEYSMAL DTAEGPSKSQ VMAHKAFDKL VYSKIRAAVG  
 GDVQYAITGG SAMGQELLHF FRGVGMTIYE GYGLTESAAA AAVDFTDQKI GTVKGPMGGM  
 TIKINEDGEI MLKGEMLFQG YWNNPEATAE ALHDGWFNTG DLGELLESCH LVITGRKKDL  
 IVTAGGKNVS PGPMEIIRA HPLVSQAMVV GDGKPFVGLL VTLDPDMLKR WKLNNHIAES  
 RTVSEIATDP ALRAEIQDAV NNANATVSHS EAIKRFYILD RDLTEEADEL TPTLKVKRNV  
 VVRRYADAID HIYNR

> RXA00899 (1-1266, translated) 422 residues  
 MEDVHDDVPD IPTGMDVSAE VESVIKLNRR LTRMPAVTGG NNGFYSDYRE SLKRMTAAID  
 EAEEYIYVEI YIMAWDSYTQ PFFAALERAH NRGVKVRLLF DHVGSWKYPG YHRLKKELNR  
 MGFAWYMLP LQPWRRRFRP PDLRNHRKML IIDGHTAFMG SQNLIAPSYL QKKNIKLGRE  
 WKDLMVELTG PIVSSMEMIF AGDWYVESNE ALDIRDHAEA HGYIGNTQKD SATNLVQLIP  
 SGPGYTTEPN LRMFNSIVHH AKERLILCSP YFIPDESLE AVTSACYRGV TVELFVSEQA  
 DQFAIDHAQS SYIQALLEAG VKIYQFPKPD VLHTKYMIAD PDDTTGNEAL GVLGSSNLDI  
 RSFGLNYSIS LMIKGNLIH ELNALTDRYR TVSFKLTLTK WNQRSWRRRY VDNVMRLTSA  
 LQ

> RXA00902 (1-1233, translated) 411 residues  
 MSSGFYVQH PRRALPPPIP ERKGPAALFL PGTFHPINPK NIAASHDQVL LSGWGKFVRW  
 LLVLLSILVI IIGINLILDG VYGFGTFTT QMYQVAKDPL IGVLLIGILAT ALVQSSTTTT  
 TLTVTAVGTG IVSVPVAIPI ILGANIGTTI TAMLVAFSYV GERREFKRAF TVAAMHWFN  
 VLVLVLFVV ELLFHPFRTI SGAIATEITL TTGGSLLPTSG VMTKIFDPPT QLLGMNGLIG  
 SIGNPSISAI VCLVVGITLI LISVRAMSSQ IRTITAATVT SIMDKVINPE NSPKATILSN  
 FWSFILGVLF TLMVTASSVT VASMOPVAAS GVVKQKPLLQ VILGANVGTG VTAMFATFAI  
 VSDQGEFAIQ AALIHLLVNF TGALLVLCIP QLANVILHLA EKTANLTARS Y

> RXA00931 (1-846, translated) 282 residues  
 VKTIEDILTL EEIDRDIYRG PVIESYLART FGGQVAAQAL VAATHTVDKA FTVHSLHGYF  
 IAPGDPTAPA IYLVDRVRDG KSYVTRSVRG IQDGEVIFSM QASFHRGDEG IEHMDKMRKV  
 PAPDEIKGTV ERMPISSRRV LDEWAEWDIR VIPQDQLELS DFTATEQAVW IRCTADLPDN  
 PTFHQCSLT Y LSDMTLLHSA LVPHPGEKMQ MASLDHAVWF LRPFRVDEWL LYDQRSPSAS  
 SGRALTHGRL FNQQGDLVAI VNQEGMTRTL HEGAQSIPMR KD

> RXA00941 (1-1317, translated) 439 residues  
 MNLTRNDRLD RLPVTSKHKH ILGGSGIGWA LDAMDVGLIS FVMAALATHW GLSPTETSLL  
 GSIGFVGMAI GASLGGLLAD KLGRRQVFAL SLLVYGVATG ASALSVSLAM LMALRFVVG  
 GLGAELPVAS TLISEFSPRK VRGRMVVILE AFWALGWIMA AIVGTFFVAG SDNGWRWALA  
 LGCVPAIYAV YVRLGLPESV RFLEKKGRHD EAEAIIVSFE EAAAAEGKAA DATTAVVHDN  
 AAEGSVSIWS AALRKRTVAL WIVWFCINLS YYGAFIWIPI LLVADGFTLV KSFQFTLIIT  
 LAQLPGYAVA AWLIEKWGRR STLATFLVGS AISAAALYGLA NVEWQILVAG CLLSFFNLGA  
 WGALYAIGPE LYPTNVRGTG TGAAAGFGRI ASIIAPLIVP PVIAFGGPIA LFALFATAFA  
 IAAIAAFTLP EQKGKSLAD

> RXA00962 (1-666, translated) 222 residues  
 DKAIKADHDI REGHDEPAGE KDLLVDRYRW ISIWALATF VTLLAWYGLG TWLPRLMETA  
 GYEFGLHMF TLALNLGAVI GSVVTAWAGD RFGPIRSGVI AAGIAGIAL LLLTYPPVTA  
 VYVILILAGV GTHGTQILII AAVANFYPSN LRGTALGWAL GVGRIGAVVA PQLAGLLLAW  
 NLGVNSNFIM FGTAALLSAL ALSVLLRLQK TYSVTHKVEI QG

> RXA01060 (1-924, translated) 308 residues  
 MNRTLRLTLGW LAAVIQEDPE PWFETDPDTP YVPYVNSFSF ESLSLVPDAL MLLKRSLHLA  
 MEQQDLVPKD LQEARHVLV FKFHFREEWE LELAWDSERT KSAVRIEST KESLADQYRD  
 YKYAFLPELI FQESRGIFDF ELEGYTLKVG QSTLSIPWDM IANGYVPASL RNFGEMLDRD  
 TGDLDADPIL RPRELKFEIH NCPDLNPWIM RETFDFMMEI ATETGWFHAL NPAYNSVYTY  
 DLISRMPEFL VEGSFRPHSV KRSWEKIQKI AKAVESYASH DYCMSTLTHD YRAIELSLTP  
 TKTEEPST

> RXA01067 (1-729, translated) 243 residues  
 VSEFQVPEIP AQFLPKHIAL VMDGNGRWAT ERGMKRTEGH KRGEAVLLDV VDACIELGVP

YLSAYAFSTE NWRRSTDEVF FLMGFNRDVL RRQRDDLHEK GVRVRWVGRR PRLWRSVIRE  
 LETAEELTKD NTTMTLAMCV NYGGRAEIID AARDIARLAA EGKLRPEQIT EKTFPNFLDE  
 PDMPDVLFL RPSGEKRTSN FLLWQSAYAE MVEYQDKLFPD FTQQDLYDAV LEYAKRDRRF  
 GSA

> RXA01114 (1-792, translated) 264 residues  
 RLAEARETAG GRNHPIPGGM IETAENLRRE YGISREEQDK ISAASQQRWG KAADAGLFDD  
 EIVPVTVPK KRGQEPTIVS RDEHGRPGTT VEKLAALRPI MGRQDAEATV TAGNASGQND  
 GAAAVIVTTR AKAEEKGLRP VMRLAGWSVA AVPPETMGIG PVPATKKVLD RLGLTLEDIG  
 AIELNEAFAA QALSVLKEWN ISWEDERVNP LGSGISMGHP VGATGARMV TLAHRMQREN  
 TQYGLATMCI GGGQGLAAVF EKEN

> RXA01136 (1-432, translated) 144 residues  
 MTLDFYKASG TDYALGLAAE SEGARRTGIT GMASAFKEFA GCGEIDLEAT RVEGGLKVSG  
 KLRWASNLCF DPVIVPAAKT AEGLQLLFAL GAETEGVTLG SSLALLGLNA TACAWVSFED  
 VFIPGAQILS HDFLTWHRC AQPS

> RXA01138 (1-417, translated) 139 residues  
 VVTTTDGEVD HGLTVSAFVS LSLEPAMVLV SIDKKSSVVP FLEQGSPVAV SVLSEEQSDL  
 AITFGRHLEN KFDGVSIRKS TNRAAVLEGA SAWLSGAVVD KYPGGDHFII TIAVEECAHD  
 EEQKPLLYHR GRLFQWQED

> RXA01172 (1-1455, translated) 485 residues  
 VLASFRAFS SPRRFRTEVL AGLVVALALI PESIAFSVLA GVDPKMGLFA SCTMAMTIAL  
 TGGRPAMISA ATGAVALVIA PVVRDHGVEY FLATVILAGI IQIALSLLGV AKLMRFIPRS  
 VMLGFVNALA CLVFFAQLPH LIDVPWMVYP LFALGIGIML FWPKLTSVIP APLIVIVALT  
 AIVWVFGINI PNVSDQGELP SSLPEFLIPN VPLTLETLKI IGPYALGMSL VGLMESLLTA  
 KLVDDITEVH SNKSREAAGQ GIANIITAFI GGMGGCAMIL QTMINVKNKG ARTRLSTFLA  
 GGFLLLLVL LGDVVGKIPM AALVAVMIIV SIDTADWHSI NPRTLKFMPL SETIVMFITI  
 IATLVTGNLA IGVILGVLT MVMFARRVAH LVSVERTTDN NISTYTVKGQ LFWASSNDMV  
 YSFDYSDEAE QIIIDLTAEE IWDASTVATL DSIIHKYAAK GKSVEIIGLD GPSRDRLERL  
 SGKLG

> RXA01191 (1-1407, translated) 469 residues  
 VSLDANTIET AGRGDVISRI ADDSREVSTA ASTVVPLMVQ AGFTVVISAF GMAAVDWRLG  
 LVGLVAIPLY WTTLRVYLPR SGPLYTRERE AFGVRTQRLV GAVEGAETLR AFRAEDTELK  
 RIDAASGEAR DISISVFRFL TWAFSRNNRA ECITLVILIG TGFYLVNIDL VTVGAVSTAA  
 LIFHRLEFGPI GTLVGMFSDI QSASASLIRM VGVINAASNQ VSGTSPASAS TALTLFDVSH  
 HYHTAPVIKN ASVQLEPGEH IAIVGATGAG KSTLALIAAG LLSPTSGQVA LGGSSFSNVE  
 PEALRQKIAM VSQEIHCERG SVLDNLRIAR PEATDADIHA VLADIGDSWL ERLPQGIDTI  
 VGDGAFRLTS VENQIMALAR VHLADLAIVI LDEATAESGS DHAKQLEDAE LKVTENRSAI  
 IVAHRLNQAK TADRIIVMDS GEIIESGTHE ELRAIGGRYE QLWTAWSAR

> RXA01205 (1-531, translated) 177 residues  
 VSAYPPAIIA AALVGICAGV LPHNFEPSRI FMGDSGSMLI GLLLAASST ASGKINMSLY  
 GAADFIALIS PIIIVLAAVA IPLLDLVMV VRRVGRGASP FSPDKMHLHH RLLSIGHTR  
 RVVLVLYTWA SAVAFGAVSF SVVPPLFATG SSICGILIAV AVTAVPVMKS RRAAKLD

> RXA01212 (1-813, translated) 271 residues  
 GLNFHVQRGE VFGLLGTTGA GKTSTLEVIE GLSAPSSGTV RISGLDPVAD RAILRPELGI  
 MLQSGGLPSQ LTVAETMDMW HGTCTYPRAI KDVLAADVLL HRENVKVGAL SGGEQRRDL  
 ACALLGDPSI LFLDEPTTGL DPESRRHTWQ LLLDLKQRGV TMMLTTHYLE EAEFLCDRIA  
 IMNAGEIAVE GTLDELVARE KSIISFVLRG GQVELPVLSG AEIIRDNNHV RIATTTLQOH  
 TLEILTAAE TGIALEGFAA KPATLESVFM D

> RXA01219 (1-882, translated) 294 residues  
 MDILLNQLVA GLSVGSVLLL VAVGLSLTFG QMGVINMAHG EFIMVGAYTA YVVQLVVGSA  
 GLSLLISIPF AFIIGGLFGV LLEQFLKYL YHRPLDTLLA TFGVGLILQQ LARNIFGAPA  
 VDVRAPEFLR GNVEVLGVLV PTARLFILAL AIASVTALAV FLNRTAWGRR IRAVVLNRDL  
 AETAGIDTRA TDRMTFFVGS GLAGIAGVAI TLIGATGPTI GQNYIVDAFL VVAAGGIGRV  
 KGAVIMAFVL GITQAFVEYT TGASIAKFIV LIAVVAFLQF RPQGLFQTQT RSLV

> RXA01220 (1-1077, translated) 359 residues  
MSTQLKLKKP AKKKTTPKLS VVNAPTLRTA ALGLAALAAV LLCAPLFLST FQLTLMSRLV  
CYAIVAVGIG LAWGRGGMLT LGQGVFFGIG AYIMAMHMLY SDSQIFGTTV PQWWSIFANP  
AVALIAVVAL PGIVAFVLGF SIFKRRIKGA YFAIVNQALA AAVVVLVVGQ QDSLGGSNGL  
SGFRSEFMGFA VYDPINRIMF YFTAVGVLLA LVAISYWLMR SRYGELLVAT RDAEERVRL  
GYDPALIKTA AYVIAAMIAG IAGALFVPIV GIISPAEIGV VPSIVFVIAV AAGGRASLFG  
PVVGALVLGW VESTLAQTFP SMWSYFQGAI LVLVIVLLPG GIASIKLSAL KNKARKATS

> RXA01221 (1-726, translated) 242 residues  
MSLKITNLKV AFGSFIIVNE ISFQVLPGHV HFLIGANGAG KTTCIDAIISG LAPGQGSVQL  
DGTEILGTPV HRIARMGVGR TFQTASVFEE LSVLQNLDA CGIHRPLRAL LGVRHRIDPR  
IEHALEVTGL ADLVNAQAGT LSHGQKQWLE IAMLLVQDAQ VLMLDEPVAG MSEEERVATG  
ELLQRVARGR VVLVVEHDME FMRRFATRVV VMNRGTILCE GSVDEIQANP DVQSIYLGTA  
GK

> RXA01222 (1-699, translated) 233 residues  
MLEITNLCAG YGRTQVLHSL SISTSSNGIL SILGHNGAGK STLLRTAVGL IKPTSSEVVKL  
FGQDVTSLST HERVKRGMAY VPQGQSQFTQ LSCMENLQVV ADLQGRVGKA RIAEALDRFP  
ALTQVLDRQA GLLSGGQRQQ LAIARALITA PKLLLLDEPT EGIQPSVVAE IQQTIIDLAK  
DGMSIVLVEQ NIGFALDAAT SYAIVARGQV VESGQGAETT AEKQTKVRES LAI

> RXA01235 (1-972, translated) 324 residues  
VVLFSGFSGV IDLSPTAVIR HLSGQDTLTP RDQAIFFDIR LPRIIAGVIV GATLAISGAA  
YQAVFRNPLA DPYLLGVSA SGLGVTAIVV GGTVLGFSAP SIGVIGAAEV GGVA AVLATL  
MVS RGVGQGS STTVVILAGV AVAAFASSIQ TYIQQRHIDT VARVYVWMLG NLNVTNWMSI  
FIVAVVAGLC AAVIMSCARL LDVMAVG DVE ARTLGVD PGL VRIGIVIVAT LGTAAVVSIS  
GLIGFVGIIIV PHALRLIVGP GHRILLPLSF VWGAIFLVLA DTAGRTL MAP QELPVG VVTA  
ALGAPFFLFI LRRTSRQ RVP KRSA

> RXA01260 (1-1182, translated) 394 residues  
VTFNYEDA HK RSRGVSDKIV GGVHYLMKKN KIIEIHGLGN FKDAKTLEVT DGKDAGKTIT  
FDDCIIATGS VVNTLRGVDF SENVSFEEQ ILNPVAPKKM VIVGAGAIGM EFAYVLGNYG  
VDVTVIEFMD RVLPNEDAEV SKVIAKAYKK MGVKLLPGHA TTAVRDNGDF VEVYQKKGS  
DKTETLTVD R VMVSVGFRPR VEGFGLNTG VKLTERGAIE IDDMRTNVD GIYAIGDVTA  
KLQLAHVAEA QGIVAAETIA GAETQTLGDY MMMPRATFCN PQVSSFGYTE EQAKEKWPDR  
EIKVASFPFS ANGKAVGLAE TDGFAKIVAD AEFGELLGAH LVGANASELI NELVLAQNWD  
LTTEEISRSV HIHPTLSEAV KEAAHGISH MINF

> RXA01261 (1-171, translated) 57 residues  
VTEHYDVVVL GAGPGGYVSA IRAAQLGKKV AVIEKQYWGG VCLNVGCIPS KVSDQKR

> RXA01269 (1-441, translated) 147 residues  
VVFEMIKFRT MLEPDEKHVT DEQRLTKVGK LLRETSDEL PTLWNVFKGD MSLVGPRPLL  
VSYLEHYSSE QARRHEVRPG ITGLAQVNGR NQTTWDERLK LDVEYVDRCS LKLD FKILIA  
TVKTVLSKKG ISNEGHVTMP SFIEERK

> RXA01291 (1-933, translated) 311 residues  
VADQQDFLGR FDAMSSKATA TVIAHYSSSF TLASKLLSPK IRRDIEALYA MVRVADEVVD  
GAAAAAGCAP DAVAEILDNY ERQVLLSLV PFHTDPVIHA FGNTARKCGF EQAHIVAFD  
SMRRDLSQTS YDPTQLDEYI YGSAEVIGLM CLKIFLQDST ASPQDRATME HGARRLGAAF  
QKVNFLRDLA EDREGLGRSY LPVFTEEMRD EIVTDIREDL DAARLSIPLL PFGARTGVRA  
ATDLYGCLVD NLESASLEDL KNGRDFVPSL KKPAWQPKQC GKKCFKNDKS SGHRRGTSRT  
SHHRTALTRR I

> RXA01292 (1-1185, translated) 395 residues  
MTKAVVIGGG LAGLATTALL LREGYEVHLV EQNEHLGGRA GTFELDGFRW DTGPSWYLM  
DAMSHFFKLC GTSIDHDLDL VPLEPAYRVI DDHGEFIDVT SDIDAMAELE ESREPGAGAK  
LRTYIDSATQ VYNLAIDGFL YTNFTNFIPY LSPGMLRLLP KLLASLSTSL KVKVNTQFRD  
TKLRQILSYP AVFLSSDPSH TPALYHLMSH TDLVQGVSY RGGFTAFIKA LISLIDDAVL  
HLGTPVSAIT TQGRNATGVQ VGSEFIEADI VISCADQHHT ETQLLPASLC AKPETS WKNK

QPGLSTVLVL AGVKGEHTLL FPPTGTKISA KFSTAPPQNS RLQNPSRSPR PPQQIPMPHP  
KATRTSSWS QYPPMSPLVT GPLTEKNLTW WAGSQ

> RXA01293 (1-327, translated) 109 residues  
MVGRIAAV AQIGRWAGID GLESRIVVQR TIGPADFADR YNSWSGGSIG PSHTLAQSAF  
FRGSNKSARKV DGLYDAGDTT VPGVGVSML ISAENVLKRL RGDNSVDRT

> RXA01339 (1-1245, translated) 415 residues  
MTTESIVAHN AAGTAPQNV SAKKKYLSVA QGVALIYGTN IGAGVLSLPY AARNGGFLAL  
VVALLIAGTL TTISMLYIAE VSLRTKKPLQ LSGLAEKYLG QWGRWLVFIA IVVNSVGALI  
AYASGSGILI GNLTGLPPIV GTLGFFVLGT LIMWKGLHTA SFVEALITTG MATIIIVLCG  
WTVLGPGISA DNLIVFHPPF IVPIMNLAVF TFLAQYVVPE IARGVNPATP KAVPRAIIIG  
MVATGVTLAA VPFAALGLLG TGVSEVVTIS WGEALAPVAY YMANAFALLA MFTSFIAIGF  
TAMRNVLDIG HWPQHGWRQS VAVGLTVLPP LAISLAGLGG FVAALSYAGG FAGAIMSIIP  
VLLLRNSRKS GDQEPVWKAT WQAHPIFQIL LIVVYSLAFV YSVLAIVGLM PAGWA

> RXA01382 (1-1062, translated) 354 residues  
STSTAAGTGT ANEEGTITAA ISYELGTNGY DPMTTTSALT VAANWHTLEG LTEIDPATGE  
VYAALASALP SADATSLDIK LRDGATFHNG DAVTADDVVF SFERVLDPAN NSLYASFIPF  
IKSVTKKDDT TVTIDL DYAT GIISERLAVV KIVPKSVVEA DASGFDANPI GSGPYKMTDN  
GASKVVKFER NDDYNGPRPA RAAKMEWQII PDASTRTNSL QSGSTMAIDS VPYLSIPQLE  
ATSTVESVQG FGLLFAMFSC SEGNPFNDVR NRQAFLYALD MDKIVKTGMS DQATPATSEV  
QKEHPNYNQA STVYSLDADK AKALFAETGL TSLNLLCTDH DWVKNCTPLI QESL

> RXA01399 (1-1119, translated) 373 residues  
ILSPATALVL AIGLIAAAII PPLLAARGVK TAEARRAESS EAYLSSLDQV LSNQAALRVR  
GEMPAALSKA DVAARSYSSS LEAGAKDTAI GAASSLWIHG FTVIGVLMVS ASLYADGSHS  
PQWFGVLVLL SLAAFEAVSV LPDAAIARTR AADATRLAE ISALPESVSL ELRTASDQPV  
LRAENLVYGW DSDLGTSNLD LTFGSRHEII APSGTGKTTL LLTLAGLLEP RGGQVLIDGT  
NPSELKNAVL FSPEDAHIFA TTVRDNLALG APEATDAEMT SILEHVGLSE WVQGLPDGLG  
TVLD SGADSL SGGQRRRLLL ARVLLSDAPI LLLDEPTEHL DTAGSSEILS MLASDELPGK  
RARRTVVIIVR HVR

> RXA01419 (1-264, translated) 88 residues  
MLLSARTHTS FQELGLNASR RKAINWTLAL TVVLIASMFV GVLIGASGTS VFSTWTVISH  
HLFGTELGGG DTADAIWYI RTPRVLLA

> RXA01420 (1-759, translated) 253 residues  
VTLGGLNVPS WSLGAEMLFY LTFPLFIPLV RKVKGVGNWW AFGITFAVSL ALITVIHFYA  
DGPKGIEFF VPRLWDTNVS PVAEVHADPV WFMQEEIPVL ESYWLSYYFP LTRLIEFYLG  
VFGAKLVAEG MFKNTNITIP LIALAVSFVA TWFVPLAFKM SVIMSLPMAF VVATLAVRDI  
EGKSGEIASP RAVLLGNISF AFYMVQFPVM VFVQRYFIAG KEYGFLGWAF YAVVCFIVSV  
ILAWVLLPSL MIL

> RXA01467 (1-291, translated) 97 residues  
MDFNDKAASE NAVKTGAEGP NVFASVAKIL QDVGGISAED VTPESRFTED LAVSSLNYIE  
LIVNAEDAFG VRIEDADAKD LTTVQDLIDF INTNKAD

> RXA01538 (1-390, translated) 130 residues  
MADNKNADDS QLVSASTGTP GPGDIAKANA PSLKQAAVTA SGRSALMGAI FLMATSAIGP  
GFLTQTAVFT NQLGAFAFA ILVSILIDIA VQLNVWRIIG VSEMRAQELG NTVIPGFGWV  
LAVLVCIGGV

> RXA01576 (1-759, translated) 253 residues  
VAPNRKISHH ALGSIPIMDA SKNSDFKDTW LVVPCYNEAT VIREVLENAL KTFPNIVAVN  
DGSPDNSAEE IHAAGAHLVN HPVNLGQGAA IQTGIEYARK QPGAKYFVTF DADGQHVKD  
VIRMVERLRA EDVDIIVGTR FGRPRQADDQ VPLIKRLVLR TVVLLSPKTR RLGLTDAHNG  
LRVFNQKVAQ EMNIRMNGMS HASEIVDQID ERGWRISEEP VDILYTEYSM SKGQSLLNGV  
NILADGFLAR RLP

> RXA01580 (1-702, translated) 234 residues



MYKNMHIVAH RGAEDLHLEN TMTAFQAAAP ADAFELDIHA TADNQVVVIH DRTAARVAAP  
 DSLHRDTPVA RLSAAQIKEI TLIDGSPVPT LEEVLLQTSI PIQVEIKSAG AVPAAAALLQ  
 KYPEHLERLL FISFIDAALV EIVDRLPEAR VGILRDASMD DLRILDYIPL KNVGAILPSW  
 KALNVASIAD LHTKGIKVC WTIRDENAFG IAQQAGVDYP TVSDPSRFSR PPLL

> RXA01584 (1-543, translated) 181 residues  
 VVFLGALLGA VIMGGFYPAF IQAGSTVFGG GHVVLPLEK LVVAPGFIKE TDFLSGYSA  
 QAVPGPMFSF ASYLGAIYGG IGGAVLASLA IFFPAALLSI SGMFWGRWR KAPRIQAAVT  
 GINAGVVGLL GAALYDPVFT HGITSVSALA IATVCWLGLA HWKIPPWAIA AGAALAGWVL  
 L

> RXA01591 (1-945, translated) 315 residues  
 ASLNWSVIVP ALVIVLATVV WGIGFKDSFT TFASSALSAV VDNLGWAFIL FGTVFVFFIV  
 VIAASKFGTI RLGRIDEAPE FRTVSWISMM FAAGMGIGLM FYGTTEPLTF YRNGVPGHDE  
 HNMGVAMSTT MFHWTLHPWA IYAIIVGLAIA YSTFRVGRKQ LLSSAFVPLI GEKGAEGWLG  
 KLIDILAIIA TVFGTACSLG LGALQIGAGL SAANIIEDPS DWTIVGIVSV LTLAFIFS  
 SGVGKGIQYL SNANMVLAAAL LAIFVFVVGTP TVSILNLLPG SIVNYLSNFF QMVGRTAMSA  
 DGTPGEWLGG CTIFY

> RXA01604 (1-606, translated) 202 residues  
 DTPFADVEIA PDSGLTLLST GRESQSSSFS LVLSGRMRAS TGTIELNGEP IKATKLAKHV  
 ALAGIPEIDS LERLVTVRTV VREQLAWSPP WYLMVPRDIS DSGRWVDVEK HLGLNLNPKT  
 LIGDLSVLER FKLRIALALL ARPEAQLLVV DDPDQVRSME LRAEVLHALK GVAEDLPVVV  
 VSTNPDEFDSL ADTALTITGA GN

> RXA01614 (1-1023, translated) 341 residues  
 MNQMQQWKPD FLGEGYQNL IELGDDPDNE TDVVTTVVRY NPDNHADESF AARPALLWVH  
 GMTDYFFHTE FAEFFHNAGF AVYGIDLRKC GRSYRPGQWQ HYTSDLAHYF PDLTAAAEVI  
 SSTHPELVVP AHSTGGLIVP LWMSQMRTSN PAAIEKIPAL VLNSPWLDMM YPPLFIKLIT  
 PMVRVLGKRS PTTIIPGGGL GAYGKSIHKN FYGEWDFDTT IKPVEGHKKS IGWLRAVMAG  
 QAEIHHDHVN VGVDVLTLCN KSWLKSEYT EDTNTSDAVL DVKHIQKWAP HLSSPSSRVD  
 VEIIDNARHD IFLSRKPARD HASEVLNNWL QSKLSSLKPS Q

> RXA01629 (1-1512, translated) 504 residues  
 VSPIRSKKKI KNEPRLTVDD VNVVPPKKIR PAIKGTVVGN FMEWYDFGIY GYLTVTMTAV  
 FTQGLPQEWQ LLAVMFGFAV SYLVRPLGGL VLGPLGDKVG RQKVLYVTMA MMAVSTALIG  
 LLPTAASIGA WALVLLYLLK MVQGFSTGGE YAGATTYVAE FAPDRRRGFF GAFLDMGSYL  
 GFAAGASVVA ITTWVTTHFY GATAMEDEGW RIPFLTAIPL GIIAVYLRTR IPETPAFENN  
 QDEPNAVVEK DTEDPYARLG LAGVIRHHWR PLLIGIAIVA ATNTAGYALT SYMPVYLEEQ  
 IGLHSASAAA VTPVILVMS LLLPFVGMWS DRVGRKPVYA TAVAATLILM VPAFLIMNTG  
 TIGAVLIAIS MVAIPTGLYV ALSASALPAL FPTASRFSGM GISYNISVSL FGGTTPPLITQ  
 FLLQKTGLDI VPALYIMFFS AIAGVALLEFM TESSQKPLLG SFPTVETKSE AVEIVKNQDE  
 DPNIDLSHMP FPDEENVGAE KQNA

> RXA01644 (1-1278, translated) 426 residues  
 MTIADIVEAT TTAPIPFIHT AFDGSFTGPE DAPYQLFVAN TDAVSYIATA PGDLGLARAY  
 LMGDLIVEGE HPGHPYGIFD ALKEFYRCFK RPDASTTLQI MWTLRKMNAL KFQEIPPMEQ  
 APAWRKALIN GLASRHSKSR DKKAI SYHYD VGNEFYSLFL DDSMTYTCAY YPTPESSLEE  
 AQENKYRLIF EKLRLKEGDR LLDVGCGWGG MVRVAAKHGV KAIGVTLSEQ QYEWGQAEIK  
 RQGLEDLAEI RFMDYRDVPE TGFDAISAIG IIEHIGVNNY PDYFELLSSK LKTGGLMLNH  
 SITYPDNRPR HAGAFIDRYI FPDGELTGSG TLIKHMQDNG FEVLHEENLR FDYQRTLHAW  
 CENLKENWEE AVELAGEPTA RLFGLYMAGS EWGFAHNIVQ LHQVLGVKLD EQGSRGEVPE  
 RMWWTI

> RXA01667 (1-1206, translated) 402 residues  
 MILGPKVLGL IGWSDHLSTY TTVLIAIVFA SMPYSMKFDR GVRTGMKTMW AYSTAMFVGQ  
 WGLFILLGLF LFQPVWGTDE WFGMMLPVGF VGGFGTAAAV GTALESSGAE AAMSLGFTSA  
 TVGTFAAIVG GIIFTTWGIK KGKTAAMPAQ LPWDLRSGYI DKLSDRPSIG KASTNPSAIE  
 PLALHTGIIL LTVAVAYSIN QWLGSMEPTV QIPLFAMSFV VGIVGMGIMR LLKKPEYLDL  
 DTVNSVSGAA TDYLIAFGIA SIAPAAIADY WVPLVVLVFL GTINCCFFFF WVAPRFFGEK  
 WLERAIFGWG WATAAVATGI ALLKIVDPKL KSGALNEYGV AYIGFAPFEI GMTIIAPIAV

LAGFTMGLGW ASLIVAIVIF GLAWGLKWLP ERGHVRGEGK PQ

> RXA01722 (1-1725, translated) 575 residues

MLSTMQDVPL SLTRILEYGS TVHGDTLITT WGGADGIEQA QQTFSAVGAR AAALAHALHD  
SLGITGDQRV ASMLYNCAEH METMFAVACM GAVFNPLNKQ LMNDQIVFIL NHSEAEVVIA  
DPRMAEQLGE ILKETPKVRA VVFIGPNDFS SAAAHMPEGM KLYSYEALLD GRSTVYNWPE  
QDERTAAAIK YSTGTSGPPK GVVYSHRSLY LQSLSLRTTD SLAVEHGETF LCCVPIYHVL  
SWGVPAAAFM SGTPLVLP GP DLSAPTLAKI ISTTLPRVAH GVPTLWIQLM VHYLKNPPER  
MSLRELYVGG SAVPPIVITM WEQRYGVDV HVWGMTETST VGTVSRPPSG VSGESRWNRY  
VSQGRFPASL QYRIVNDGQV MASTDRNEGE IQVRGPWVTA SYFHPDVEKE GGTASTFRDH  
DVEEENDEL TADGWLRTGD VGSVTS DGFL TIQDRARDVI RSGGEWIYSA QLENLIVAXE  
EVVECAVIGF PDDKWVERPL AVTMLYPGIE RTRETAERLR DQLRDRLPNW MLPEYWTFVD  
EVDKTSVGKY DKKDLRNHLR NGDFEVIKLG GPGXK

> RXA01727 (1-1278, translated) 426 residues

MSKKSVLITS LMLFSMFFGA GNLIFFPMLG LSAGTNYLPA ILGFLATSVL LPVLAIIVAV  
LSGENVKDMA SRGGKIFGLV FPIAAYLSIG AFYALPRTGA VSYSTAVGVD NALYSGLFNF  
VFFAVALALS WNPNGIADKL GKWLTPALLT LIVVLVLSV AKLDGTPGEP SSAYAQQPAG  
AGLLEGYMTM DAIAALAFGI VVISAFKYQK VNKVVRTATV SAFIAGILLA LVYLGLGSIG  
QVVNGEFADG TAILNYAALS TMGQAGRIMF VAILILACMT TAVGLISATS EFFNSLLPGV  
KYHVWATVFA LISFGVATMG LDTVLAVAAP VISFIYPSAI TLVFLSLIEP LLFRLKWTYL  
FGIWTAVVWA LFMSIPALNP FIEWAPLHSM SLGWVVPVLV ASAIGLAIDW NKKGAQSVAK  
KESISV

> RXA01737 (1-1059, translated) 353 residues

MGRMKNDGEL ADLPDHALLS IIRIPQAAKR SPWALILTRI GYAMVLLVIV TMVVYFDRNG  
YSEDLTFIDA LYYSTVSLTT VGYGDITPVT QSARLINIIV LTPARIGFLI LLVGTTLSVL  
TEESRRALQI QRWRKMRNH TVVVGYGTKG RSAVAALLGD GVPANQIVVI DTDQVSLDAA  
NNSGLVTVKG SATKADVLRL AGVSRARAVV VAPNLDDTAV LVTLSVREIA PQAMIVASVR  
ESENQHLLEQ SGADSVVISS ETAGRMLGLA TVTPSVVEMM EDLLSPDEGF SVAERLVGED  
EIGSNPRHLA DIVLGVVRSG ELYRIDSPEA ETVEPGDRL YVRRVFSEEV NDK

> RXA01755 (1-348, translated) 116 residues

MSTPDIKEGS AESPGVMV GDRREWRRQA TGIIAGLVLA ALVYLLFPSN SVETVMQSSG  
VDPETEYTN AMRLTAAVTI LMAVWWMTEA IPLAATALIP LVAFFPAFQVV DFGKAA

> RXA01762 (1-1263, translated) 421 residues

MKVNLGIGSY PRRRATVRPE STAIEFEGTS ITYGEFSKRV NRLGHALLDL GVAHQDRVAY  
VGFNHPALLE VFFSTNLIGA TPVLVNPRLS ANEIDYIIQD SGASIVFYGI DLIEHATYLO  
ELHPEIIMVA VEGDEGPGLR RKALIEAASD ADIDLEVSD DLVLLMYTSG TTGRPKGAML  
SHRNLFNYF NALLSQEIEQ GAVLLSTAPL FHIAGLNMTT IPVMMKGGKV IIHREFRAEH  
VLDEIERSKV SESFMVPAMI DMLSNHPSFA ERDLSSLRAI MVGGSPLSER ALRIWQGRDV  
KIVQGGFMTE TAPGACILEA TDTSTHLGTA GRAHFFTDIK LVDPKTGEEV PTGEAGEVLI  
RGPHVMTGYW NRPEDTASAL QNGWYHSGDI AIKDEDGYIT IKDRIKDMYI SGGENIYPAE  
V

> RXA01764 (1-933, translated) 311 residues

MSLNGKVAIV TGSGAGLGRS FAQELARQGA SVIVNDVNQA AADETVAAIT EAGGKAAAVI  
APVGPSESAA LLVREAVDKF GSLDILVTNA GILRDRSLLK MTDDDFDAVI NVHLKGFTFC  
VREAFGYFKE NGIAGRIVTI GSPTGQRGNE GQSNYAAKA GIVGMVRTWA LEMKRAGVTI  
NAIIPAAATD MTKTVPYFQK AVEADERGEA MPAFFRET LG FGTPQDVAGL VAFLLSSDEAA  
NISGQAIGAG GDRMQVWKHP EPAVTEFNPG GWTYEALQER GKNIIIEGNLQ SVGVVFPELP  
AELQPQIPVK A

> RXA01766 (1-291, translated) 97 residues

MRDPHQGAVI PSDLFGFAEV LTEAERAVLL ETRRVLEEEV KPYINEAWDK AVFPDEIVQP  
LQDLQLLDP ALREAGESVR DIFTGFRNFE LARCDIN

> RXA01801 (1-1017, translated) 339 residues

MSNVVNTFVQ NSTGMVELNR PKALNSLNQE MIDLVQEALT TWADDDQVQQ VLIYSSSERA  
FCAGGDVRAV RESVLEGDVA AGDKYFIDEF AMNNTLGTYK KPVISVINGV AMGGGMGISM

HGSHRIVTEK AFASMPEMAI GYVPDVGFTY FGQRASSLAI ATFLAVTGWR MSPADMLWAG  
VATHFVEDAQ GFIDAVLNE LDGALEKFST QPTGSSELAG VASQIEETFG HSSWALIDAS  
LRSHPDAEFV AKVDGLMASA APASVVATVK LMHQNSEATT LREGLDNELA MSLYMIRQPD  
FAEGVRAVLV DKDRNAAFSP ANYEDVDESH FVTLFQRSS

> RXA01823 (1-777, translated) 259 residues  
MLQAHDLTLS YGGRNIVEGL SLDLPERGLS IIIGPNGCGK STVLKALGRL LKPQLGKITL  
GGRDISSMGT KHVAKHIGVL PQPPYAPDGV SVTELVSRR YPHQHLLSQW SKDDEAIVAR  
SLAEVGMHTH AEHLVSELSE GQRQRAWIAM ALAQETDILL LDEPTTFLDV AHQISVLDLC  
SDLHQGRRTL AIVLHDLNMA ARYATHIIAM RDGTIIDQGK PEEILTKALL KEVFDLDAI  
LKDPNNGRPL IVPTDRRNS

> RXA01833 (1-1407, translated) 469 residues  
MLFERIYEEG LAQASYFIGC QREGKAIIVD ARDIQTYLD LAAKNNMVIS AVTETHIHAD  
YLSGTRELAA ATGAEIFLSG EGGADWQYGF TGTTLMHNST IKLENITITA KHTPGHTPEH  
LSFLITDGAV SKDPGFMLSG DFVFGVDVGR PDLLEAAGG VDTRFAGAQQ LFHSLKEQFL  
ALPDHIQVYP GHGAGSPCGK ALGAIPTTV GYEKANAWWA PYLRSDDEAG FVEELLDGQP  
DAHAYFARMK KQNKQGPVAVL STLSPLVKLE AEEVVEKLGS EAVFVDTREQ NQVHLGTVVG  
ALNIPRGAKA SNFAAWVIDP QKDAQDLIVL APDANTAADF RDALLRVGID TVRYFTNSID  
GLPTFVPELI SPAELAETNY DALIDIRAKS EFAAGSIPGA QQLSGGSAMW RLNELPAGGT  
LVTEFCQSGAR NTVVANALRR AGFTVIELEG SYAAWEKSAA NPKNLQTAV

> RXA01853 (1-552, translated) 184 residues  
MEILGFAAGP YKTNCYVVRG ENEVAIIDPG MHAHDDLVEY ITNNLSVDK IVLTHGHIDH  
TRDAGVVAKR FNAPVYIHPD DAFFLEVYKG SGTKTAMLF DADNMVSPDPE SLRDLVDGET  
ITLAGEEFTL KHAPGHSPGC TLIVGKEYCF SGDVLFKSGI GRTDFEWSA DAMNESLRTA  
VLPL

> RXA01881 (1-441, translated) 147 residues  
MANLINLENV SKTWGLKTLL DGVSLGVQTG DRIGVVGLNG GGKTTLLEVL TGIEKPDQGR  
VSHNSDLRMA VVTQRAELND DDTVADVVLG PLGLEVFWEA SNATVRDVLG GLGIVDLGLD  
TKVGQTFSGG RSADAPTWP RWFATLT

> RXA01894 (1-855, translated) 285 residues  
MPKPKNNAGR DLKAAIAVGI GLGVLVLLGI VLSPWGWYIL VAGFMAAATW EVGSRLKEGG  
YHLPLPIMII GGQAIWLSW PFGTMGILAS FVATVLVLMY FRIFYNGTEK EARNYLRDTS  
VGIFVLTWIP LFGSFAAMLS LMQNSIPGT YFILTFLMLCV IASDVGGYIA GVFFGSHPM  
PLVSPKKSWE GFAGSIVLGS VTGALSVHFL LDHHWWMGVI LGCALVVCAT LGDLVESQFK  
RDLGIKDMNS LLPGHGGLMD RLDGMLPAM VTWLILSVIS SSYPS

> RXA01897 (1-543, translated) 181 residues  
MKIGVILGSI REGRFGQGVA DWVMEQIGAY DAPDVEFELI DLKAFNVPLL ESATVPGSAD  
KQYDDPRVTA WSQAIDACDA FLFITPEYNH GVPAGFKNAY DILGNEWLNK TVGFISYGAV  
EGIRVVEQWR QIVATFNMYD IRSQLSFSTF TENNNGTFAP NDRRPGELIR LLDSLLTAVR  
D

> RXA01946 (1-1275, translated) 425 residues  
IRKYSRLEEQ FQSLGGYEAD AEAAQICDNL GLEARILDQQ LKTLSGGQRR RVELAQILFA  
ATNGSGKSKT TLLLDDEPTNH LDADSITWLR DFLAKHEGGL IMISHDVELL GAVCNKIWYL  
DAVRSEADV NMGFSKYVDA RALDEARRRR ERANAEEKAG ALKDQAARLG AKATKAAAK  
QMIARAERMI DNLDEIRVAD RAANIVFPEP APCGKTPLNA KGLTKMYGSL EVFAGVDLAI  
DKGSRVVVLG FNGAGKTLL KLLAGVERTD GEGGIVTGYG LKIGYFAQEH DTIDPKSVW  
QNTIEACADA DQQLRSLLG SFMFSGEQLD QPAGTLSGGE KTRLALATLV SSRANVLLD  
EPTNNLDPIS REQVLDAIRT YTGAVVLVTH DPGAVKALEP ERVIVLPDGT EDLWNDQYME  
IVELA

> RXA01980 (1-633, translated) 211 residues  
MQIIDLSHAF APGQPHYPGD PDQEIKTVST IENDGFLMHQ YRLVGPWGTH VDAPAHFDPQ  
GRTLDQIPVE ETHLPLYCLR FSRPDLCTAA DIEAFEHTHG KIEPGSFVAL HTGWEWGKQG  
IAPGWSIEAL EILHARGVIA IGHDLPTDTP SLEAQRWWLC RDHWQIENLT NLDKVPATGA  
MIACPWPVPK DGASFPVRPI ALVPEHLSPT R

> RXA01983 (1-507, translated) 169 residues  
 MEGYGPTQIE KLLPAYTQVN TAGNNPATTP EQDLLGGAAT SPENYDHQLQ YAVDASPVHQ  
 NAAQAPPFLI MHGTGDRMVP PEQSAALHTH LVQAGRQSTL VLIEGFGHGF LNPGEVAELG  
 PNVRLDNGRL EREPQTNFSA QQSPGNPFEL QGLAADHEMI KRFFTLHLR

> RXA02020 (1-1011, translated) 337 residues  
 MAKSENEGLGT GLRTRHLTMM GLGSAIGAGL FLGTGVGIRA AGPAVLLAYI IAGAIIVVLVM  
 QMLGEMAAAR PASGSFSRYG EDAFGHWAGF SLGWLYWFML IMVMGAEMTG AAAIMGAWFG  
 VEPWIPSLVC VVFFAVVNLV AVRGFGEFEY WFAFIKVAVI IAFLIIGIAL IFGWLPGSTF  
 VGTSNFIGDH GFMPNGISGV AAGLLAVAF AFGGIEIVTIA AAESDKPREA ISLAVRAVIW  
 RISVFYLGSV LVITFLMPYE SINGADTAAE SPFTQILAMA NIPGTVGFME AIIIVLALLSA  
 FNAQIYATSR LVFSMANRQD APRVFSKLST SHVPTNA

> RXA02029 (1-1314, translated) 438 residues  
 MAEARLRHLE PIDVEEWPGV ASVPNLAFAG ARARQAEYRF AKACSNAGLV LLGNPDPLII  
 DHEELFSRLA ASGWLGLAES YMAGEWRSER LADVLTALLG TGFKPRGKLS GSFTLPGQAV  
 DAGGALPNEL IRLSSGDGMS AFGGVFASGV PTTLRTAVKS HVPGAGRNR PASHFVDITK  
 ISEPVAVERE DLGEAQRRRA SFLLDGAKVK AGSHVLEFPS SGGALAILAA RRQGTVDALT  
 ADPAQVSSLE ETFVLAGEVE DIHIEVIPQA IPSPREWGGA YDSIVAMEKL EVVGKHGSKR  
 FIKAIDRMLT TGGNVAMQSL VATDQWSPVC SEASILLKAY IWPALHYPTV DEVHQLVDRD  
 SSLRVVKETH FAGHYLKSQV LQREVFEGQI REAAADGFDA VYRRMWVYHY ALIEALLRLG  
 CLNAVQFALT TRNRRGR

> RXA02030 (1-1386, translated) 462 residues  
 VTTTDHSTEL NPSDPGGQTA TLVIDKKTKR RVAAASTIGT TIEFYDFYAY AAAAVVVFPS  
 LFFPANDNPT VNLLASFATF GLAFVARPLG SIIFGHFGDR VGRKATLIGS LLTMGIATIL  
 IGLLPITYGQV GIIAPALLAL MRFCQGLGLG GEWSGAALLA GENAENTHRA RAAMWPQLGA  
 PFGFFLANGF MLILVGVLAH QDGDHLGAFM TWGWRLPFLS SAIMIAVGLW VRFSLEETPV  
 FKQAVDQGKK VKSPLKELFK TSPGPVVQAT LIMLSTYTLF YLVTTWILSY GIGNRSTGNG  
 LSIPYFEFLQ LQLATIVFFA IMIPVSGWLA DVWGRKNTLT LASVLLLGFG LTFNLLLDPE  
 TATKTTVFIF LFVGMSIMGL IFGPMASAILP ELFPTNVRYT GSGIAYNVSS ILGAAIAPFI  
 ATWLVSEFSV AYVGYYLIIV TAITFVAVLT MKENKNHDLR EV

> RXA02073 (1-1530, translated) 510 residues  
 MISRLQLAK KVPPELGAST LLRLNQLLT AALIVFPWV LSRKPDISLL AVAIIMALIA  
 LTAAVCRWGE QVCGHRAAFG LLAHMRVMY DALVHKGSPS PIHGSGSIMS VATRDINSIE  
 VFFAHTIGPT VTAVLLSAGG VITLATLDPV AGLIGLLGVL IAWLIPLIGK QSSSSEATSR  
 GHIAQHLED AAGRLEINSH GAQATRLNAL EVKEQQLEQV VTRQGLIVGI RQGAALLWPW  
 ISAVLLVALV PHVGIVAAAI ILGISPALDA VEGFARTMPT ALNSAQRYFQ IIDAPVAIAE  
 PDEPKPLPKG PLKLIRSRVP VSAKGTVSLE VAAGEHIGII GSSGSGKSTL AKLILKLAQL  
 RSGTITIGGV DIAEVSSAEL RKSRTLVEQK SVLFRASVLE NLRMGNPESL EDEAREALRL  
 ASISELPLDA DALRLSGGQQ QRLCLARALA RTPQVLIVDE ATSHQDALNQ ADLSQTLATL  
 KDTTVIIIAH RTAALTHVDR IIDLEEIKNP

> RXA02074 (1-1623, translated) 541 residues  
 MRSLLRDIPA VGWLITATIV VRTLVALVI VGIGLLIDVP SPAHSAMLWW VLAGATAAAA  
 LLCAEAVLPQ RIRARVERSW RRQLAAKNLE LNSSSSDDAQ LITLATEATS KASTYTMFL  
 GPYFAVFLAP LTVIAVVGAA ISWPIAGILC LGLCVIPFVI SWAQRMKGA GAGYGRASGQ  
 LAGVFLESVR TLGTTMMLNA AGQRRQIITQ RAENMRSQVM SLLYRNQLMI LVTGDFVGA  
 TTMVAAVFAI GGFSGSLTL QQAVALLA RLLIDPINRM GRTFYTMAG KPSLIAIEKA  
 LATTFDQPT QQQRHDGDL VVNNLKIARD HRDIVHGIF SIPRGSHIAV VGPSGAGKSS  
 VALALSGLE FDGAISLGGH NCEMLDLRAS VSFVPQSPTL FSGSIKSNID LARTGVDSH  
 IHAALLGEEL PADLKVGETG KGVSGGQAR ISIARGLVKN AAVIVLDEAT AQLDYTNARQ  
 VRHLAKSLEC TLVEITHRPS EALDADFIIV LEDGQLTMMD TPSNVSQHNA FFRTAVMEEE  
 Q

> RXA02095 (1-1404, translated) 468 residues  
 MKTEQSQAQ LAPKKAPEKP QRIRQLISVA WQRPWLTSFT VISALAAATLF ELTLPLLTGG  
 AIDIALGNTG DTLTTDLLDR FTPSGLSVLT SVIALIVLLA LLRYASQFGR RYTAGKLSMG  
 VQHDVRLKTM RSLQNLDPGQ QDSIRTGQVV SRSISDINMV QSLVAMLPL IGVVVKLVLT



LVIMLAISPP LTIIAAVLVP LLLWAVAYSR KALFASTWSA QQKAADLTTH VEETVTGIRV  
 VKAFAQEDRE TDKLDTARE LFAQRMRTAR LTAKFIPMVE QLPQLALVVN IVGGGYLAMT  
 GHITVGTFVA FSSYLTSLSA VARSLSGMLM RVQLALSSVE RIFEVIDLQP ERTDPAHPLS  
 LPDTPGLGSF NNVDFRGILN GFELGVQAGE TVVLVGPPGS GKTMAVQLAG NFYQPDSGHI  
 AFDSNGHRTR FDDLTHSDIR RNLIADFDEP FLYSSSIPRE HLDGFGCQ

> RXA02099 (1-273, translated) 91 residues  
 MGADQIAAVS GNSAWMLMSA SLVLLMTPAL ALFYGGMSRQ KSVLNMMMS FGALGVVTVI  
 YLLWGWSMSY GTQSIAGIFA NPFEFFGLKD S

> RXA02115 (1-1197, translated) 399 residues  
 TRATKSVGTV LALLWFAIVL DGFDLVVLGA TIPSMLEDPA WDLTAGQATQ ISTIGLVGMT  
 IGALTIGFLT DRLGRRRVML FSVAVFSVFT LLLAFTTNVQ LFSLWRFLAG VGLGGALPTA  
 IAMVTEFRPG TKAGSASTTL MTGYHVGAVA TAFLGLFLID GFGWHSMFIA GAVPGLILLP  
 LLYFFLPESP QYLKISGKLD EAQAVAASYG LSLDDDLRE HEEELGESSS LSSLFKPSFR  
 RNTLAIWGTS FMGLLLVYGL NTWLPQIMRQ ADYDMGNSLG FLMVLNIGAV IGLYIAGRIA  
 DKNSPRKTAL VWFVFSAFSL ALLAVRMPLI GLYGIVLLTG IFVFSSQVLI YAFVGENHPA  
 KMRATAMGFS AGIGRLGAIS GPLLGGLLVS ANLAYPWGF

> RXA02128 (1-1695, translated) 565 residues  
 MRGYQRSWLK GDVIAGITVA AYLVPQVMAY AVIAGLPAVV GLWGV LAPMA LYFFLGTSRN  
 LSVGPESTTA LMTAAGVGAL VGAAGGPERY AEVAALLAIA VGIVCAVGFI GRLGFLTRLL  
 SRPVLVGYLI GIAVLMIVSQ LSKVTQVNVE SGQWQEIIS FIKVAGQAH I PTVILAVVVL  
 SLLYLANWLT PKFPSTLMVL LLSAAAVGFF HLD RFGLEVI GEVPRGLPQP SIPSIGDLEI  
 WSLLPYAVGI AIVGFSDNVL TARAFA SGKD EVIDSNQELL ALGTANLANG FFQGFVSSS  
 GSRTVLGDTA GARTQVHSLV VVALVIMVLL FAGPVLESFP DAALGALVIY AATQLIDIAE  
 IKRIARFRKS ELVITAATAA SVVASGVLG IGVAVTSLIL DLIRIRITRPY ADVLGYTPGM  
 AGMHSLEDYP ESTAVEGLVV FRYDSPLFFA NADDFSKRAI EAVDEATQPV HWFLLNAEAN  
 TEVDLTAVDA MEALRKTLEE RGIRFAMARV KQDLRRSLEP AGFIESVGEE YIFATLPTAV  
 KGYSVEFRDR FGNYPEGVPK EILEL

> RXA02133 (1-306, translated) 102 residues  
 ENPYIGGAGY NAAKFGVAAF NRVLRLETHQ QTLRVSEIDP GRVATEEFSL VRFGGDKERA  
 EAVYDDVLNL TAEDIAESVR WVASLPKHMN IDRM RITPRD QV

> RXA02150 (1-801, translated) 267 residues  
 VGNVFLEVPT AVKREEGVNP NIMKNNWYRL FKYVLIGPFL RVYNRPEIEG KENIPAEGAA  
 IMASNHEAVM DSFYFPLLCP RQLTFPAKAE YFTSPGIK GK MQKWFFTSVG QVPLDRTADN  
 AMDSLMNTAK MVLDRGDLFG IYPEGSRSPD GRIYKKGKTGM AYVAMETGTT VIPVAMIGSR  
 DANPIGSWFP KPAKVRIKVG SPIDPLAFVK EHGLKPGTYE AARKLTDHVM FILADLTGQP  
 YVDAYS KDVK NALEEGKGYP EGTAPSQ

> RXA02171 (1-1653, translated) 551 residues  
 MNSTILLAQD AVSEG VGNPI LNISVFVFI IVTMTVVL RV GKSTSESTDF YTGGASFSGT  
 QNGLAIAGDY LSAASFLGIV GAISLNGYDG FLYSIGFFVA WLVALLLVAE PLRNVGRFTM  
 ADVLSFRLRQ KPVRVAAACG TLAVTLFYLI AQMAGAGSLV SVLLDIHEFK WQAVVVGIVG  
 IVMIAYVLLG GMKGTTYVQM IKAVLLVGGV AIMTVLTFVK VSGGLTTLN DAVEKHAASD  
 YAATKGYDPT QILEPGLQYG ATLTQ LDFI SLALALCLGT AGLPHVLMRF YTVPTAKEAR  
 KSVTWAI VLI GAFYLM TLVL GYGAAALVGP DRVIAAPGAA NAAAPLLAFE LGGSIFMALI  
 SAVAFATVLA VVAGLAITAS AAVGHDIYNA VIRNGQSTEA EQVRVSRITV VVIGLISIVL  
 GILAMTQ NVA FLVALAFAVA ASANLPTILY SLYWKKFNTT GAVAAIYTGL ISALLLIFLS  
 PAVSGNDSAM VPGADWAI F LKNPGLVSIP LAFIAGWIGT LVGKPDNMDD LAAEMEVRSL  
 TGVGVEKA VD H

> RXA02173 (1-1452, translated) 484 residues  
 MVWGMEHTSA LTLIDSVLDP DSFISWNETP QYDNLNQGYA ETLERARSKA KCDESVITGE  
 GTVEGIPVAV ILSDFSFLGG SLGTVASVRI MKAIHRATEL KLPLLVS PAS GGARMQEDNR  
 AFVMMVSITA AVQRHRE AHL PFLVYLRNPT MGGAMASWGS SGHLTFAEPG AQIGFLGPRV  
 VELTTGHALP DGVQQAENLV KTGVIDGIVS PLQLRAAVAK TLKVIQ PVEA TDRFSPTTPG  
 VALPVME AIA RSRDPQRPGI GEIMETLGAD VVKLSGARAG ALSPAVRVAL ARIGGRPVL  
 IGQDRRFTLG PQELRFARRG ISLARELNLP IVSIIDTSGA ELSQAAEELG IASSIARTLS

KLIDAPLPTV SVIIGQGVGG GALAMLPADL VYAAENAWLS ALPPEGASAI LFRDTNHAAE  
 IIERQGVQAH ALLSQGLIDG IVAETEHFVE EILGTISNAL SELDNNPERA GRDSRFRFE  
 RLAQ

> RXA02224 (1-1797, translated) 599 residues

MAQHERVADA LQPASLAESW RELKTMPSGP KAWWYVSFVV ISVVTVVAMV GTSNLLGYSV  
 DLINGQSLPL IGSGSTAMIW LLGLVGAGIL AETAGRALLQ LVINTLARRL SVDLRKAALS  
 SALRAPVPDV MELGTGNVIS RLTQDIDNTV RIVGMVGVRL VITILILPSS LFALMTIHW  
 FVILFIAVIV VLIPSGRKAV RAIPSATNIV SSTEARRNNL LLDITIRGIET LRVLKLGA  
 VQRMQRASWT AVQATADRAP IFTRLLALGS IAYGLLLIGV FGLSAFWVAQ DAMSIGAATA  
 AVFVVVRMEI HVFNVLFAS EIQSASTSLG RAVSLAQMAR RTEQLSESAD CTEPPSVTVQ  
 DVTFKYPGGV AILEDENLV EAGTTTALVG TSGAGKSTLA GVIAGLQRPD SGAVLVGGIN  
 TATVTDTWTT RQVALISQEV HLFAGTLAED LRMANAHATD AQLHAALESV GLGQMTTAFR  
 RFFPSGLDTK IGAGAEELTP EIQQQISLAR IVLRNPPVLI MDEATSEAGS DDARMLEKAA  
 TEIARNRTTL VVAHRLDQAV VADRIIVMEQ GTITEDGTHQ ELLAFEGRYA QLYQRWSAQ

> RXA02225 (1-882, translated) 294 residues

QTEERFGAAA DEALAIMLKE ARLQSLTFV RQLVPAVFSV GLLAYASLLA FDGDITGGEM  
 ISVTLVPPS LTVLGVS LGM MTEIWARGQA STKRQNLVT ELDKAAAEPR PQPATFEFEE  
 GITVWDPSTP EARDVIDREL EALQVREDVI VAPHRVSVFE GVLKDNLNP GTIAPEMLRA  
 ALHAASCEDI LSRLGADLNM PGEFELPDTL IGEAGLNLSG GQRQRIALAR FLAVDPEVLI  
 LDEPTTGLDA VTLDEVAHRV EKLRRGRKT VITSNPTWHG VAKQMQSDFS EGVK

> RXA02233 (1-1212, translated) 404 residues

VLVTSTWGT VHGDGKKIEP GAVVAPKERL SWGRTIGIGM QHVIAMFGAT LLVPTLTGFP  
 VNTLLFSGL GTILFLLITR NRLPSYLGSS FAFIAPLTAT QVHGIGVQIG GILVAGLVLV  
 AIGFVKAAG KRVIDAVMPP AVTGAIVALI GLNLAPTAAG NFSSQPLVAT ATLFALIAT  
 VAGRGMIALR GILIGVVIGW VFAAITGNLS EGAADTIREA AWFGLPQFHK PEFQLSAILV  
 TLPVIVLIA ENVGHVKA VS EMTGEDLDDL AGDALIADGF GTTLAGAFGG SGTTTYAENI  
 GVMAATRVYS TAAYWVA ACT AIALAFIPKF GALIFTIPAG VLGGACLVLY GLIGMLGIRI  
 WQDNKVNFN PVNLTMAAVA LVAGIGNLTL TVFGVTLEGI AWAL

> RXA02253 (1-927, translated) 309 residues

MIQSTGVTHT DKSAQENPVK YRDNFTPVII TGMSGAGLST AARVLEDLGW YVAHNIPPQI  
 ILELIDMCAR EDSPVDKVA VCDVRSREFR GSLTQVSEL RDKQLDPTVL FLEARDEVLI  
 KRFDNVRTH PLQGSQTLQV GIERERTVLS PVKEDASVVI DTSDLSVHDL RRAIESSFRT  
 IATRTQHVTI ESFGFKHGSP RDADEVVDVR FLPNPFVWPE LRPFRGVDPK VSDYVLSQKG  
 AEEFLNNFVD MLKDMLPGYR HEGKNFITIG VGCTGGHRS VAVSEELAKR IADQTTLDVS  
 VVHRDINRH

> RXA02261 (1-1356, translated) 452 residues

MDPSDLAWIL AAFALVSLMF PGLSLLYGGM LGGQHVLNTE MMVMSSLGII SLVYIIYGHG  
 LVLGNSIGGW GIIGNPLEYF GERNIMEDDG TGDLMWAGFY ILFAAISLAL VSSGAAGMR  
 FGAWLVFVGL WFTFVYAPLA HWVFAIDDPE SGYVGGWMKN VLEFHDFAGG TAVHMNAGAS  
 GLALAIVLGR RHSM AVRPHN LPLILIGAGL IVAGWFGFNG GTAGGANFLA SYVVVTSLIA  
 AAGGMMGFML VERVFSGKPT FFGSATGTIA GLVAITPAAD AVSPLGAFV GALGAVVSFW  
 AISWKKGHRV DDSFDVFAVH GMAGIAGALF VMLFGDPLAP AGVSGVFFGG ELSLLWREPL  
 AIIVTLTYAF GVTWLIATIL NKFM TLRTS EA EYEGIDRA EHAESAYHLN SNGIGMATRT  
 NFGPEIPEET VPDVQVGVD KQKIADTRKA SK

> RXA02268 (1-900, translated) 300 residues

MSQENSGLFK RAITRGVAKV RRPREDFAE EFTQELYDHA TNITLPLTAR LKPNGFFQDD  
 WRARPSGARP WPIVLIHGSG ASKGSWEEMG AELRSKGAV FAPDFGTRAT EPIAASAAQI  
 GAYIDAVLLV TGAAQIVLVG HSQGGVVARY WMRTYGGYMK VRHMISISTP NHGTLMGIL  
 NPM TKVSGE GTIEKLMHRL FGPTGFEQLR GHDIIEFLAD GGDLDPGVTY TCIGTHFDPF  
 IQPPEVAFLE VNEDDDPNRV HNIWVEDEHP RAMIAHNDMV RDPRVIEIVR AELDRVARLG

> RXA02269 (1-972, translated) 324 residues

MVDALNDLRR ELTNALRSVW KNLP TDNAPQ ADALPDDVVE EIAINFYRDP KNRGKL NEDK  
 TDSLPLMARI RSRGLFEDDW RARPTEDRPV PVVLVHGTGS TKGDWQDLGA DLRRDGWAVE  
 APEFGQRATG SVAESSAQIG AYIDTVLLAT GASKVIVVGH SQGGVLLRYW MRVLGGASKV

KHMOVSLAVPN HGTTMGGIVS PLIRNNRGES VVNSVVQSWF GEAGFEMIRG HDTINAINEG  
 GDLDPDVTYL CIATHFDTVI QPPETCFLEA RNPEELKRVQ NIWVENLDPN SVVLHEAMPY  
 DPRVRALVRA DLSKLVEISE TAEN

> RXA02309 (1-975, translated) 325 residues  
 MSSGRTVPTR SHGLGKEGVS TTGASQVEFG DPELTARIND AMVQVEELLH TELSSGEDFL  
 VDIVMHLTRA GGKRFRPMFA LLASEFGEKP LSENVIKAAV VVEITHLATL YHDDVMDEAS  
 MRRGVPSANA RWDNSVAILA GDILLAHASG LMSQLGTDTV AHFAETFGEL VTGQMRETVG  
 PRDTDPIEHY TNVIREKTGV LIASAGYLGA MHAGAAPEHI DALKNFGAAV GMIFQIVDDI  
 IDIFSETHES GKTPGTDLRE GVFTLPVLYA LREDTPVGAE LRDILTGPPE DDETVNHVLE  
 LLSQSGGRQA ALDEVYRYMD IANAE

> RXA02310 (1-1263, translated) 421 residues  
 VSTTFDVLII GAGPSGASAA VHAARTGLQT LLIDASSFPR DKTCGDGLTP RAIHQLELLG  
 VADQVTGDYF NKGLKLHGFG GSVEAPWPET YFTNKGSAMS RMEFDDLLFR LAKSHEEVTT  
 WENASAQDPI LRGNFLEGVV INHAGQEKTV KAKHVIIADG VRSPFGKKLG RQWQRDEVYV  
 IAARAYCETP LSDEPWIHSH VELRDEGTVV QPGYGWIFPL NGTGVNLGCG ALSTDTRPAK  
 INTKKLLSFY AGQRRKAWQL GPEHVASAL LPMGGAVSNV AGANWMLIGD SAACVNPLNG  
 EGIDYGLETA AMAVDTLVEN PKRDLTLVWP HRLRDAYGET FMLARTAARL LTYPQFLPMA  
 GPLAFRGPLQ KAIMPAAARL MGNLITEEDK DLLARGWQAA GSAISWARKG SPLWDSTSSL  
 V

> RXA02320 (1-588, translated) 196 residues  
 MTAAQTKPDL TTTAGKLSDL RSRLAEAQAP MGEATVEKVH AAGRKTARER IEYLLDEGSF  
 VEIDALARHR SKNFGDLAKR PVTGCVVTGY GTIDGRKVCV FSQDGAVFGG ALGEVYGEKI  
 VKVMDLAIKT GVPLIGINEG AGARIQEGVV SLGLYSQIFY RNTQASGVIP QISLIMGACA  
 GGHVYSPALT DFIVMV

> RXA02321 (1-444, translated) 148 residues  
 EYGGILRRGA KLLYASXEAP VPKITVTMRK AYGGAYCVMG SKGLGSDINL AWPTAQIAVM  
 GAAGAVGFIY RKELMAADAK GLDTVALAKS FEREYEDHML NPYHAAERGL IDAVILPSET  
 RGQISRNLRL LKHKNVTRPA RKHGNMPL

> RXA02335 (1-1773, translated) 591 residues  
 VSVETRKITK VLVANRGEIA IRVFRAARDE GMGSVAVYAE PDADAPFVSY ADEAFALGGQ  
 TSAESYLVID KIIDAARKSG ADAIHPGYGF LAENADFAEA VINEGLIWIG PSPESIRSLG  
 DKVTARHIAD TAKAPMAPGT KEPVKDAAEV VAFAEFGLP IAIKAAFGGG GRGMKVAYKM  
 EEVADLFESA TREATAAFGR GECFVERYLD KARHVEAQVI ADKHGNVVVA GTRDCSLQRR  
 FQKLVEEAPA PFLTDDQRRER LHSSAKAICK EAGYYGAGTV EYLVGSDGLI SFLEVNTLRQ  
 VEHPVTEETT GIDLVRMFR IAEGHELSEIK EDPAPRGHAF EFRINGEDAG SNFMPAPGKI  
 TSYREPQGPV VRMDSGVVEG SEISGQFDSM LAKLIVWGDV REQALQRSRR ALAEYVVEGM  
 PTVIPFHQHI VENPAFVGND EGFEIYTKWI EEVWDNPIAP YVDASELDED EDKTPAQKVV  
 VEINGRRVEV ALPGDLALGG TAGPKKKAKK RRAGGAKAGV SGDAVAAPMQ GTVIKVNVEE  
 GAEVNEGDTV VVLEAMKMEN PVKAHKSGETV TGLTVAAGEG VNKGVVLLLEI K

> RXA02343 (1-414, translated) 138 residues  
 MTISSPLIDV ANLPDINTTA GKIADLKARR AEAHFPMGEK AVEKVHAAGR LTARERLDYL  
 LDEGSFIETD QLARHRTTAF CLGAKRPATD GIVTGWGTID GREVCIFSQD GTVFGGALGE  
 VYGEKMIKIM ELAIDTGR

> RXA02364 (1-627, translated) 209 residues  
 MEPLFQSLAE SDNISVIGGF TQGTRNLYTT DAPVKRPADL AGKKIRVQES AMHIRMIELM  
 GGSATPLTYG EVYTAMQSGV LDGAENNEIS YVTQNHFEVA RYNSNTNHLV GLDYMVMRHD  
 LLDAMSEPDR ELFLEWDAA MTEHTDLWNT ETDVIEKAK AGGAEFVEVD AQAFTDALAP  
 IKDEFILTSEF QRELYEAVRA ADTSGGAAS

> RXA02372 (1-555, translated) 185 residues  
 DAVNKMDRTD FVETFAPLFN SKTWPLETAW ESQPFANVTE LREAIQVAVL TAPLSDREEL  
 IHDYPDMAQL ILATEEEAAT ISQDRGSIGL DDLDDVDQEK LITVTEQYRE RFNMPYVAYF  
 DTMDSDVDTVV AAGLRRLDNS DEQEHRQALS EIIEIANDRF DILLADANPA RSAFDRKFTE  
 TDFLG

> RXA02377 (1-1191, translated) 397 residues  
VPPAPKLAAL GLQHVLAIFYA GAVIVPLLIA QSLNLDATT IHLINADLLT CGIATLIQSV  
GIGRHIGVRL PIVQGVTTTA VAPIIAIGLG VTDGQGGVAS LPAIYGAVIV SGIFTFFAAP  
VFARFLKFFP PVVTGTVLLV MGASLLSVSA NDFVNYADGV PAARDLAYGE GTLAVIILAQ  
RFFRGFMGTL AVLIGLVGGT AVALILGDAN LDEVGNAAEF DITTPFYFGV PEFNAVAIFS  
MIIVMIITMV ETTGDVFATG EIVGKRTRRS DVTRALRADG LSTLMGGVMN SFPYTCFAQN  
VGLVRITGVK SRWVAAAAAG FMILGVLPK AGAIVASIPS PVLGGASLAL FANVAWVGIO  
TIAKSDLADS RNSVIVTSAL GLAMLVSRP DVAQGV

> RXA02397 (1-996, translated) 332 residues  
MNDFETTIDR ISKEQDPAAR SRVEQFIVET VRALPNLTTK QGASLAIQLL DAVQLADAAG  
TKGGASTSNA SSLPDTFDAL TSLIGKLDVR SDSEWRSFGF QPSETAHPLM IAIPEIEIFY  
QHTDVEPGSD DAVAPDFQEN QDMWRRRLGS VTEPNLIYKE FSGPGKAQRA VEMLGNLWKI  
GVVVSRTES RLGLTRVEYT PTPGEVPVPL MSEKNCWYSI RVSETIGENQ VPEIVRCLGE  
IFCGYLPQMW LKEPVKAGKL RIQSEAAAY IAMARLDLSP RTGNTTWTNS YISTRPLSPA  
FRWDVVLEAS HQLENLLRGD TGPVTATQSA AG

> RXA02424 (1-381, translated) 127 residues  
TGATHYAPFL EVPALPSAVD VELHHGDSIE FEGHVFPI SI LRGHTPGGAV LTAEIDGKTH  
LFVGDSLFPGL GLGKTSSEGD FVRLFNDVKE RIFDTYDDDS IVWPGHGKET TLGAERPQLE  
IWWERRW

> RXA02426 (1-1533, translated) 511 residues  
MLITLLLATV IVVAIGDKTG LPWPALMTIV AAGGALLPFL PEFTIPADLM LPIFIPPLW  
ALARKSSWAV IRSQMSTIIT MSVLLVFVTI AALTGASMLL LPGIGLAGAI MLAAAIAPPD  
PVAVDVAEP AGIPKRITTT LQTEGLFNDASIVAFHVAL AALVAGEDLS WSTGVLEFLW  
SCLAAVILGL VIGRAAAWFT DHVSSVEARN AFTWVLPFAI YVVAEEIGGS GVIAIVIAAV  
EMNSRASIGA EDRLTGSAFW GTIEVLFTGV AFGLIGLNVR AAIDEVGSSEL WHAVVVGIVL  
SVVAIVVRGV WMFAAYKRNK FKIDKKGATN SSLRAPRLQ ESLLMTWAGM RGLVTLALVL  
SIPEDIFPYH HELQVIALVV LLITMVGPGL TLPWLMRKLS LDKGPDAAGD ESIAALTERA  
HKAATTYLVD TTELPMEQMV AIKNWFSQEI DADELQENV D KLHQRAHHAR VGAIKAAQEE  
LLKARRERGV NPAYVDEVLT NIDRMLVAAE R

> RXA02487 (1-288, translated) 96 residues  
VYPAEVEEVL AEHPDIEDSA VVGIPREDGS ENVVAAITLV EGAALDPDGL KEFARKNLTR  
YKVPRTFYHF EEMPRDQMGK IRRREVQAE LKKLGK

> RXA02490 (1-813, translated) 271 residues  
MSAYETKEWL QHYPEWTPHS LEYGDTTLLD VYDNNLAINA DKPATYFFGR SQTGELDKE  
VRKTAAGLRA LGVRPGDHVA IILPNCPQHI AAFYAVLKL AVVIEHNPLY TAHELLEPFK  
DHGARVAIVW DKASPTVEQL RGQTQLETIV SVNMINAMPP LQRLALRLPI PALRKSRESL  
SGAAPNTVPF ETLTSAAMGG DGDDVVSEPT VTKEVALIL YTSGETTGRPK GAQLTHGNLF  
SNLLQKGHWV PGLGDKPERM LAALPMFHAY G

> RXA02511 (1-657, translated) 219 residues  
MLGLHGRKPA QVIVEPVAKL MIKLVTPNQ LTLVSAGLTV GVALLLIPTG HLIWAAVLTG  
LFAAFDMIDG TVARMQGGGT KFGATLDATC DRITDGALFG AITWWLVYSY DAPQALVAAS  
LVCLVASQVI SYVKARGEAS GFTMDGGLVE RPERLIVSLV GLGLTGMGVP YAIIDVALWAL  
AAGSIYTVVQ RLVMAKGSPL AKEFTKAPAG AKADYSNTK

> RXA02512 (1-957, translated) 319 residues  
MKPKDFCTAE NWAENLSALG YLAGWRFVRM LPLPIARRVF DLGADLASKS GKMGQRLAN  
LARVVGAEV TQALVKQATR SYARYWLEAF RLPALARDPE LLARLRKGTV GLDLLDESLA  
AGKGVVLTLP HSGNWDMAA FLISHHGQFT TVAERVKPER LFEAFVEFRE SLGFEVLPLT  
GGERPPFEKL KERLTSGGIV CLLGERDLRH SGVETTFEKE KTSMPAGPAQ LAIETGAALH  
VVHPWFDDDG WGLSVSDAVT VDNLSDTVQR IAHLFMANIT AHPADWHMLQ PLWFGDLDP  
RLKRSREQTN VHKPVALQE

> RXA02527 (1-1329, translated) 443 residues  
MFGLFIATIV AIILKPMMPG AVTIIGMIAA VLTGLVPLTA SSDDPGAVYG LIGFSNGTIW



LIVMAFLISR GFIKTGLGRR IALFFVSKVG GKMLGVTYGL ALADLV LAPA IPSATARGGG  
 IMAPIMKSVA LTYDSTPGPT RRRAGAF LAL NVGQVNAITC AMFLTAMAGN PLIASLASQM  
 DVNITWTNWA VGAIVPGLVA LIVVPWVVYK IYPPELKDTP EVKKMASDEL KQLGGFTYGE  
 KVLAGTFVVL LLLWTGGDLV LGISATTTAF VGVIILLVAH VLTWEDI IQE KTAWDTMVWF  
 AVLYMMATAL SQYGFIAWIS EVIASSLGGM NWVVALVVLV LIYFFSHYFF ASATAHISAM  
 YLAFLGAAIA IGAPPLMAAL VLAYTSNLFS SLTQYSGGPS PTLFGLNYIT VGEWWRTSAI  
 AGAVSITIWL VIGGLWMNVI GLW

> RXA02547 (1-2124, translated) 708 residues

AARLTVDEYP AAREALESAG QRNVEDRTRA VDEFKAADQE LSSLSKGSSN IEYRLLQVRE  
 NLCQDLGVSP RDMPFAGELI DPNNAEWEPV VQRILGGFAA EMLVPHGLLP RVRDWVNAKH  
 LAALLKFNGV VTTGEYKTSR FPADSLIRKV DVVESPF RDW VNQELGKRFN IRCVRTPEEL  
 SALGPRDQGV TILGVRKFAQ QTGDPTTRWE KDDRRKL GDR STYRLGSTND AKVETLRET V  
 KAGKAVVQAA DNRIAANRAE LRELERQYQA SQEILKVS WA QIDVESADAA IAELDR LLEE  
 LNNTPEATEL SARHEAAKQT LARVSDLLVA AQSEETVASM NLKRAETELK RLESLPVAEV  
 SEEIAREVEK LFLANTRRVH AANVDEQTIA LREDLDKQID ANEAELRRCE NQIVGILRSY  
 IETWPANRAD LQAEPEFVGE AINRLGELRS DRLAEFTAKF LGLMNEMSTR NLGQISRRLR  
 DARREIEERI EPINASLAQS EFNEGRFLHI DIRDQSGPIV REFQOKLDAA TSGDLGTSTE  
 KQAFARYALI AEIISK LASH DSADARWRNT VLDTRRHVRF IGLERDSDGA TVNTYVDSAS  
 LSGGQAQKLV FFCLAAALRY QLAEPGAHYP TYATVILDEA FDRADPAFTR QTMNVFHSFG  
 FHMVLATPLK LIQTLGDYVG STIVVSYTEK PNAQGAIQGN SSFSRIEK

> RXA02561 (1-660, translated) 220 residues

MVGASNGVTL SMGSLLAHL AGASWGG SAA TLTTIGAAIF SIPLARMVST YDRRTSLSTG  
 MLLGCVGALL AILGAQFGLF PVVLLAFLFL GSMSAVNLQA RFAATDVASE ETRGRDLSIV  
 VWSTTIGAIA GPNLFEPSAR FSETLGLEQH AGAYLLCLFG QLIAIAVWRF TLPKGLKPEA  
 TPNAPTEKKR LTPKALQAIT SVATAHFSMV GLMSMAAIHM

> RXA02566 (1-438, translated) 146 residues

ISLHVAGMYA LSPVFGLLTD KLGRNVTIYS GFAMLATSAA FLIIWPEPQW AMITSMILLG  
 LGWNSALVGS STLLVDATPI HRTYAQGRS DLT MNLAGAS GGLIAGPLIA MGGMPLLAGV  
 VLAVVALQTV LSFRTSIEK TPASCF

> RXA02571 (1-1029, translated) 343 residues

VVALTQIVGP SGSGLTRELE KRYRETPGAV MLTADPRAHI TYLRATVAEE LAFGLEQ RGI  
 VPAQMWERVR NIGLLENLL DRAPAQLSGG QTRRLAIGTV AILEAPTMLL DDPLSGLDTS  
 SRAQLITMLE SYEGDVIVAA HKRWLDAPTV YLGDLEELSL PARVEFSGPS RTFSAITGTR  
 GQORRRWWQF NESQPQFQIG PLDITVSAGQ VLWLQGPNGS GKSTLLRGLA NEPGTEMLQ  
 NPSDQVIDST VANWVPGSNS EEHPLDLSQR ELRLAQCDAA LGNNPEVLLA DEPDVGLDVG  
 GRNAIHQRFA DFLGNNGALI LTCHDET FVA EVAEYAI VKE MGL

> RXA02578 (1-1104, translated) 368 residues

MSTQSYAPIR HRGFISSLEG LRAIASLGVL ATHVAFQTSV DPASNIGAVL ARFDEFFVAVF  
 FALSAFVLWR RRAGQPVGLY YLKRLARIMP AYWATVIAVL LFIPTGPWLA NLTMTQIYWP  
 DGLMTGLTHL WSLCVEVAFY LVMPLLA WVL DRFGRPVRIL LIVGGAVLSL AWPWIPLVEH  
 ALDEGWANMQ IWPPAYACWF AVGMIAAEIE GVRFRVPSPF VWVGLALVVA WIAGQEWFGP  
 LGLVHPSPWE FNLRLVAGTL FAVFLVVPYA LGTPSRLLDS SWMKT LGTWS YSIFLWHL PV  
 LTIVFPLLGL PLFSGN FLLV FIVTVLLTIP VAAISYTFIE EPISGGPGAP FRLGVVRIHH  
 FSGGRSGK

> RXA02581 (1-1527, translated) 509 residues

VPVPLYDPNE PGHADHLNAV FADSEPVVVL TNSKSAGAVR KHFS SLPAAE RPRILSVDSL  
 PDSLADSYEN PMLTEAGRRL AALRQSAPID LTAFLQYTS G STRTPAGVVL TNRSILT NVL  
 QIFSAAQLKT PLRLVSWLPL HHDMGIILAA FVTMLGLDNE FMNPRDFVQQ PSRWIKQLNR  
 RESDVDVNVY TVVPNFAL EL AARYAKPAEG ETLDLSALDA IIIGSEPVTE NALTTFREAF  
 EPYGLPVQTL RPSYGLAEAS LLVTTPQ TEN RPLISYFDRE ALAENRVELV EKGNNKAVAF  
 VSNGQVAAPQ QLVIVDSETG TELADGQIGE I WTHGENTAA GYLDREEDTA ETFRNRLTTR  
 LEENSRAEGA ADDNYWMATG DLGVI VDNEL YITGR LKDLI VVAGRNHYPQ DIEYTVQAAS  
 AHIRADSVAA FAVPGDDIEK LIILAERDTT ANEADDAAAE EAIRSAVGTA HGVVP EEIRI  
 LAPDEIARSS SGKIARRVNQ RNYIQEQAN

> RXA02582 (1-4830, translated) 1610 residues

```
MEQSQSSDQK MTVEQVRTWL RDWVVRTTGI PVEEVTDDKA METFGLSSRD VVVLSGELEN
LLDTSLDATI AYEYPTIRSL AQRLVEGEPR RAHTQRELNF SAVSDSPGSH DIAVVGMAAR
YPGAESLEDM WKLLVEGRDG ISDLPIGRWS EYAGDEVMSR KMEEFSTIGG YLSDISSFDA
EFFGLSPLEA ANMDPQQORIL LETWEALEY ARIAPNTLRG EAVGVFIGSS NNDYGMMIAA
DPAEAHPYAL TGTSSAIVAN RINYAFDFRG PSVNVDTACS SSLVAVHQAV RALRNGEADH
AIAGGVNILA SPFVTTAFAE LGVISPTGKI HAFSDDADGF VRSDGAGVVV LKRVDDAIRD
GDKIIGVIKG SAVNSDGHSN GLTAPNPDAQ VDVLQRAYVD AQVDPTTVDY VEAHGTGTIL
GDPIEATALG AVLGYGRDAS TPTLLGSAKS NFGHTESAAG IAGVIKVLLA LQNKTLPTTV
NFAGPNRYID FDAERLEVVE DPREWPEYNG HAVAGVSAFG FGGTNAHVVI SEYNAEDYET
RAPKEALLPD QQVALPVSGH LPSRRRQAAA DLADFLEGRK DCDLTPVARA LAGRNHGRSR
AVVLASTIEE AVKRLRQVAE GKVSVGISAA DSPAANGPVF VYSGFGSQHR LMIKELCSIS
PQFRERIEEL DEMVKFESGW SIMKLVLDDE QTYDTETAQV VITAIQIALT DLLASFGVKP
AAVMGMSMGE IAAAYAAGGL SDRDTMLIAS HRSRLMGEGE KSLAEDQLGA MAVVEFAAAD
LDKFIEENPE YKGIEPAVYA GPGMTTVGGP RDAVVQFVEK LESEDKFARL LNVKGAGHTS
AVEPLLGELE GEIAGIEPLP LQIPLESSVD QGVTPVGAV VHDADYMLRC TRQSVYFQDS
TEAFAAAGHN TLVEISPNPV ALMGMMNTAF TVGKPDAQLL FSLKRKVPEA ESLRDLLAKL
YVNGANVDFS ALYGEGETID PPHITWKHQR FWTSARPSSG ASLDLPGFRV NLPNNTVAFS
TAAELAPSAV AIMEAAAMAV TPGSSVDAVD ERDMLPPSGE ITTIVTRSLG GLSLSVYKIE
GTTSTLVAEG FAANPGFAAA SSFDGPGYDG FNTDYSQPD PRSDLPLDIE AVRWDPATET
VEERMRAIVS EAMGYDVDDL PRELPLIDLG LDSLMGMRIK NRIENDFQIP PLQVQALRDA
SVADVVMIMVE NMVAGRSSET LVDATPQVPA EAAGEAQAAE SSASGEDVQG VGVAPRDASE
RMVFGTWAGL TGAAAAGVTS KLPQIDVDTA TAIARLTER SGIEISTEQV LAAETLEPLS
DLVREGLETE VQGNIRVLRG RAEGSTKPAV FMFHPAGGSS VVYQPLMRRL PEDVPVYGVE
RLEGDLADRA AAYVDDIKKY SDGFVVLGG WSFGGAVAFE VAHQLVGSDV EVATVALLDT
VQPSNPAPDT AEETRARWTR YADFAKKTYG LDFEVPFEIL DTIGEDGMLS MMTDFLANTD
ASEHGLSAGV LEHQRASFDV NRILAKLNFA DWANVEAPVI LFRAERMHDG AIELEPNYAK
IDQDGGWSGI VNDLEIVQLN GDHLAVVDEP EIGTVGAHLS RRIDEISRKN
```

> RXA02583 (1-1548, translated) 516 residues

```
LSNTTTAEKL ADLRARLEIA KDPGSERARK KRDEEGRTTP RQRIDALLDA GSFVEIGALG
RTPDEPDAPY SDGVVTGYGR IDGRPVAIYA HDKTVYGGSV GMTFGRKVSE VMDMAIRIGC
PVIGIQDSGG ARIQDAVTSI AMYSEIARRQ LPLSGRSPQI SIMLGKSAGG AVYAPVTTDF
VIGVDGETEM YVTGPAVIKE VTGEQITSAP LGGGAQQMQN GNISYLASSE EEALNMVKDL
LDFLPLTCND PAPVFAAPTD EEIAYDEALN SFMPDDTNQG YDMHDLLDKL FDDANLLEIQ
EEYAPNLITT FARVDGKAVG VVANQPMDKA GCIDADAADK GARFIRICDA YNIPPIIFVVD
TPGYLPGVDQ EKVGLIHRGA KLAFAVEST VPKISLIVRK AYGGAYAVMG SKNLTGDLNF
AWPTAQIAVM GAAAAVVMIQ GKQLEAAPPE QREYMKKLFM DFYDENMTSP YVAAERGYID
AMIEPAETRL VLRRAVRQLE TKAVRDLDDK HTIMPM
```

> RXA02599 (1-477, translated) 159 residues

```
MDQLILDAFI GLRVTWLSPV IILFTQLTGP TLMFVYALVW GLLRKSATAP IAVGLANLIS
HFLKRAFERP RPNTAEHLVV ETNFSFPSGH AVGAAACAVA VGYSVNRWWK LTLWVIALLV
GLSRLYVGVH WPSDVLGWA IGALTSVVVF TSWNLLQRR
```

> RXA02618 (1-438, translated) 146 residues

```
MTNTPFPLEL QNISCAFGE PRHVSALNNV SLAVNPGEVL AIMGPSGSGK STLLNVAGLL
QRATSGHVLI DGASASDLNA KRAAETRRRH IGVIFQNYNL VPTLTVGENI GLPLELDGKT
DRQAVAIALA EVGLKGSTTA FPERSL
```

> RXA02634 (1-1611, translated) 537 residues

```
MRDLLPSRDD YQLLRFSWKM DIAAGVTVGI VALPLALAFG VSSGVGAEEAG LVTAIAGLV
AAIFGGSNVQ VSGPTGAMVV VLAPIVAQYG VGAVALLSLM AGVIVLVAGV LRLGRTVSFI
PWPVIEGFTA GIGVIFLQO VPAAFGYSGH LPTNALLAAI HTVSHATKDA ILPLLIIVT
AAIMIVLGKI APKLPASFIA ILVVSIGVAL LKLPVELIGE LPNSLPAPHL PDVNLEMFTS
LLGPAFAVAA LAIESLLSA RVAASMADTG PYNADRELVG QGLASISAGF FGGMPATGAI
ARTAVNVRSG GRTRIASIIH ALVLLGVVYV AANIVAVIPL AALSGVLMVT ASRMVSIEVI
SRVMRSTRSD AIVFVITAIV TISVDLVIAV GIGIAVATFF MLRRMSMNAG VFRETLPPEA
TLNDEKIGLF RIEGALFFGA AERLSQQILD YEDLEVILR LSHIQMIDAT GAHQLTLELVN
ALERKNVTVL IKGVRKEHIH VLGVLGAIRS LRHENHLEDD LAPAVEHARK HVKIDNS
```

> RXA02638 (1-504, translated) 168 residues  
 MARKRLNAGS LVGIFPEATV SRSFEIKELK TGAVRIADSA NVPLLPLIIW GGQRIITKDI  
 ERDFGRSHIP VFISVGEPVD ASGDPDEATE RLYEAMKKLL DETRTAYEQK YGPFEGGELW  
 RPKSLGGGAP TLEQAKMLEI AERERRQAKR AAKVAKKRTT FIRKIFKK

> RXA02659 (1-312, translated) 104 residues  
 FGNDPDLLMR WWYAGDVWTD SRMHWKGSSES YDQVQNLEEE GIRATDKAEQ QDIWNRTFDV  
 ISDNVPLYPL FHRKVPTAWN SNALVDFKPI SLTGLNFSGV ATTE

> RXA02676 (1-1389, translated) 463 residues  
 MDTWEQTLGT GPLLGIAAGA IALILVLVIV FKLHAFLLTI LVSIIVTALAA GIPVTAVVDT  
 LLDGFGKTLA SVALLVGLGA MLGRLVETSG GAKSLADTMV RIFGEKRAAF ALGVASLIMG  
 FPIFFDAGLV VMLPVIFAVA RRLNGSVLTF GIPAAAGAFSV MHVFVPPHPG PIAASEFFGA  
 QVGYVLIAGI IVALPTWYLT GYLLGKFLGR KFPLPVPDLL SGGAQEDDQP QNPANAVSII  
 VILLIPMLLI FGNTGTSMAY SAGLLDAEST MVKILGFLGE TPVALLITLI IALFFLGNRR  
 GINGSALEKT IEGALGPICS VVLITGAGGM FGGVLRSTGI GGALADSMAD LGLPVIAGCF  
 IVAAVLRVAQ GSATVALTTA AALMAPAVAA ADFNEFQLAA IVISTAAGSV IASHVNDSGF  
 WLVGRLMNAD VPTTLKTWTV NQTCIAIVGF VMAYAMFGLA SLA

> RXA02677 (1-759, translated) 253 residues  
 MKVIAHRGLS SRFPELTESA FRAALELPIH GIETDVRLTK CGEVVNVHDP IVDRVSNGRG  
 RVSRLDLESL LSLNFGTKET PEKVLTLNNL LDIFEDYDPK HLYIETKHPM RYAVMLEEEI  
 TKILKYRGLT EDPRIHIISF ALPAMYRMAR LAPQLDRIHL RRSWERWGNP RDVRCGVPTG  
 LGLSLERAKM DPRMIGAKGL PTYLFRTVDKQ KDMLWAREQG VDMLATNYPD RAAELLNAHP  
 KPAMYANAAG KED

> RXA02691 (1-807, translated) 269 residues  
 MNTMPDQPLN QDGFPTASKG VEPDNLPRDV LVDGLKPKHQ QLREILEEIC TTQLQPGDML  
 PGERILEEKY GVSRTIVRRA IGDLVASGRL KRARGKGTFFV AHSPLISRLH LASFSAEMAA  
 QKLSATSRIIL SSSRGPAPDD IADFFGTDRRA AQHITLRLRL FGNGRPYRID NGWYNSEFAP  
 DLLENDVYNS VYSILDRVYG VPVTQAEQTV TAVAAEDETA RLLDVTPGAP LLRILRQSLS  
 GDKPVEWCVS LYRTDRYSK TLVTRSED

> RXA02718 (1-1047, translated) 349 residues  
 VRDRLTQFLD AQELTIADIG APVTDVAHL RSFVLNGGKR IRPLYAWAGF LAAQGHKNSS  
 EKLESVLDAA ASLEFIQACA LIHDDIIDSS DTRRGAPTVM RAVEADHRAN NFEGDPEHFG  
 VSVSILAGDM ALVWAEDMLQ DSGLSAEALA RTRDAWRGMR TEVIGGQLLD IYLESHANES  
 VELADSVNRF KTAAYTIARP LHLGASIAGG SPQLIDALLH YGHDIGIAFQ LRDDLLGVFG  
 DPAITGKPAG DDIREGKRTV LLALALQRAD KQSPEAATAI RAGVGKVTSP EDIAVITEHI  
 RATGAEEEEVE QRISQLTESG LAHLDDVDIP DEVRAQLRAL AIRSTERRM

> RXA02749 (1-876, translated) 292 residues  
 MSPILKVRDL VKRYGDTVAV DGLNFDVSQG EIFAFLGENG AGKTTTISCL IGIDQATSGE  
 IELQGGQVDS EKLGVVFQQS VLDPLLSAKE NLETRGQLYP GVGKQ RVAQL IEQIGMEGFA  
 DRRYGVLSGG EKRRTDIARA LLHSPDILFL DEPTAGLDPR SRRQVWDTIN SLRNDVGLTV  
 FLTTHYMEET ELADSVLIID RGKEVASGTP MELRARYTTT ELTLRTNDPT HSGKELAHLS  
 PEIDGDLRI KLENGLEAAR LATELDGVLD VEIRHGSMDD VFLAVTAERK RS

> RXA02762 (1-285, translated) 95 residues  
 MLSELFPLAM RGFAIGISVF FLWIANAFGL LFFPTIMEAV GLTGTFMFMA GIGVVALIFI  
 YTQVPETRGR TLEEIDEDVT SGVIFNKDIR KGKVH

> RXA02767 (1-783, translated) 261 residues  
 MRELALNMAG VTVRRGEKLL LDDISLSIPQ GSHWAVLGPN GAGKTTMLKI AATLLYPSEG  
 TVDILGHRFG RVDTRELRKT IGLVDPKQRF TNLPAHEIVL SGLTASNGLL PRWSASASEL  
 ERCALMLELV GMTARADRYW ADMSQGEKAR TLIARALIIS PTLILLDEPT TGLDLPGRET  
 LLSVIDGLRA ALPGLTTVMI THHVEEIAAS TTDILMIKDA RILASGTVSE VMTPENLGAL  
 YDMSVSLETV RSRWFAFDAL H

> RXA02792 (1-753, translated) 251 residues  
 MIEATHLRHS FGDNIVIDDV TLHLPAHGTV SLVGPNNGSGK TTLRLALYGA LQPNEGHIHV

DGVPLISLHR KDI AKTMAVV IQEHSD LPM TVADLVLLGR LPHQKMFAGN SQADQLLVKE  
ALTRVGAIHL ADRQFGALSG GERQRVLIAR ALVQNATHIL LDEPTNHLDI RYQHEVLHLV  
RELSSSSIIV LHDNLNLAGAY SDHIILLDQG RVVTQGTPSE VLTPEHLEPV YGVRVERFDL  
GDEVHLRFKR H

> RXA02794 (1-621, translated) 207 residues  
MAASGLIFFV ARAAGRISST RLLMSGVAIG YMLSAATSFL IFSSDSAEGS RSVLFWLLGS  
LGLAAWNGPM AIIFLIVGIA LALLMVLGPQ LDALNSGDET ALT LGVSPDR LRILLVITC  
LLVGSMVAMA GSIGFIGLVI PHLARRFVSG KHRLMLPVSA LMGAILLIWA DIAARTLLAP  
QEIPIGIITA LIGAPFLIL VRRMHTY

> RXA02809 (1-273, translated) 91 residues  
AALTNALSYL SAEWNNKAAG IVSYGSAMGV RAAEHLRGIL SELQIAHVQK TGLLSIFTDF  
EYPNFKPSEQ GISSVDAMLE QLVVWTKAMS T

> RXA02811 (1-384, translated) 128 residues  
VTESTLGASN SSQTIENKGL TILGISGRRL AAVLIGWFFV IFDGYDLIVY GTVQSALAKE  
WNLSSATLGT IGSTAFFGMA IGAVFIGRLS DRVGRKAAVI GSVLILSVFT MLCAFAPNPW  
VFGAFRFI

> RXA02836 (1-306, translated) 102 residues  
MTIDEGRRQF EVNVFGAMAL TRLVLPHMQK QKWGTIVNIT SMGGKIYTPL GGWYHGTFKA  
LEALSDALRL EVAPFGIDVV VIEPGGIATE WGGIAADNLD AV

> RXA02850 (1-492, translated) 164 residues  
EELGGATTHM VTAGNSHYTA ATDEEALDWV QDLVSFLPSN NRSYAPMEDF DEEEGGVEEN  
ITADDLKLDE IIPDSATVPY DVRDVXECLT DDGEYLEIQA XRAENVVIAF GRIEGQSVGF  
VANQPTQFAG CLDIDSSEKA ARFVRTCDF NIPIVMLVDV PGFL

> RXA02851 (1-519, translated) 173 residues  
PRQKADIMIG SIQENINDVD LELDTIIPDS PNQPYDMKEV ISRIXDDAEF FEIQEDYAEN  
ILCGFARVEX RXVGIVANQP TQFAGXLDIK ASEKAARFIR TCDAFNIPIL EFVDVPGFLP  
GTNQEFDGII RRGAKLLYAY AEATVGKITV ITRKSYGGAY CVMGSKDMGA GLV

> RXA02865 (1-1017, translated) 339 residues  
LSRTGVSKKP KLTAPVVIIG TLVLLIIAFT ASLMLGPVTV PLNELATNPV VTDIRAPRII  
IAALVGAALA VSGAIMQTVF HNPLADPGIV GVSSGA AVAA VLAIVTGASF FGQWTVPFAA  
FVGALVTVAV VYLIASSRAM DGRGADPATL VLVGMAITAF LGAVISSATA NAPQDSELR  
VTFWLNGDLV SRTWEHVGVA IIPIIIVGLIL AIGGSRDNL LLLGDSTAQT SGLNVNRARI  
ILLALAALLT ATAVAVSGTI TFGVLVPHL VRIVLGADHR ALLPAAAILG ATFVIVSDTV  
ARMIFSPIVL QTGVVVAFIG SPIFLYLLLS MRKRRLGL

> RXA02900 (1-852, translated) 284 residues  
MSNPAASTPA NNSDDVAKEN WDSSFTPKTD IDSSQPVNNS TGEAAARAVN LYKAYGQGDT  
TVTALDHVNV EFEKNKFTAI MGPSGSGKST LMHCMAGLDA ATGGS AFIGD TDL SRLKDKE  
MTSLRRDRLG FIFQS FNLVP TLTASENITL PTDIAGR KID QSWFDEITSR LGLTERLKHR  
PAELSGGQQQ RVACARALVS RPEIIFGDEP TGNLDSNSSR EVLDILRTAV DQDDQTVVIV  
THDAKAASYA DRVIFLADGR IVNQLFDPTI EEILATMNGI EDIA

>RXN00024 TRANSLATE of: rxn00024.seq check: 2799 from: 1 to: 945  
MEHGVTVIKGTEFDVFPLNLGGNTFGWTSNREQTF AVLDAFVAAGGNFVDTADSYSAWVE  
GNEGGESERELGA WIKER GADKLIIATKSGALEPVAGRSREATFKAVEGSLERLGVESID  
IFYYYHYDDEAVSIDEQVAIANDLIAQ GKIKHLALS NYSAERLAEFFEKSVGTPAQPV ALQ  
PHYNLVS RKDYENVQPLAEKHGVAVFPYFALAAGLLTGKYTSKEDISG KARAGQLDRYA  
SDEAFAVVTELRAVADELGVAPTTVALAWLVAHGVTAPIASVSKVEQLKDLMAVKDVELS  
AEQLARLDKVSE PFA

>RXN00092 TRANSLATE of: rxn00092.seq check: 5543 from: 1 to: 666  
MTNTPFPLELQNISCAFGEGPRHVSALNNVSLAVNP GELVAIMGPSGSGKSTLLNVAGLL  
QRATSGHVLIDGASASDLNAKRAAETR RRHIGVIFQNYNLVPTLT VGENVGLPLELDGKT  
DRQAVAI ALAEVGLGEGFDDRFP EEISGGQAQRVAIARALIGPRKILLADEPTGALDTSTG



DAVLRVLRQRIDSGAAGLLVTHEPRFAAWADRTIMLRDGEIQ

>RXN00099 TRANSLATE of: rxn00099.seq check: 3872 from: 1 to: 1173  
 VKNPRLIALAAIILTSFNLRITAITALAPLVSEIRDDLGVASLIGVLGMIPTAMFADAAAF  
 ALPSLKRKFTTSQLLMFAMLLTAAGQIIRVAGPASLLMVGTVFAMFAIGVTNVLLPIAVR  
 EYFPRHVGGMSTTYLVSFQIVQALAPTLAVPISQWATHVGLTGWRVSLGSWALLGLVAAI  
 SWIPLLSLQGARVVAAPSKVSLPVWKSSVGVGLGLMFGFTSFATYILMGFMPQMVGDQPQL  
 GAVLLGWWSILGLPLNILGPWLVTFTNCFPMVVIASVMFLIGNGGFCLAPDVAPWLWAT  
 LSGLGPLAFPMALTINIRAETSAGASALSSFGQGLGYTIACFGPLLTFIVDATGSFRT  
 IFVLFAVATLFFVIRGGYFATRQVYVEKLLNR

>RXN00113 TRANSLATE of: rxn00113.seq check: 9363 from: 1 to: 5622  
 VRIVLTTEGEVAAKLVTFRFAIRGRITTNEMAAPADSYGARDEVVEATPRSFIRQATVSAP  
 ADMTPFAMVSGDYNPIHTSDNAAKLVLGLDAALVHGMWLSATAQHLAGLGSEVIGWTYSMY  
 GMVQLNDVVDITVERVGRAGLKPAYEVTCTRIDGNVVSRRGQALLKAPSTAYVYPSQGIQAK  
 GMGQGDRTASAEARAVWERADAHTRANLGFSIQQVIDENPTELKVGDTTFVHPAGVLNLT  
 QFTQVALAVVAYAQTERLKAANAIVDGSLYAGHSLGEYALASLGNIFELEGVIDVVFSSR  
 GSAMHSLVPRDEKGRSNYGLAAFRPNMINVAATEVENWVDRVAEESGEFLQIVNYNVDGQ  
 QYAVAGTLAGLKALKASASANPRAYVNI PGIDVPFHSSVLRPGVPAFAEKLDELLPETID  
 IDALRGRYIPNLVARPFELTQSFVDAILAVVPSERLKGIKVEDTDENTLARLLLIELLSW  
 QFASPVRWIETQALIIDTVDQIIIEVGLAASPTLTNLALRTMDVIGKSRPVFNVERDQDTV  
 MLNDVRQAPVAEVEEEEAVEEAPAAAAAPAAEAPVAAAPVAAAAPAPVGNAPELKFNAANA  
 IMVLFVQNKINIDQITAADTSETLTNGVSSRRNQMLMDMSTELSVPTIDGAADADVATL  
 QGRVVTAAAPGYKPFPGPVLSETVRARLRALTGAAGLKTSYIGDRVTGTWGLPESWTAHVEV  
 ELLLGTTREGESVRGGNLGSLPANASSKGDVDALIDAAVQNVAAANGTSVSMSSGGAASGG  
 GVVDAAALDAYASTVTGEEGVLANVARGILSQLGLDTKDEVEGAEIDTELYDAVEAELGT  
 GWLKLVTVPVFSADRAILFDDRWAASAREDLARLANGEDIAVERFAGTGETVVKQAAWWAEH  
 VEDTALAATLKQVSEVAAKPANEPHIDDVALVTGAAPESIAGAVARLLSQGATVILTAS  
 NVSQARKEYARKLYAANATPNAKLWIVPANMSSYRDVDAVIDWIGNEQRTVVGSTVTVTK  
 PALTPTLAYPFAAPSVSGTLADAGPQAEQARLLLSVERTIAGLADLASRGVDGRVHV  
 LPGSPNRGMFGGDGAYGEVKAADFADAILAKWGSETGWPQFVSLAQARIGWVAGTGLMGRND  
 VLI PAAEKLGIHVYTPPEEISSELLGLASAESREKALEAPIDYDLTGGLSGGVSI AALAAS  
 LESDAVETTSAAEDTIKALPSPKHPEQPVGTPVGEVKTDLDMVVMVGVEVSSWGSGR  
 RFEAEYGIQRDGSVDLTAAGVLELAWMMGLISWSEDPKPAWYDADGTEVPEEEIYERFRD  
 EVIARCGVRELVDDAFLVDGGSLDAAEVFLDRDISFSVTSAAEAQAYVDADASVTVEEAD  
 GEWIVTKKKGSTSFVPRKATLTRSVAGQLPTDFDPAKWGIPAS MIDALDNIAAWNLTAV  
 DAFLSSGFSPAELLQSIHPADVSTQGTGIGGMQSLRKL FVNRF LGQDRPSDILQETLPN  
 VVAAHTMQSYVGGYGQMIHPVAACATAAVSVEEGVDKIRLNKADFV VAGGIDDIQVESLT  
 GFGDMNATADTQAMLDKGI DPRFISRANRRRAGFLEAAGGGTVLLARASVAAELGLPVL  
 AVVAHAQSYADGAHTSIPAPGLGALGAARGGKKSVLARELNKLGLTPDDVRVVS KHDTST  
 NANDPNESELHNLLWKTIGREADNPMFVVSQKSLTGHSKGG AALFQIGGLVSILETGKLP  
 QNASLDCVDP EMEAKGENFVWLRKPLDLGAGSIKAGVLTSLGFGHVAAVVVLATSGIFEQ  
 AMRNAGLDVEAWRARATQRLRTGANRLEAGMVG RAPLFEQVDGRRLPEHGAHQAEINLLI  
 DADARLGADGIYQG

>RXN00164 TRANSLATE of: rxn00164.seq check: 2228 from: 1 to: 1689  
 VGRIPRAKWWFLGALVLLSAGAYASVLVPQVLGRIVDLVSDGAQMRDFVELSVILIAVAI  
 AGAVLSACGFYVVSRISEKIIANLREDMVG TALGLPTHQVEDAGSGDLVSRSTDDVSELS  
 AAVTETVPILSSSLFTIAATIIALFSLDWQFVLIPVVVAPVYFASKHYLSKAPDRYAAE  
 RAAMAERARKVLEAIRGRATVRAYS MEDAMHNQIDQASWSVVVKGIRARTTMLILNMWML  
 FAEFLMLAVALVIGYKLVIDNALTIGAVTGAVLMIIRLRGPMNMFMRVLDTIQSGYASLA  
 RIVGVVADPPPI PVPDSGVKAPQGKVELRNVSF SYGDSWAVKDIDITINSGETVALVGASG  
 AGKTTVAALLAGLRVPDQGQVLVD DFPVSHLSDRER IARLAMVSQEVHVFSGTLRQDLTL  
 AKPDASDEELAHALGQVNALDWLESLPEGLDTVVGARGIQLEPVVAQQALARVLLNPA  
 IVIMDEATAEAGSAGASALEEAADAVSKNRSALVVAHRLDQASRADQILVMDKGEVVEG  
 THQELLDHGGIYQRLWTAWSVGR

>RXN00193 TRANSLATE of: rxn00193.seq check: 1918 from: 1 to: 594  
 KAFXQREGFISAFGFTVLVVI SVITVNI FAFL LAWLLTRKLRGTNFFRTVFFMPNLIGG  
 IVLGYTWQTMINAVLSHYATTISADWKFGYAGLIMLLNWQLIGYMMIIYIAGLQNVPEL  
 IEAAELDGVNWKWEMLRHVTIPVMPSITICLFLTLSNSFKLFDQNLALTNGAPGGQTEMV

ALNIINTLFNRMNVEGVG

>RXN00201 TRANSLATE of: rxn00201.seq check: 716 from: 1 to: 192  
VADCGLPPEHVEIIDLALVFGIPTFEQVLNALKPEVVVEGAVIAEGAPQRIREMVDTDV  
EVCA

>RXN00243 TRANSLATE of: rxn00243.seq check: 3186 from: 1 to: 1017  
VTSEQALDPIHPGQFRLSRIQLINWGTFHGTVDIPVTREGILVTGGSGSGKSTLIDAITA  
VLLPQGKLRFNAAQANTPRNKGRSLVTYIRGAWRAQEDPLQDQIVSTYLRPRATYSLVG  
LTYSNGEGVEHTLVAFYLYKSGHNLTSDISSYYGVFPVDQDINALDLDLKEGIDKRQIRA  
AFKEAIFSEQHSVFSGRFRSRLGISSEEALLLHRAQSAKDLQSLDDLFRDYMLVEPDTF  
SIAKTAVEQFQDLEGAYEQVEDIKRQIHTLDPLVQLKNRREKAQQSKDHANALKKALPTV  
GNRIKKEEQEPLVRQFTVEQTQRSRRWSPPKLRQIVPAK

>RXN00297 TRANSLATE of: rxn00297.seq check: 2827 from: 1 to: 912  
MGFTVVFFIVIGIGWILGRRDTLGTHAQKPLSLFVYYVATPALLFDRVTKSDTSTIFSLNF  
VVIALSALIVGFLFFLLMRVFIKRTAAVSVIGMLAASYANAGNLGIPLAAYILDDFTVVI  
PVILFQVAFYAPITMTIMEMLTNKKSTNLVRNLLVTPLTNTMVLAAGIAVSLTSMSVP  
VVIAQPVEMLANASVPLALVVFGLSLSKSKILEKGQVSRROVFTAALFKNVLHPIVAGLL  
ALAFGMEGTALLSAVILGALPTAQNVYTYALRFTAESMARDTGVVTTLISFPVLVAVSI  
IFGS

>RXN00298 TRANSLATE of: rxn00298.seq check: 2826 from: 1 to: 1845  
MSSNIAITTEPEGKNKKGLKSDPFIFSI SVGFIVVFIATIALGEKARTTFSAIAGWLLE  
NLGWMYIGGVSLVFIFLMGIFASRYGRVKLGDDDDDEHTLIVWFCMLFAGGVGAVLMFW  
GVAEPINHAFNVPMANEESMSEAAIVQAFAYTFYHFGIHMWVIMALPGLSLGYFIYKRKL  
PPRLSSVFSPILGKHIYSTPGKLIDVLAIVGTTFGIAVSVGLGVQLQINAGMNKLWSTPQV  
SWVQLLIILIIITAVACISVASGLDKGIKLLSNINIAMAVALMFFILEFTGPTLTLLRFLVE  
SFGIYASWMPNLMFWTDSFQDNPGWQGWTFVYFAWTICWSPYVGMFVARISRGRVREF  
IGGVLLALPAIFGVVWFSIFGRAGIEVELSNPGFLTQPTVVEGDVPAALFNVLQEYPLTGI  
VSAFALVIVIFFITSIDSAALVNDMFATGAENQTPSYRVMWACTIGAVAGSLLIISPS  
SGIATLQEVVIVAFPPFLVQFVMMFSLKGMSEDAAVRRVQTRQWEKTDTPKLEEHS  
SQPAPGYDDEGNPLPMPALEHDEDEGNIVIPGNVIEGDLGVVGDVDDPEEAQEMGSRFK  
IVEQTRPQSRDEYDI

>RXN00349 TRANSLATE of: rxn00349.seq check: 102 from: 1 to: 1467  
MLSFATLRGRISTVDAAKAAPPSPLAPIDLTDHSQVAGVMNLAARIGDILLSSGTSNSD  
TKVQVRAVTSAYGLYYTHVDITLNTITIFTNIGVERKMPVNVFHVVGKLDTNFSKLSEVD  
RLIRSIQAGATPPEVAEKILDELEQSPASYGFPVALLGWAMMGAVAVLLGGGWQVSLIA  
FITAFTHIATTSFLGKKGLPTFFQNVVGGFIATLPASIAYSALQFGLKPSQIIASGI  
VVLLAGLTLVQSLQDGITGAPVTASARFFETLLFTGGIVAGVGLGIQLSEILHVMLPAME  
SAAAPNYSSTFARIAGGVTAFAVGCYAEWSSVIIAGLTALMGSAFYLLFVVYLGVPVS  
AAAIATAVAGFTGGLLARRELIPLIVAIAGITPMLPGLAIYRGMATLNDQTLMGFTNI  
AVALATASSLAAGVVLGEWIARRLRPPRFNPYRAFTKANEFSEFQEEAEQNQRQRKRPK  
TNQRFGNKR

>RXN00368 TRANSLATE of: rxn00368.seq check: 9416 from: 1 to: 1575  
MRLGVWLIVAGLFITPLALVVGLALGGNQFPALWDSGLGKALWNSAYTTVLSAVGATIIG  
TIMALTLDRTDVFGRALRLFLLSPLLIPIFIGAIAWLQFLGKNQGINRFFGTEVWDIYG  
ADGVTFLLIVHSYPTVYIIVSAALRQLPSDLEQAARIAGADTFTVLRITITLPLLKPALLS  
AFTLTTVANLADFGIPALLGSPARFETLATMIYRFMESGTVSNPLQVVSTIGIVLLFLGI  
AAVTADYLVSLYAASKLQDAGTPHRTLNKSRIPVSVITWIIALIITAAPLLGLAYRALL  
PAPGVFPNLDNITLNNFEAALSNNPRVIEGFSNSLMLSLGAALICGVLGWLIGVLITRTQH  
FANVPLTLTVLLPTALPGMIIGVGWLILGRYTGIIYNTPWVILGAYVCAFTALVVQAVRGP  
LSQAPEAIEEAARISGAGRLRSIMDTTGAMAI PAAFAGAVLVAVTAVRELTVSILLIAPG  
TTTLGVQVFNLQQAGNYNQASALSMLFAIIGIVALALTVRSQKEF

>RXN00378 TRANSLATE of: rxn00378.seq check: 9591 from: 1 to: 2610  
VDKAVNTAISDAKTAALKAGVGLNRATASEEEEDLSSSIKVSALAFELEGLSNAPSLMVVE  
KALEKIPGVSADLIYPSQTAWITATDRVHPETLIEVFQFGIKAHLNSSSLRRHQQLSA  
EVNREARLDYRSMRMDAKRISPRVRRHNRQEMVHAVRARESGWIKRRNHTTSQHEDPMSG

DVLFTARALITPKRLWVSLPFALIVLALSLNPSWQFDYWQWLSAVLAI PVVVWGAWPFHR  
 AAAGGIRRGISALDATSSIAIAAAYAWSIAMLLFETPGGKSWRSYPSWFAFDHGTLTQNE  
 IYFDVACGITVLLLAGRLLTRRRSQSSLLAELGRLQIDPQRIVTVVRKHRLKRVVQELNI  
 PVQEV RVNDDVKVPPNTTIPVDGTVIGGGSRIAASIIMGQDQRDVKVNDKVFAGSLNLES  
 EIKVRVIRTGHRTRIAAVHRWVKEATLKENRHNRAAIRSAGNLVPITFTLAVVDFCLWAL  
 ISGNINAAFTTTLAVLACVAPVALALSAPLATRNSIEAAARHGILVRSGEIFRVLDDVDVT  
 AVFN RVGTLTLDGEMTVETVTADKGEDPELVLRVAGALAMESHHAISKALVKASREARDTG  
 AGGEDVPHWIEVGNVEITEAGSFQATIELPLIKPSGEKIMRTTEALLWRPRSMTEVREHL  
 SPRLVAAATSGGAPLIVRWKKGKDRGVITLSDHVRSDDSDAIIAIEEQGIETMMLSRDTYP  
 VARRYADSLGITHVLAGIAPGKKAQVVRAVHTRGSTVAMIGDESVMDCCLKVADVGVLMGV  
 DRPSDLRDDSDPAADVVMREEVMSVPTLFKLARRYAKLVNGNIALAWIYNGVAMVLAV  
 SGLLHPMAATVAMLASSLLIEWRSRGRARKY

>RXN00410 TRANSLATE of: rxn00410.seq check: 1977 from: 1 to: 666  
 MMIYKGKSTEVRLDGISVQIQSDKWT SIMQSGSGKTTLLQCLSGLAQPTSGRVTLNKN  
 NITLSSLSENKRAKLRRTHISMVFQDFNLVPILSVKDNILLPLRLAHRRVKQWFEHITS  
 VLKIDNRMRLPGELSGGQQQRAAIARALMSRPDIVIADEPTGSLDSVTSDAVLNLFRSI  
 VDDFGQSLVFVTHDKDAAHRGDVLITMRDGKIIDTADLRVGR

>RXN00411 TRANSLATE of: rxn00411.seq check: 5242 from: 1 to: 675  
 MNEMILAADWNRLGPTFQTAIIDTLLMVIITMVVAGLLGLLVGLLLYTTRAGGILKNKVI  
 YTILNLVNVFVRPIPFIIILIAAIKPLTVAVMGTSIGRDAGIFVMVVAIFSVARIVEQNL  
 VSIDPGVIEAARSMGASPMRIIATVIIPEALGPLVLGYTFLFIAIVDMSAMVG YIGGGGL  
 GDFAI VGYRAFDNEVMYVAVLVIVIIVQAAQLLGNWLSKKIMRR

>RXN00412 TRANSLATE of: rxn00412.seq check: 7568 from: 1 to: 1080  
 VSHTASTPTPEEYSAQQPSTQGRVEFRGITKVFSNNKSAKTTALDNVTLTVEPGEVIGI  
 IGYSGAGKSTLVRLINGLDSPTSGSLLNGTDIVGMPESKLRKLR SNIGMIFQQFNLFQS  
 RTAAGNVEYPLEVAKMDKAARKARVQEMLEFVGLGDKGKNYPEQLSGGQKQRVGIARALA  
 TNPTLLLAD EATSALDPETTHEVLELLRKVNRELGITIVVITHEMEVVR SIADKVAVMES  
 GKVV EYGSVYEVFSNPQTQVAQKFVATALRNTPDQVESEDLLSHEGRLFTIDLTETSGFF  
 AATARAAEQGAFVNIVHGGVTTLQRQSFGKMTVRLTGNTAAIEEFYQTLTKTTTIKEITR

>RXN00419 TRANSLATE of: rxn00419.seq check: 8218 from: 1 to: 759  
 MLNAVKGAKQNILLGGTSEIGISIVSRFLKQGPSHVTLAARKDSPRVDAVAEIKAAAGAA  
 SVAVVDFDALD TESHPAAIDA AFENGVDVDAIVA FGILGDNEAQWRDQALAVEATTVNYT  
 AGVSVGVLLGQKFEQQGHGTIVALSSVAGQVRVRSNFVYGSAGAGFDGFYTQLGEALRGS  
 GANVLVVRPGQVR TKMSADGGEAPLTVNREDVADAVYDAVVNKKDII FVHPLFQYVSFAF  
 QFIPRAIFRKLPF

>RXN00432 TRANSLATE of: rxn00432.seq check: 8334 from: 1 to: 1485  
 MELLETFTD VINDNLWMILPFLLVAAAGLYFGGRTLLVQIRMIP EMFKAVVEKPAKDGEF  
 ADKQDISAFKAFTISAASRVGTANVAGVALAITLGGPGAVFWMWIIALVGGATSFIESTL  
 GQLWKVKDGD SYRGGPAYYMTLGLNARWLAVVFGVAITLTFGFVYNALQSNVAVEAITVS  
 LGTPSTTAKAFVGLGMAGLSALVIFGGVQRIANVTQWMVPFMAGAYII VGVVVIVINIQQ  
 VPTMINDIIAGAFGFRPVATASVWGAFWLA FMNGMRRGLFSNEAGEGSPNAAATATVSH  
 PVKQGLVQTLGVYFD TLLVCSITAFVILLSGVEYATGDIQSSSLTQSALASVVGWGTHF  
 ITVVMFFLAFSSVLGNYYLAQANIQYFTDSKTVMTVFRLLVLLSVFSGAVASVPLIWALG  
 DTFAGIMVLINLAAI IPLGGVAVKLLKNYTIQKKAGLDPVFHRDMMPEVRNIACWNGKDA  
 ATSNYHEAMEVIKKS

>RXN00443 TRANSLATE of: rxn00443.seq check: 5344 from: 1 to: 804  
 VNKSIRRALYSFITISAGISLVACSSSDTASTTTQNASATEAAGVSGTASVFAAASLTNV  
 AEDLAAAFNEDNPDAKLEFN FAGSSALVRQISEGAPSDLFISADIANMDDALALPEFAGA  
 TSKVIATNKLVLVTADGNPGEISELADV KDSLVAICAPEVPCGTITHEALDYADIELNTS  
 SEEANVADVATKISTGAVDAGFVYQTD AQSLAKTQDNTVIELEGIDANEYPMALTTTGED  
 NEVAKAFAEFLSSDRAKEILASYGFGTN

>RXN00444 TRANSLATE of: rxn00444.seq check: 7535 from: 1 to: 837  
 MVLAQTKKARRSENHILPGWLLIPATLAMLLIIGPIFALLLQIPWDRSWELLTAPESLGT  
 ARLSIGTALFESTALCAIVGFPLALALHLYERSHPRVTSVLTVLVYAPLVLSPPVVSGLALT



FLWGRRGFLGSWLDQVGLPIAFTTTAVVFAQVFVALPFFISTVTTALRGIPKQFEEIAAT  
EGATRWEIMHKMIIPLAMPGIFTGMILGFARALGEYGATLTFAGNIAGVTRTIPLHIELG  
LSSNDMDKALGAVIMLLAVYVLIIGAIGALRLFSKVRKV

>RXN00449 TRANSLATE of: rxn00449.seq check: 92 from: 1 to: 1581  
MSTPDIKEGSAESPGEVMVVGDRREWRRQATGIIAGLVLAALVYLLFSPNSVETVMQSSG  
VDPETEYTNAMRLTAAVTILMAVWWMTEAIPLAATALIPLVAFPAFQVVDGKATAPYA  
NPTSFLFLGGFLMALGLQKWNLHRRMALAVVLAVGTPKPKQLVLGFMVATGFLSMWVSNTA  
TAVVMLPIGMSVLALTAETVGGMKNQKKFATGLMLSIAYSASISGLGTIGTPPNALLAA  
YMSESHDIHIGFGQWMILGVPIAVVFTIIAWLVLTTFVKPEMKEIPGGRELKREIAEMG  
PWTAPQVTVGVIFAAAALAWVFIPLTLDTGSQLSINDSLIGIAAGLLMFIVPANFKTGE  
RILDWRTAGELPWDVLLLFGGGLSLSAMFTSTGLSLWIGELAKGLDALPIFILIFAI AVL  
VLFLTEFTSNTATAATFLPIMGGVAVGIGLTAGGEQNVLLLTIPVALSATCAFMLPVATP  
PNAIAFGSGYIKIGEMVKGGLWLNIIAVILITIFTYFVAIPLFGIML

>RXN00456 TRANSLATE of: rxn00456.seq check: 2097 from: 1 to: 1377  
VLQALLAIMVSLSVAAILEGNRALVGLLLATTLGLGVAQWIQKVVAEDLGQHYVHEVRRE  
LVGAALVPGNTASLGVTVTRASNDLTAVRNWVALGIVPMVTGLPLIAIVLVALFIQDLRT  
GVAVTVPLLMCVAVLPVVARWTLKRARELRKKRGRMAARIADSVMAGELLHATGAIDREL  
NAVTRDSRVVIAAVRRSWATGFSRALMAMAASLGTVSIVISGHLEVSEVAGIMMLLGVL  
ATPVAELGRVVEYRQNYKAATRILIPLLQRGSEFKHSQQKLPGLOATEGIPGVYVKGISA  
LPGERIYHLGSADATRKWVTSLSAMEEGTDVIVNGQRLSQLPLKQRRALIGIASAHHHLS  
RGSVSRLVGLRVPDATVEEIEQALEQVGLNNTGKQRLKNGGHPWSTSQINKLKIATLR  
TPPLLVLGITPENLLNYPGVIIISTVQENPSETWRQVNI

>RXN00466 TRANSLATE of: rxn00466.seq check: 8825 from: 1 to: 996  
VQSRLSKILRSSVVGVAVLALLAGCSNNADDTADSTSTGNSAFPVSIEHEFGTTTIDDV  
PERVVTLGVTADIVLALGTVPGVNTGYKFFENGLGPWTDELVEGKELTLLDSDSTPDLE  
QVAALEPDLIIGVSAGFDDVVEYQLSDIAPVVARPAGTAAYAVAREEATNLVARAMGQSE  
KGQELNEETDALIQAARDENPSFDGKTGTIVLPYQGYGAYLPGDARGQFLDSLGLISLPE  
AVLSRDTGDSFFVDVPAESVKDVGDLVLSNDENLDITAENPLFETLNVVQKDAVIVA  
TTEERGAITYNSVLSVPFALEHLAPRIAEALK

>RXN00477 TRANSLATE of: rxn00477.seq check: 7063 from: 1 to: 1644  
MKVSTKTPRSSGTAVVIGAGVAGLATSALLARDGWQVTVLEKNTDVGGRAGSLEISGFPG  
FRWDTGPSWYLMPEAFDHFALFGACTSDYLDLVELTPGYRVFSGTHDAVDVPTGREEAI  
ALFESIEPGAGAKLGNLYLSDAADAYDIAIDREFLYNNFSTLGPLLHRDVLTRAGRLFSLLT  
RSLQKYVNSQFSSPVLRQILTYPAVFLSSRPTTTPSMYHLMSHTDLVQGVKYPGIGFTAV  
VNALHQLALENGVEFQLDSEVISINTASSRGNTSATGVSLHNRKVQNLADLVVSAGDL  
HHTENNLLPRELRTYPERYWSNRNPGIGAVLILLGVKGELPQLDHHNLFSEDDWTDFAV  
VFDGPQLTRPHNASNSIYVSKPSTSEDGVAPAGYENLFVLIPTKASSSIGHGDAYMQSAS  
ASVETIASHAINQIATQAGIPDLTDRIVVKRTIGPADFEHRYHSWVGSALGPAHTLRQSA  
FLRGRNSSRKVNLFYSGATTVPVGVI PMCLISAENIIKRLHADTSAGPLPEPLPPKTP  
SQKTSYDH

>RXN00523 TRANSLATE of: rxn00523.seq check: 9218 from: 1 to: 1026  
MSLSHQLKRQRASRNSRRWLIVAALGVVTLGIFAFSLMWGEVFGPAQVLKVLSGQQVPG  
ASYSVGLRLPRAVMGLTAGLAFGAAGVIFQTVLRNQLASPDIIIGISSGASAAGVICIVF  
FGMSQSAVSAISLCASLAVALLIYLVAYRGGFSATRLILTIGIGIAAMLNSLVSYLSKAD  
SWDLPTATRWLTGSLNGATWDRAMPLIVTTVLIPLLVANARNVDLMRLGND SAVGLGVA  
TNRTRVIAIIAAVALIAVATAACGPFAFVAFVSGPIAARILGSGGSLIIPSAIGGLIVL  
IADLIGQYFLGTRYPVGVVTGAFGAPFLIYLLIRSNRAGVTL

>RXN00525 TRANSLATE of: rxn00525.seq check: 5915 from: 1 to: 1263  
MSLAESILLALTSLRSNKMRALLTLGVIIGIASVIGILTIGKALQDQTLNSLES LGAND  
LSAQVEERPDEDSPEPDMFAFSGAANSSGNLIPEETVDTLRDRFAGSITGISVGGMGTQG  
TLIGDTADLKSDLLGVNEDYMWNGVEMNYGRAITQDDVAAQRPVAVIAPDTFNTLFDAN  
PNLALGSEVAFELNGQETFLRVIGVYKEAAAGGLVGSNPTVHTYTPYTVANDITHTEDGL  
NTLSIRAAQGVDDQSLKGSQTYFDALYANND SHHVAMLD FRKQIEEFNTILGAMSLGIS  
AIGGISLLVGGIGVMNIMLVSVTERTREIGVRKALGARRRDIRLQFVVEAMIICFIGGIL  
GVLLGGILGLIMSSAIGYISLPPLSGIVIALVFSMAIGLFFGYYPANKAAKLDPIDALRY



E

>RXN00559 TRANSLATE of: rxn00559.seq check: 9522 from: 1 to: 1017  
 MSDNPHENPRENPHRSPEVVLRFMAAPTDLVLMAGSHGVGGGRVLEWIDKAAYACATQWSG  
 TYCVTAYVGHIFTRPIPSGHMVEVRSRIAMTGRSSMHIVNEVLSADPRDGNVTRACDCL  
 VIFVAKDTATGRATPVPSFTPKNEEEEQRVLEAANSRIGLRKAIEAEMEKQTYNGPSEAPR  
 LITRFLAKPTDINWGGKVHGGTAMEWIDEAGAACTMEWSGNHTVAVYAGGIRFYQPIQIG  
 DLIEVDARMMRTDKRSMQMSIHVRAGDAHRGRAELETAIHATVTYLGIDVDGEPLPAPQF  
 VPRTPEDIQLAEHANILRDLRADYTPMPLFQRRVPLQID

>RXN00563 TRANSLATE of: rxn00563.seq check: 2005 from: 1 to: 2739  
 FYKDLYARSARGTAALWIVAANLSSYSDIDAIINWVGSEQTTTVNGASKLVKPALVPTLL  
 FPFAPRVSGSMADAGPQAESQMRLLLWSVERLIAGLAPLGSSINVGHRLHVVIPGSPNR  
 GRFGGDGAYGESKAALDAVVTRWNAEQAAWGAHTSLVHAHIGWVRGTGLMGNDPLVKAA  
 EEAGVETYSTQEIAEKLLSQATSTVREQAASAPITVDFTGGLGESDLNLAEMARAEAAKA  
 ANAPVVEAPRTVAALPTPYRPVVQTTPDFAGQVTQNLDEMVMVIVGAGELGPLGSARTRFD  
 AELNGSLSAAGVIELAWTMGLIHWEDEPKPGWYDDSDDAVAEEDIFDRYHDEVMAVGVGR  
 KYNDMPPEYGMIDNFAPELTTVYLDQDLTFNVGSREEALTYVDSEPELTFASFDEAAGEWK  
 VTRKAGSAIRVPRRMAMTRFVGGQVPKDFDPAVWGIPADMVDNLDTVLWNIIVCTVDAFL  
 SAGFTPAELLASVHPARVSSTQGTGMGGMESLRGIYVDRI LAEPRANDVLQEALPNVVAA  
 HVMQSYVGGYGQMIHPVAACATAAVSVEEALDKIRIGKSDFVAGGFDALSVEGITGFGD  
 MAATADSAEMEGKIEHRFFSRANDRRRGFFIESEGGGTVLLARGSLAADLGLPVLGVIG  
 FAESFADGAHTSIPAPGLGALGAARDGVESRLAVALRSVGVSADEISIISKHDTSTNAND  
 PNESDLHERIASAIGRADGNPMYVISQKSLTGHAKEGAAAFQMIGLTQVLRSGLV PANRA  
 LDCVDPVLSKSHSLVWLRKPLDLRAKAPKAGLVTSLGFGHVSALVAIVHPDAFYEA VRVA  
 RGAEAADVWRASAIAREEAGLRTIVAGMHGGVLYERPVERN LGVHGDAAKEVEAAVLLDS  
 RARLVDGVLRAEG

>RXN00570 TRANSLATE of: rxn00570.seq check: 2677 from: 1 to: 852  
 TRPRPQEIGNGLVALIFSASGPIAVILAAAAAGNLSPDQTSSWIFGAFLGNGLLTLWLTY  
 MYRSPQAYFWTIPGTIVIGDSLTHLSFAEVIGAYLVTGVVVFALGWTGLIGRIMAVLPPT  
 IVMAMVAGIFLREGLDLIDASVTDPLIALPMVIVFVALSMSPRLASIAPPVAVAAVGTI  
 VAIASGKLASGILDNGIISRPFVTAPEFSFAAIMELVPLAITVVIVQNGQGVAVLKAAG  
 HRPGVNLAAAASGLWSLPMALIGNITTCLTGPTNALIVAGAKSH

>RXN00571 TRANSLATE of: rxn00571.seq check: 33 from: 1 to: 1257  
 TLVPQVYEIVIIYGAVLSAVHEDPTQIGALSPAVAGTLGSYAMIGVMIGALSAGAVGDRLG  
 RRKVMLTAIVWFSVGMALTAFASSIALFGFLRFLTGLGVGMIVATGGAI IAEFAPANRRN  
 LFNAIVYSGVPAGGVLASILALLFEDVIGWRGLFLIGGSPLLFLPLAYFFLPESPRWLT  
 SRGRAADAKALCARYGLPTEEFVVEKQQETKGTGFAGIFSSKYLMTILIGAMSFIGLLS  
 TYGLNTWLPKIMESNGATSHDSL YSLFLNGGAVFGGLIASWFADRIGAKTVITSTFALA  
 AICLGVLPNISSWPMYTAIAFAGVGVLTQVLT YGLTSNFFGTECRAAGVAWCAGFGRL  
 GGIVGPAIGGLIIGAGFGPSSAFLIFAAAAAIGAVCTLLIPRSPAEEVEVKVAQEPLARV

>RXN00590 TRANSLATE of: rxn00590.seq check: 3570 from: 1 to: 1188  
 MADNKNADDSQLVSASTGTPGPGDIAKANAPSLKQAAVTASGRSALMGAI FLMATSAIGP  
 GFLTQTAVFTNQLGAFAFALVLSILIDIAVQLNVWRIIGVSEMRAQELGNTVIPGFGWV  
 LAVLVCIGGVVFNIGNIAGGGLGNALLGWDVKVGGVITAAIAIAIFL FKRLGAALDKFL  
 VVLGVVMILLTVYVAFVSQPPVGSALKNAVLPDTIDWLVTITLVGGTVGGYITYAGAHM  
 LDSGRTGPNNVKAVSNSSITGILITGLMRVVLFLAVLGVVAGGVTLSTTGNPAEAFQHA  
 AGDIGLRIFGAVLWAASISSVIGASYTSATFLVENKPEKKRLQNWVTIIFILISCSVFIM  
 LGTAPAILLVFAGAFENGLVLPVGFTLMIYVAIFRQK

>RXN00661 TRANSLATE of: rxn00661.seq check: 3591 from: 1 to: 690  
 MNPITELLDATLWIGGVPI LWREIIGNVFGLFSAWAGMRRIVWAWPIGIIGNALLFTVFM  
 GGLFHTPQNLDLYGQAGRQIMFII VSGYGWYQWSAAKRRALTPENAVAVVPRWASTKERA  
 GIVIAAVVGTL SFAWIFQALGSWGPWADAWIFVGSILATYGMARGWTEFWLIWIAVDIVG  
 VPLLLTAGYYPSAVLYLVYGAFVSWGFVWLRVQKADKARALEAQESVTV

>RXN00733 TRANSLATE of: rxn00733.seq check: 1945 from: 1 to: 885  
 MSNTAGPRGRSHQADAAPNQKAQNEGPSAKRLEFGILGHDRNTLIFVIFLAVLSVGLTVLG

PWLLGKATNVVFEGFLSKRMPAGASKEDI IAQLQAAGKHNQASMMEDMNLVPGSGIDFEK  
 LAMILGLVIGAYLIGSLLSLFQARMLNRIVQSAMHRLRMEVEEKIHRPLSYFDSIKRGD  
 LLSRVTDVDNIGQSLQQTLSQAITSLLTVIGVLVMMFIISPLLALVALVSIPTIVVTV  
 VVASRSQKLFAEQWKQTGILNARLEETYSGHAVVKVFGHQKDVQEAFFEEENQACV

>RXN00784 TRANSLATE of: rxn00784.seq check: 3499 from: 1 to: 735  
 MSIEFSAPAKMKIEVWSDIMCPFCYIGKKRLDDALSTFDQAGRIEVEYKSFELMPGLETH  
 PLRSDVEYLADAKGMSLEQARQMNGQVQAMAQATGLEMNPDETIAANTINAHRLTHFAKA  
 HGKQQEVAQELFKAHFVDGKNVDDLDVLVSIAAEVGLDASAAREALESVDYTNVQQDVH  
 EARQLGVQGVPPFFVDRKYAINGAQQEEVFTGTVEKAFFEEWAAENPVSPFEVIDGQSCSV  
 DGTCN

>RXN00792 TRANSLATE of: rxn00792.seq check: 6734 from: 1 to: 1197  
 MSQEILSHFAPALERIRSGAVEREQQRALPVEEIKELVELGFTGLRVPEELGGAGASLES  
 VVELLIEIAGADSNIAQALRGHFAFVELLLEAPESEFRTHWLREVATGRLVGNAESEKRG  
 VYGDPTQTFIDEVETENGPIFVLNGTKFYTTGTTFADYTWTALLRNNGQETLVSLPVDL  
 HAPGVDVADDWSGFGQKLTAAGTTTFKDLEVDPRWIIPTDAPTLVWTYLQLSLLTVLVG  
 SAAADEVVVARAQSSSTRNAWNPGVERRSDPAATIAIGDARSRTVIRGALLDATRHVSN  
 AATIVTPEAFNEADAIVAALWPIVSGQALVVTSNVFDAVGASAVLGEHSIDRHWRNVRTV  
 SSNNPVFLAKNAVGEYALNGTPVGTNIGKALSRRPVSLS

>RXN00819 TRANSLATE of: rxn00819.seq check: 3788 from: 1 to: 1329  
 MRDPIQGAVIPSDLFGFAEVLTEAERAVLLETRRVLEEEVKPYINEAWDKAVFPDEIVQP  
 LQDLQLDPPALREAGESVRDIFTGFRNFELARCDINVTYNNASAGLFTACMVGGSP  
 QAQRDLAQIKSGEVKGVFALTEPDHGSIDAGGLATTATKDADTGEWI INGEKRWIGGAST  
 ADLIATFARDTADNQVKCFLVAPQAEGVSMEIIDRKASLRIMQNAHITYNNVRVSGDARL  
 HNINSFKDVSECLRRMRSDVAVMAVGAQAGAYEAAVKYVRSREQFGRPIAGFQLIQEKLA  
 LMLGNLTASLGMVVKLTDDQQQAGIFKEENSALAKMFTSLKLRETASWAREICGGNGIILD  
 NDVARFHADAFAVSYEGTHEINALIVGRXILGXLFLLYXXFEEDLHDYFHHPKPSFSL  
 KTHQPSPARTWAFRSGALSPRRW

>RXN00832 TRANSLATE of: rxn00832.seq check: 2297 from: 1 to: 1050  
 MPFSWLKPIDYARIFVGWASIFIPLITLPSIIEALIVAVILFCAFGVVKMAERLAHIL  
 GDFPGSLILTLISIVIEVILICAVMLGPADSTTAGRDSVMAVSMIIMGLVVGLCLLIGGL  
 RHGSMPHNGVGTPTYLVLIAFVSIAFAVPAFRGEYSTGQALVISTLTAVVYGFFLFRQM  
 GAQAGEFQEVEVAEKADDAKWEVPFRGLILITVLPIVLLSHDMATVMDEVLASLGAPV  
 AMAGLIATIVFLPETITSLKAAWTGEIQRVSNLAHGAQVSTVGLTIPAVLVIGVITGQD  
 VVLGETPINLLLGTITIAVTAIAFSSKKVSAVHGSVLLMLFGVYMMSMFA

>RXN00842 TRANSLATE of: rxn00842.seq check: 5448 from: 1 to: 1200  
 MIIQILRVAFVGIIVGAGFASGQEVQYFVAFGIDGIWGVIVSAVIMSVMALIILQLG  
 SYFNAGEHGEVFRRVSHPVFSKILDIGVVVTLFSTGFVMFAGAGSNLNQWGLPLWIGSV  
 IMVLLVLAAGMLDVKVTTVIGAITPFIIIFITAASIYTLVGNFSSVEQLDSAALEVGT  
 LPHWAVAAVNYVGFNLMVAVSMVAVVIGGSMFNPRVAGRGLLGGLILGLIIISALTIFA  
 TVEEVGQDDMPMLTIINNINPLAGQVMAVVIYGMIFNTALGMFYALGRRLTAKNPQRFRP  
 VYVVTVLIGFVLSFVGFKNLVGYVYPVLGYIGLLIIVMMVAVVRGRVRIYKESERRMRI  
 ADLLQIGHDGALSGAELAVLNQEIQDSNLDEEQIKA AVRK

>RXN00931 TRANSLATE of: rxn00931.seq check: 6454 from: 1 to: 846  
 VKTIEDILTLEEIDRDIYRGPIVIESYLARTFGGQVAAQALVAATHTVDKAFTVHSLHGYF  
 IAPGDPTAPAIYLVDRVRDGKSYVTRSVRGIQDGEVIFSMQASFHRGDEGIEHMDKMRKV  
 PAPDEIKGTVERMPISSRRVLDEWAEWDIRVIPQDQLELSDFTEQAVWIRCTADLPDN  
 PTFHQCSLTYSMTLLHSALVPHPGKMQMASLDHAVWFLRPFRVDEWLLYDQRSPSAS  
 SGRALTHGRLFNQQGDLVAIVNQEGMTRTLHEGAQSI PMRKD

>RXN00934 TRANSLATE of: rxn00934.seq check: 9723 from: 1 to: 1083  
 VRIGMVCPYSFDEPGGVQAHILDLARTFIAQGHEVQVLGPCSADTQVPDFVVRGGGSIPI  
 PYNGSVARLSFGPKMFKAVRTFLREGNFDVLHIHEPNSPSFSMAALRFAEGPIVATYHAS  
 SSGSKLLKAFLPVLSPLMKVRAGIAVSEMARRWQVEQVGGDPVLIPNGVETSMFKAAARQ  
 IEPNDPVEIVFLGRLDESRLKGLDILLRALTRLDPRFTCTVIGGGTPREVAGINFVGRVSD  
 EEKAAAILGRADIYVAPNTGGESFGIVLVEAMAAGCAVVASDLEAFSLVTDSEAAQPAGVL

FKTGSDADLAKKLQALIDDPSSRSTLIAAGLKRANAYDWSTVSTQVMAVYETIAIDKVRL  
G

>RXN00960 TRANSLATE of: rxn00960.seq check: 4118 from: 1 to: 1035  
MARHCCSNRYASTVFSGLIAYGASQALYPWLLKDHQSVTEIDLDAGALQPYFNIEMPPPF  
EVMTALLLAFCLGLGMAVIKSDTLFKVTRELERVVMKTITAFVIPLPLFIFGIFLGMGM  
NGGLEIMSAFGKVLILAVVGTLLEFLAIQFIIAGAVSKKNPWKLFKNMLPAYFTALGTSS  
SAATIPVTYQQTLKNDVDVNVAGFVPLCATIHLGASMMKIGLFTFAVVFMVDMEVGVGL  
SIGFLLMLGITMIAAPGVPGGAIMAATGMLASMLGFNTEQVALMIAAYIAIDSFGTAANV  
TGDGAIAVIVNKFAGKQLHTTSPDEIEEDDRVAFDITPSDVEHHK

>RXN00980 TRANSLATE of: rxn00980.seq check: 2367 from: 1 to: 1794  
MLADAFMIAAAIVAGWPPIAQSAQALRIRMVSIIDLLVVVAAGVAMFINNYWESAATVFLF  
ALGKALERATMNRTRKALSDLVDAAPETATRLNADDSTEVVELWELEPGDIVLVRNGEQI  
PVDGNVIAGVGGIDESNITGESMPAEKGQGSVDYAGTWLRSGVLRVEATGIGSDSTLAKI  
IHRVEDAQDDKARTQTFLEKFSKWYTPGVMIAAAVVGLITWDVELALTLVIGCPGALVI  
SIPVSIVAGIGRAARDGVLIKGGEYLETAAKVDVVVDKTGTLTTRPELTDVEVIEPAY  
SQGEVLELAARAETASEHPLADAIIRGAQDRGLSTTLVEAAENITGRGIIANVDGQAVAV  
GSAELLDHEPDSTRILELNAEGKTAMFVGUNGHAGIVAVADAVRSDSASAIESLHKAGI  
QVVMATGDAHRVAQNVAASKLGVDEVYSELLPEQKLELVRDLQAAGKTVAMVGDGVNDTPA  
LAAADIGVAMGVAGSPAIAIETADIALMADRLPRLAHAVTLAKRTVRTMRINILIALATVM  
VLLAGVLFGGVTMSVGMVLVHEASVLLVISIAMLLLRPTLKDAAQASDIKRSEIQQIA

>RXN01000 TRANSLATE of: rxn01000.seq check: 4854 from: 1 to: 846  
MSTLTSHRTVPAPSSPPARPKNKLARNIVAIVAALIVLIATGTLKIEWNELPQMPAQVWHY  
LELMFSDPDWSKFGRAVQEMWRSIAMAWLGAILCVVSVPLGMLAARGVGPYWLRTVLRF  
VFAVIRAFPEVVIAIILLTVTGLTPFTGALALGISGIGQQAQWYEAIESTPTGPSEAVR  
AAGGTTPEVLRWALWPQVAPSIASFALYRFEINIIRTSVAVLGIVGAGGIGSMLANYTNYRQ  
WDTVGMLLIVVVVATMIVDLISGTIRRRIMKGGASDRVVAPSN

>RXN01002 TRANSLATE of: rxn01002.seq check: 1757 from: 1 to: 804  
MNSDASATTNSWAINFDHVSVTYPNGTKALDDVSLTINPGEMVAIVGLSGSGKSTLIRTI  
NGLVRATEGTVTVGPHQINTLKGKALRDARGQIGMIFQGFNLSESSVFQNVLVGRFAHT  
AWWRNLLGFPTTEHDKQIAFHAEISVGILHKVWTRAGALSGGQKQORVAIARALSQDPSVML  
ADEPVASLDPPTAHSVMRDLENINNVEGLTVLVNLHLIDLARQYTTRLVGLRAGKLVYDG  
PISEATDKDFEAIYGRPIQAKDLLGDRA

>RXN01007 TRANSLATE of: rxn01007.seq check: 4278 from: 1 to: 1707  
VFKKHRHGLGSPETKPRSITRFFTAATAATLAGLAVLSGCTAQPSQAEDNTLTYLEPQFF  
RTLYPPSAGFYPNGSVVNNIADRLLYQDPETLELKPWIATELPEVNEDATEFTFNIRTDV  
TYSDBGTPLTAEENVVKNFDLYGLGDQDRRLTISEQITNYDHGEVVDEDTVRFHFSEPAFGF  
AQATSSFNAGLYADSTLEFANEDFAPGNAQNVIGSGPFVITDETGLTNLTLTAREDYDWA  
PPSREHQGRAKLDAVNYVLAGEESVRIGAIIVAGQGDIARQIEAPVEAHLKDAGIPIISAA  
TNGVNNSFNFRFKNELLSDIRVRQALIHAIIDREKIMRVLFSDSYPLATSVLAQNALGYKE  
QVDAYVYDLKATALLDEAGWTLDSGDMRRKDGELELTFNEALPQPRSREVVTMVQEQL  
GDLGIKVNLPNGDQAAQDADSKDLNKIQVRHTMVGRADYDVLKSQLYSTNRNELLNMTVE  
GETADIGDPHLEELLMAIASSPREEDRAAASAAAQDYITEQAYVLPLFEPPVYGVQPYV  
KGFSPEVIGRPSFYETYIDHSSDHSSEED

>RXN01090 TRANSLATE of: rxn01090.seq check: 2624 from: 1 to: 798  
MALPLPSKSARALVTGASQGIGLAIKDLARYGHNLILVARREDVLKEIAADLEKKHGV  
VEVRPVDLSDEPARKVLIDEIKTREINIIINSAGIASFGPFKDQDWSYETAQFSLNATAV  
FELTHAVLGGMIDRGTAICNVGSAAGNVPIPNATYVLTAKGVNAFTEAMHYELRGTV  
ACTLLAPGPVREAEIPESEKSIVDKVVPDFLWTTYESCSAETLRALSKNQRRVPGPLSK  
AMNFVSSVAPTAVLSPVMGWVYKMG

>RXN01114 TRANSLATE of: rxn01114.seq check: 9460 from: 1 to: 1224  
MNPQDIVICSPLRTPVGAYGGSFTGVPVEELATTVINAVEATGITGDDVDDLILGQASP  
NGAAPALGRVVALDSKLGQNVPGMQLDRRCGSLQAIIVTAAAHVASGAADLIAGGAESM  
SRVEYTVSGDIRWGVKGGDMQLRDLAEARETAGGRNHPIPGGMIETAENLRREYGISRE  
EQDKISAASQQRWGKAADAGLFDDEIVPVTVPKAKRGQEPTIVSRDEHGRPGTTVEKLAA



LRPIMGRQDAEATVTAGNASGQNDGAAVIVTTRAKAEEKGLRPVMRLAGWSVAAVPPET  
MGIGPVPATKKVLDRLGLTLEDIGAIELNEAFAAQALSVLKEWNISWEDERNPLGSGIS  
MGHPVGATGARMVTLAHRMQRENTQYGLATMCIGGGQGLAAVFEKEN

>RXN01139 TRANSLATE of: rxn01139.seq check: 1443 from: 1 to: 954  
MESHDLQQRSYAHNPDPDGHSHDGLGHSHAPSSLKALFAVIFTSIIFLAELIAGLISGS  
LALLADAMHMLSDSTGLIIAAVAMLIGRRARTSRATYGYKRAEVLAAMVNATVVTALSVW  
IVVEAIMRLGKDLEIQTNMLIVAVIGFVTNGISALVLMRHQDGNINMRGAFLHVLSDML  
GSVAVIIAGLVIRYTGWMPADTIASIAIAAIIIPRAFSLLKEALNILLERVPTGAEPAEV  
DAALRKVPVSDVHDLHIWSIDGKEILATVHLVVDSSNQLHSCGVLDRAEAELSGLGIL  
HSTIQLESADHSDHESVC

>RXN01141 TRANSLATE of: rxn01141.seq check: 9956 from: 1 to: 825  
LSTALAGAARYVTSTSNNEPADNTPLTIGYVPIAGSAPIAIAADALGLFKKHGVNVTLLKKY  
SGWSDLWTAYATEQLDVAHMLSPMTVAINAGVTNASRPTLSFTQNTNGQAITLASKHYG  
SVNSAADLKGMLGIPFEYSVHALLLRDYLVSNVADPIADLELRLLRPADMVAQLTVEGI  
DGFIGPGPFNERAISNGSGRIWLLTKQLWDKHPCCAVAMAKEWKAHEPTAAQGVNLALAE  
ASAILSNPAQFDSSARTLSQEKYLNQPATLLDGPS

>RXN01142 TRANSLATE of: rxn01142.seq check: 3960 from: 1 to: 498  
LTARGNIDFGLRSARPSLSKTERADITRTHLEQVGLTDAAERRPARLSGGMQQRVGIARA  
FAIDPPIMLLDEPFGALDALTRRELQLQLLNIWEASRRTVVMVTHDVEAILLSDRVLVM  
SKSPEATIITDIPVNLPRPRHELSEDAVEAETTALRKRLHLLH

>RXN01164 TRANSLATE of: rxn01164.seq check: 868 from: 1 to: 1635  
VTLFVRLAALAVGGLFVFASNEPIGWVAGIVGTALFFISLAPWDLGVPQKRRKKNEPVP  
FLQQMSTGPTVVQGMLLGFVHGLVLYLQLLPWIGEFVGSPLPYVALSVVEALYSIALGAFG  
VLIARWRDWKVLFPAMYVAVEYLRSSWPFDFGFAWVRLAWGQINGPLANLAALGGVAFVT  
FSTVLAAGVAMVVISKKRLAGAIITASVIAIGAVSSLYVDRNGTSDESIEVAIIQGNVP  
RMGLDFNAQRRAVLANHARETLKLDEQVDLVIWPENSSDVNPFSDAQARAIIDGAVEHVQ  
APILVGTITVDEVGPRNTMQVFDPVEGAAEYHNKKFLQPFGEYMPFREFLRIFSPYVDSA  
GNFQPGDGTGVVEMNAANLGRAVTGVMTCEYVIFDRAGRDAIANGAEFLTTPTNATFG  
FTDMTYQQLAMSRMRAIEFDRVVVAATSGVSAIVNPDGSISQNTRIFEATLTESIPLK  
DTVTIAARVGFYVELLLVIGVLAGLFAIRMNSRSKSAKGSARPAQVRVKKVPAKKAATN  
RRKVK

>RXN01168 TRANSLATE of: rxn01168.seq check: 6703 from: 1 to: 810  
MSSEAVDATTLVIIPTYNELENLPLIVDRVRTATPDVHVLIVDDNSPDGTGERADKLAAD  
DDHIFVLHREGKGGGLCAEYMAFGQWGLERDYQVLCMDADGSHAPEQLHLLLAIEITNGAD  
LVIGSRYVPGGRVNVWPKNRWLLSKGGNVYISVALGAGLTDMTAGYRAFRREVLEALPLD  
ELSNAGYIFQVEIAYRAVEAGFDVREVPITFTEREIGESKLDGSFVKDSLLEVTKWGLKH  
RGGQAKELSKEMVGLLNYEWHFKKRNTWL

>RXN01191 TRANSLATE of: rxn01191.seq check: 2562 from: 1 to: 1590  
VGGLVDKLLATPSMRDVVVFALLIVAGGVVSSLGTWWSALMARALEPAIAGLREDVLRA  
AVSLDANTIETAGRGDVISRIADDSREVSTAASVPLMVQAGFTVVISAFGMAAVDWRL  
GLVGLVAIPLYWTTLRVYLPRSGPLYTREREAFGVRTQRLVGAVEGAETLRAFRAEDTEL  
KRIDAASGEARDISISVFRFLTWAFSRNNRAECITLVLIILGTGFYLVNIDLVTVGAVSTA  
ALIFHRLFGPIGTLVGMFSDIQSASASLIRMVGVINAASNQVSGTSPASASTALTFLDVS  
HHYHTAPVIKNASVQLEPGEHIAIVGATGAGKSTLALIAAGLLSPTSQVALGGSSFSNV  
EPEALRQKIAMVSQEIHCFRGSVLDNLRIARPEATDADIHAVLADIGDSWLERLPQGIDT  
IVGDGAFLRLTSVENQIMALARVHLADLAIVILDEATAESGSDHAKQLEDAALKVTENRSA  
IIVAHRLNQAKTADRIIVMDSGEIIESGTHEELRAIGGRYEQLWTAWSAR

>RXN01212 TRANSLATE of: rxn01212.seq check: 3583 from: 1 to: 924  
MPMTTTPAIDVTDLVRTYGDYTAVKGLNFHVQRGEVFGLLGTNGAGKTSTLEVIEGLSAP  
SSGTVRISGLDPVADRAILRPELGIMLQSGGLPSQLTVAETMDMWHGTCTYPRAIKDVLA  
DVDLLHRENVKVGALSGGEQRRDLACALLGDPSILFLDEPTTGLDPESRRHTWQLLLDL  
KQRGVTMMLTTHYLEEAFLCDRIAIMNAGEIAVEGTDELVAREKSIISFVLRGGQVEL  
PVLSGAEIIRDNNHVRIATTTLQQHTLEILTAAETGIALEGFAAKPATLESVFMDIASL  
ENTSLQTA



>RXN01285 TRANSLATE of: rxn01285.seq check: 1049 from: 1 to: 726  
 LNV TIPDNTFTAIIGPNGCGKSTLLRGFSRVLPQHGVLLDGRQLDSFKPKKEIARELGL  
 LPQTSIAPEGIRVYDLIARGRAPYQSLIQQWRTSDEDAVAQALASTNLTELAARLVDELS  
 GGQRQRVWVAMLLAQQTPIMLLDEPTTFLDIAHQYELLELLRAFNEAGKTVVTVLHDLNQ  
 AARYADHLIVMKDGHVHATGTPEEVLTAEMVQGVFGLPCIISPDPVTGTPTVVPLSRSGA

>RXN01298 TRANSLATE of: rxn01298.seq check: 8940 from: 1 to: 930  
 VSTLISEPEVDKLRKRAKRSRTEWWLAAALLAPNLLLLAIFTYRPLLDNFRLSFFNWN  
 SSPTSTFIGFDNYVEFFTRSDTLQVVLNTVIFTACAVIGSMVLGLLLAMLDDQKLFGRNF  
 VRSMVFAPFVISGAAIGVAFQFVFDPNFGLVQDLLGRIGVDSPQFYQNPWALFMVTFTF  
 VWKNLGYSEFVIYLAALQGLNKDLSEAPVDGASAWTRFWKVTLPQLRPTTFFLSITVTLN  
 SVQVFDIIHTMTRGGPLGNGTTTLVYQVYTETFTNYRAGYGATIATILFLLLLIIITVIQV  
 RYMDKENKQK

>RXN01338 TRANSLATE of: rxn01338.seq check: 9102 from: 1 to: 1902  
 KTYTPNPWMLFIRSFDTGIITVAALVAIAIHLILWLALDLDGLAKNWPLIAIVIVGGIPLM  
 WDVLSAIAKTRGGADTLAAVSIITSVLLGEWLVAIIIVLMLSGGEALEEAASRRASGTL  
 ALARRAPSTAHRLLGATILDGTEEIAVEEITVGDVAVLPHELCPVDGEIVAGHGTMD  
 YLTGEPYVVSLSKSGSQAMSGAVNGDTPLTIVATKLAHDSRYAQIVGVLHEAENNRPEMRR  
 MADRLGAWYTVIALALGGLGWIVSGDPVRFLAVVVVATPCPLLIAPVVAIIGAISLAARR  
 GIIVKNPGLMNASGVKTMFDTGTLTGRPVITDIHTAPGVEEDTVLALAASVERYSR  
 HPLADAIREGAKARELHLPDVVEVSEPRPGQGLTGTVEHLVRITNRRSTLEIDPDSKNYI  
 PVTSSGMESVVLVDDKYAALIRLRDEPRASASEFIAHLPPKKHKVDKLMIIISGDRASEVRY  
 LADKVGIDEVHAEASPEDKLNIVNRHNEHGATMFLGDGINAPAMAVATVGVAMGADSDV  
 TSEAADAVILDSSLERLDDLLHISARMRRIALQSAGGMALSVIGMILAVFGFLTPLMGA  
 IFQEVIDVLAILNSARVALPRGAISDFDTQEKVS

>RXN01382 TRANSLATE of: rxn01382.seq check: 7830 from: 1 to: 1092  
 MCTNNTGTSGSTSTAAGTGTANEEGTITAAISYELGTNGYDPMTTTSALTVAANWHTLEG  
 LTEIDPATGEVYAALASALPSADATSLDIKLRDGATFHNGDAVTADDVVSFERVLDPAN  
 NSLYASFIPFIKSVTKKDDTTVTIDLDYATGIISERLAVVKIVPKSVVEADASGFDANPI  
 GSGPYKMTDNGASKVVKFERNDDYNGPRPARAAKMEWQIIPDASTRTNSLQSGSTMAIDS  
 VPYLSIPQLEATSTVESVQGFGLLFAMFSCSEGNPFNDVRNRQAFLYALDMDKIVKTGMS  
 DQATPATSFVQKEHPNYNQASTVYSLDADKAKALFAETGLTSLNLLCTDHDWVKNCTPLI  
 QESL

>RXN01411 TRANSLATE of: rxn01411.seq check: 3735 from: 1 to: 765  
 MLGVGWRIPLMAVPLGLIGWWIRTGAQENVRPASERPEAPIKQALRTEWKMLRVGGFI  
 SCTGLSFYIFTTYMTTFLRSTVGLEGLVLVAGNIIALSMAAIVAPFVGRAIDKFPRRNIM  
 AFATLSTVIMAIIPAYIIAGQGTLTASLIAQVMLGIGAVTANCVTSVMMAEVFQEVTRGTS  
 AGITYNVTYAIFGGSAPFISTALVSWTGSPLAPAVYMIIIALFAFTASRFIPETSPVFVT  
 ATPAIKAPKVLVNPG

>RXN01421 TRANSLATE of: rxn01421.seq check: 1863 from: 1 to: 387  
 MTSKSIISGKRPNLPSLTGARWLAALAVYFLHALVFLSVYPFQQSELFATIHKFVPMQLGS  
 AGVTFFFILSGFLIYWSNSQLKGMKNVLYYCKRRITKIYPMHLIALPMFIEASAKFTTTG  
 ITWVLILRE

>RXN01602 TRANSLATE of: rxn01602.seq check: 2220 from: 1 to: 1530  
 MAKTHIRLQDLSLSYTSTPLITKLNITVSSGQCAVIVGENGRGKTTLRALAREFPPSAG  
 EILTHGTVAIAHQHMPAGDLSVGEICDEAIRDSKNALEELERAGALLETNTAHALDGYQQ  
 ALDAAEVLDANNAEHRLEKALRSFGAITDRSRALSELISIGQRYRVRLACLIGGDADILL  
 DEPTNHLDRGALNYLTEAITSHKGVVLVSHDQALIKDVADFIIDIDSTPDGLPRIYHEG  
 FDSYRRQRSALLETRQDYAAAQTVQQQLQEDLEHARQVRNSSWKPPKGTGKHTRASRAP  
 GVVQALKRAQDALDSKALDVPPAPAPLLPTLKVRPDKPMVDFSDLFVPHRLRLPGSHSV  
 VSGDKIVITGDNGAGKSTLIEVLSGVLTASGVSANHARTGVLGQESLVGEVPSIARDHA  
 VKWGLLSVEESRFALQEFISIGQRRRLDLAMSLAGNPELLLLDEPSNHLSMHLVSALTEWL  
 DTTAAAVIMVTHDRQLLRDTAHRHIELKS

>RXN01604 TRANSLATE of: rxn01604.seq check: 7962 from: 1 to: 648  
MNTPLLRSSGLSIRDTPFADVEIAPDSGLTLLSTGRESQSSSFSLVLSGRMRASGTIEL  
NGEPIKATKLAKHVALAGIPEIDSLERLVTVRTVVREQLAWSSPWYLMVPRDISDSGRWV  
DVEKHLGLNLPKTLIGDLSVLERFKLRALALLARPEAQLLVDDPDQVRSMELEAEVL  
HALKGVAEDLPVVVVSTNPDFDSLADTALTITGAGN

>RXN01722 TRANSLATE of: rxn01722.seq check: 9580 from: 1 to: 1725  
MLSTMQDVPLSLTRILEYGSTVHGDTLITWGGADGIEQAQQTFSAVGARAAALAHALHD  
SLGITGDQQRVASMLYNCAEHMETMFAVACMGAVFNPLNKQLMNDQIVFILNHSEAEVVIA  
DPRMAEQLGELKETPKVRAVVFIPNDFSSAAAHMPEGMKLYSYEALLDGRSTVYNWPE  
QDERTAAAICTSTGTSGPPKGVVYSHRSLYLQSLSLRTTDSLAVEHGETFLCCVPIYHVL  
SWGVPAAAFMSGTPLVLPGLDLSAPTAKIIISTTLPRVAHGVPPTLWIQLMVHYLKNPPER  
MSLRELYVGGSAVPPIVITMWEQRYGVDVVHVWGMTETSTVGTVSRPPSGVSGESRWNYR  
VSQGRFPASLQYRIVNDGQVMASDRNEGEIQVRGPWVTASYFHPDVEKEGGTASTFRDH  
DVEEENDELFTADGWLRTGDVGSVTSDFGLTIQDRARDVIRSGGEWIYSAQLENLIVATE  
EVVECAVIGFPDDKWVERPLAVTMLYPGIERTRETAERLRDQLRDLPLNWMLPEYWTFVD  
EVDKTSVGKYDKKDLRNHLRNGDFEVIKLGPGKEK

>RXN01732 TRANSLATE of: rxn01732.seq check: 6268 from: 1 to: 1050  
MFKLSKPSKSMRVAVSTLAISTLALVGCSSSDESSSSSSASSSSDAASQWPESITLSLVP  
STEGEDLAEALAPLTDYLSENLGIEVNGVVASDYAATVEALGADQAQVIITDAGSLYNAI  
EQYDAQLILRDVRFGATSYSAVAYTNNPDKYCDDAPVAASDYAASDVMMLYCNGIETEGQA  
ATGEGPAALDALEKIESGDKVALQAATSPAGYQYPIVAMQDLGMDTDSAFVQVPVEGNNN  
AVLSVLNGDAEVSFGFWDARSTVLSEAPNAAEDVVAFAYTEMIPNGGVAASKSLPSDLVE  
KLTLMDDYADSSEEAKDVMFDMVGLSDWTADTAQDEITRYGEILKKFSN

>RXN01762 TRANSLATE of: rxn01762.seq check: 8097 from: 1 to: 1536  
MKVNLGIGSYPRRRATVRPESTAIEFEGTSITYGEFSKRVNRLGHALLDLGVAHQDRVAY  
VGFNHPALLEVFFSTNLIGATPVLVNPRLSANEIDYIIQDSGASIVFYGIDLIEHATYLO  
ELHPEIIMVAVEGDEGPGLRRKALIEAASDADIDLEVSDDDLVLMLYTSMTTGRPKGAML  
SHRNLFNFYFNALLSQEIEQGAVLLSTAPLFHIAGLNMTTIPVMMKGGKVIIHREFRAEH  
VLDEIERSKVSESFMPAMIDMLSNHPSFAERDLSSLRAIMVGGSPLSERARLIWQGRDV  
KIVQGFMTETAPGACILEATDTSTHLGTAGRAHFFTDIKLVDPKTGEEVPTGEAGEVLI  
RGPHVMTGYWNRPEDTASALQNGWYHSGDIAIKDEDDGYTIKDKRIKDMYISGGENIYPAE  
VEQALQELEAVLDAVIGVNDERWGETGIAFVSIRESYLTNPPTGPPELRELLGSVLARYK  
LPREIHIIIEELPRNATGKIQLNLRDFTIPVS

>RXN01881 TRANSLATE of: rxn01881.seq check: 7932 from: 1 to: 435  
MANLINLENVSKTWGLKTLTDGVSGLGVQTDGRIGVVGLNGGGKTTLLEVLTGIEKPDQGR  
VSHNSDLRMAVVTQRAELNDDDTVADVVLGPLGLEVFEEWASNATVRDVLGGLGIVDLGLD  
TKVGKPFPPVGEAPTHQPGRRAGSRP

>RXN01936 TRANSLATE of: rxn01936.seq check: 5923 from: 1 to: 1272  
VSFRDIFADTRPLKEPAFKRLWLGNVATVIGAQLTVVAVPVQIYQMTGSSGYVGLTGLFG  
LIPLVIFGLYGGSIADAFDKRIVLICTTIGMCVTTAGFWVLTLGNENIWLINFLSLQQ  
AFFAVNQPTRTAILRSILPIDQLASATSLNMLLMQTGAIVGPLIAGALIPLIGFGWLYFL  
DVVSIIPTLWAVWSLPSIKPSGKVMKAGFASVVDGLKYLQAGQPVLLMVMVLDLIAMIFGM  
PRALYPEIAEVNFGGGDAGATMLAFMYSSMAVGAVLGGVLSGWVARISRQGVAVYWCIIA  
WGAVALGGVAIVVSPGAVTAWAWMFIIMMVIGGMADMFSASVRNAILQQSAAEHVQGRI  
QGVWIIIVVVGPPRLADVHLGWAAEPLGAGWTVLWGGVAVVVLTAICMVAVPKFWKYEKPK  
ITGI

>RXN01946 TRANSLATE of: rxn01946.seq check: 7246 from: 1 to: 1275  
IRKYSRLEEQFQSLGGYEADAEAAQICDNLGLEARILDQQLKTLSSGGQRRRVELAQILFA  
ATNGSGKSKTTLTLLDEPTNHLDAISITWLRDFLAKHEGGLIMISHDVELLGAVCNKIWYL  
DAVRSEADVYNMGFSKYVDARALDEARRRRERANAEEKKAGALKDQAARLGAKATKAAAK  
QMIARAERMIDNLDEIRVADRAANIVFPEPAPCGKTPLNAKGLTKMYGSLEVFAGVDLAI  
DKGSRVVVLGFGAGKTTLKLLAGVERTDGEIGIVTGYGLKIGYFAQEHDITDPDKSVW  
QNTIEACADADQQSLRSLLSFMFSGEQLDQAPAGTLSSGGEKTRLALATLVSSRANVLLLD  
EPTNNLDPIISREQVLDALRTYTGAVVLVTHDPGAVKALEPERVIVLPDGTEDLWNDQYME  
IVELA

>RXN01995 TRANSLATE of: rxn01995.seq check: 3763 from: 1 to: 1338  
MDIRQTINDTAMSRQWFIVFIAVLLNALDGFVLAAMSFTANAVTEEFGLSGSQLGVLLS  
SALFGMTAGSLLFGPIGDRFGRKNALMIALLENVVGVLVSATAQSAGQLGVWRLITGIGI  
GGILACITVVISSEFSNNKNRGMAMSIYAAGYGIGASLGGFGAAQLIPTFGWRSVFAAGAI  
ATGIATITATFFFLPESVDWLSTRRPAGARDKINYIARRLGKVGTFELPGEQSLSTKKAGL  
QSYAVLVNKENRGTSIKLWVAFGIVMFGFYFANTWTPKLLVETGMSEQQGIIGGLMLSMG  
GAFGSLLYGFLTTKFSSRNTLMTFMVLSGLTLILFISSTSVPSIAFASGVVVGMLINGCV  
AGLYTLSPQLYSAEVRTTGVGAAIGMGRVGAISAPLLVGGLLDSGWSPTQLYVGVAIVIVI  
AGATALIGMRTQAVAVEKQPEALATK

>RXN02062 TRANSLATE of: rxn02062.seq check: 5414 from: 1 to: 1170  
MRVGMMTREYPPEVYGGAGVHVTELTRFMREIAEVDVHMGAPRDMEGVFVHGVDPALES  
ANPAIKTLSTGLRMAEAANNVDVHSHWTYAGLGGHLLAARLHGIPHVATAHSLEPDRPWK  
REQLGGGYDVSSWSEKNAMEYADAVIAVSARMKDSILAAYPRIEPDNVRVVLNGIDTELW  
QPRPTFDDAEDSVLRSLGVDPQRPIVAFVGRITRQKGVHELIKAAALFDESQVLVLCAGA  
PDTPEIAARTTALVEELQAKREGIFWVQDMLGKDKIQEILTAADTFVCPSIYEPLGIVNL  
EAMACNTAVVASDVGGIPEVVVDGTTGALVHYDENDVETFERDIAEAVNKMVADRETAAK  
FGLAGRERAINDFSWATIAQQTIDVYKSLM

>RXN02074 TRANSLATE of: rxn02074.seq check: 7807 from: 1 to: 1623  
MRSLLRDIPAVGWLITATIVVRTLVVALVIVGIGLLIDVPSPAHSAMLWWVLGATAAAA  
LLCAEAVLPQIRIRARVERSWRRQLAAKNLELNSSSSDDAQLITLATEATSKASTYTMFL  
GPYFAVFLAPLTVIAVVGAAISWPIAGILCLGLCVIPFVISWAQRMKGAGAGYGRASQ  
LAGVFLESVRTLGTTMMLNAGQRRQIITQRAENMRSQVMSLLYRNQLMILVTDGVFGVA  
TTMVAAVFAIGGFFSGSLTLGQAVALLARLLIDPINRMGRFTFYTMAGKPSLIAIEKA  
LATTFTDQPTQQGQRHDGDLVVNNLKIARDHRDIVHGISFSIPRGSHIAVVGPSGAGKSS  
VALALSGLLEFDGAISLGGHNCEMLDLRASVSFVPQSPTLFSGSIKSNIDLARTGVDSH  
IHAALLGEELPADLVGETGKGVSGGQAARISIRGLVKNAAVIVLDEATAQLDYTNARQ  
VRHLAKSLECTLVEITHRPSEALDADFIIIVLEDGQLTMMDTPSNVSQHNAFFRTAVMEEE  
Q

>RXN02096 TRANSLATE of: rxn02096.seq check: 3261 from: 1 to: 1692  
MGLDVSDEQIEHAARLAQAHDFFIDRLPNKYEEVIGERGLTLSGGQRQRIALARAFLAHPK  
VLVLDDATSAIDASTEDRIFQALREELHDVTILIIAHRHSTLELGDRVGLVEDGRVTALG  
PLSEMRDHARFSLMALDFQDSHDPEFTLDNGSLPSQEQLWPEVSTKQYKILAPAPGRG  
RGMSMPATPELLAQIEALPAATEETRVDAGRLRTSTSGFKLLSLFKQVRWLVAIVALLL  
VGVAADLAFPTLMRAAIDNGVQAQSTSTLWWIAIAGSVVLLSWAAAAINTIITARTGER  
LLYGLRLRSFVHLLRLSMSYFERTMSGRIMTRMTTIDIDLSSFLQSGLAQTVVSVGTLLIG  
VVTMLAITDAQLALVALSVVPIIIVLTILFRRISSRLYTASREQASQVNAVFHESIAGLR  
TAQMRMEDQVFDNYAGEAEFRRLRVKSQTALAIYFPGLGALSEIAQALVLGFGALQVT  
RGDISTGVLVAFVLYMGLMFGPIQQLSQIFDSYQQAAGVFRRITELLATQPSVQIWAPTG  
TLGRLPRSLYCLTTSPSAIQTIRS

>RXN02148 TRANSLATE of: rxn02148.seq check: 4200 from: 1 to: 1143  
VSASRKTLVVNTDFPPRIGGIQSYLRDFIATQDPESIVVFASTQNAEEAHAYDKTLDYEV  
IRWPRSVMLPTPTTAHAMAIEIREREIDNVWFGAAAPLALMAGTAKQAGASKVIASTHGH  
EVGWSMLPGSRQSLRKIGTEVDVLTYSQYTLRRFKSAFGSHPTFEHLPSGVDVKRFTPA  
TPEDKSATRKKLGFTDTPVIACNSRLVPRKGQDSLKAMPQVIAARPDAQLLIVGSGRY  
ESTLRRLATDVSQNVKFLGRLEYQDMINTLAAADIFAMPARTRGGLDVEGLGIVYLEAQ  
ACGVPIAGTSGGAPETVTPATGLVVEGSDVDKLSELLIELLDDPIRRAAMGAAGRAHVE  
AEWSWEIMGERLTNILQSEPR

>RXN02168 TRANSLATE of: rxn02168.seq check: 2810 from: 1 to: 2814  
VSISSLTPLHSFKEPAILYAGQASAWQQVIADSSSEDHITATHLRELLSRRAKTAPFARQ  
ITAIVPGSLARLEELTREDAQIGADIDAQPAVSIPGILLGQIAATRQLRDLGLDVAAASR  
LGHSQGILGVEAVDNEEDVLAFAILLGAAASQFAGKGAHMLSVRGLSREIIQDTIAGVDG  
VEVSLRNARAHFVVSGKPEALKKAAAALQRAADVYNEDINEKRKGGSLAEPKFDYLDVAI  
PFHHSSMQDAADLAVEWATTCGLNVNARALAEAILVNPADWVEQIANLKADYVLSLDAGV  
SRFTAPLLDGRGISLVPAFSAERDNLARPFGFHVPTAEDWSEFAPKLVLKLPNGEHKVLTG  
FSRLTGYSPIVLGAMTPTTVDPEIVAAAANAGHWAEMAGGGQYSEEVFTKNKEKLVSLLK



VGRSAQFNSMFFDRYMWNLQFGAQRIVSKARATGTSINGVVVSAGIPEVEEATELINDLN  
 ADGFPYVAFKPGTVDQIRATLKIADANPETKIIIIQIEDGHAGGHSWVNLDLTLTYAE  
 LRSRKNVVMIGGGIGTPAKAAYYLTGEWSTD LGFPAMPVDGILVGTAAAMATKEATTSPQ  
 VKQALVDTPGVDPHDAGGWVGRGDARGGVTSGLSHLHADMYELDND SAAASRLISSIDSD  
 DYADHREELIEAINKTAKPFFGEVEEMTYAEWIQRWVELAYPTQDPTWDDRFLDLVHRIE  
 ARLNEAEHGAIITLFPDHASVENEEEA VEKLLAAYPQAREIQVSARDAAWFIGLCRKHHK  
 PMPWVPAIDADLARWWGLDTLWQSQNERYGANSVRVIPGPVSVAGIDRVDEPVAELLGRF  
 EAACVDALDGEPEEIFARLNE SKNEREFLLATPHIVWHGNLIDNPAHVLNEGAFELIEED  
 GYWVIRILADSYFDDL PVEQRPYLVQHVDIPVELGDAG

>RXN02233 TRANSLATE of: rxn02233.seq check: 3705 from: 1 to: 1287  
 VLVSTSTWGWTVHGDGKKIEPGAVVAPKERLSWGRITIGIGMQHVIA MFGATLLVPTLTGFP  
 VNTTLLFSGLGITILFLLITRNLPSYLGSSFAFIAPLTATQVHGIGVQIGGILVAGLVLV  
 AIGFVVKAAGKRVIDAVMPPAVTGAIVALIGLNLAPTAAGNFSSQPLVATATLFAILIAT  
 VAGRGMIA RL GILIGVVIGWVFAAITGNLSEGAADTIREAAWFGLPQFHKPEFQLSAILV  
 TLPV IIVLIAENVGHVKAVSEMTGEDLDDLADALIADGFGTTLAGAFGGSGTTTYAENI  
 GVMATR VYSTAAYWVA ACTAIALAFIPKFGALIFTIPAGVLGGACLVLYGLIGMLGIRI  
 WQDNKVN FNPNVNL TMAAVALVAGIGNLT LT VFGVTLEGIAWGSVGIIVLYPIMKRLYLS  
 IGEKNAKF

>RXN02309 TRANSLATE of: rxn02309.seq check: 2713 from: 1 to: 1050  
 MSSGRTVPTRSHGLGKEGVSTTGASQVEFGDPELTARINDAMVQVEELLHTELSSGEDFL  
 VDI VMHLTRAGGKRFRPMFALLASEFGEKPLSENVIKAAVVVEITHLATLYHDDVMDEAS  
 MRRGVPSANARWDNSVAILAGDILLAHASGLMSQLGTDTVAHFAETFGELVTGQMRETVG  
 PRDTPIEHYTNVIREKTGVLIASAGYLGAMHAGAAPEHIDALKNFGAAVGMIFQIVDDI  
 IDIFSETHESGKTPGTDLREGVFTLPVLYALREDTPVGAELRDILTGPLEDDET VNHVLE  
 LLSQSGGRQAALDEVYRYMDIANAELDRLPDSTVKEALRNLATFTVKRVG

>RXN02321 TRANSLATE of: rxn02321.seq check: 7699 from: 1 to: 1629  
 MTISSPLIDVANLPDINTTAGKIADLKARRAEAHFPMGEKAVEKVHAAGR LTARERLDYL  
 LDEGSFIETDQLARHRTTAFCLGAKRPATDGIVTGWGTIDGREVCIFSQDGT VFGGALGE  
 VYGEKMIKIMELAI DTGRPLIGLYEGAGARIQDGAVSLDFISQTFYQNIQASGVIPQISV  
 IMGACAGGNAYGPALTD FVVMVDKTSKMFVTGPDVIKTVTGEEITQEELGGATTHMVTAG  
 NSHYTAATDEEALDWVQDLVSFLPSNNRSYAPMEDFDEEEGGVEENITADDLKLDEIIPD  
 SATVPYDVRDVIECLTDDGEYLEIQADRAENVVIAFGRIEGQSVGFVANQPTQFAGCLDI  
 DSSEKAARFVRTCDAFNIPVMLVDVPGFLPGAGQEYGGILRRGAKLLYAYGEATVPKIT  
 VTMRKAYGGAYCVMGSKGLGSDINLAWPTAQIAVMGAAGAVGFIYRKELMAADAKGLDTV  
 ALAKSFEREYEDHMLNPYHAAERGLIDAVILPSETRGQISRNLRL LKHKNVTRPARKHGN  
 MPL

>RXN02342 TRANSLATE of: rxn02342.seq check: 2806 from: 1 to: 807  
 MNVDISRSREPLNVELLKEKLLQNGDFGQVIYEKVTGSTNADLLALAGSGAPNWTVKTVE  
 FQDHARGRLGRPWSAPEG SQTIVSVLVQLSIDQVDRIGTIPLAAGLAVMDALNDLGVEGA  
 GLKWPNDVQIHGKKLCGILVEATGFDSTPTVVIGWGTNISLTKEELPVPHATSLALEGVE  
 VDRTTFLINMLTHLHTRLDQWQGPSVDWLDYRAVCSSIGQDVRVLLPGDKELLGEAIGV  
 ATGGEIRVRDASGTVHTLNAGEITHLR LQ

>RXN02348 TRANSLATE of: rxn02348.seq check: 8038 from: 1 to: 1884  
 MLNRMKSARPKSVAPKSGQALLTLGALGVVFGDIGTSPLYSLHTAFSMQH NKVEVTQENV  
 YGIISMVLWTITLIVTVKYVMLVTRADNQGGGILALVALLKNRGHWGKFVAVAGMLGAA  
 LFYGDVVITPAISVLSATEGLTVISPSFERFILPVSLAVLIAIFAIQPLGTEKVGKAFGP  
 IMLLWFVTLAGLGIPQII GHPEILQSLSPHWALRLIVAEPFQAFVLLGAVVLTVTGAEAL  
 YADMGHFGARPIRVAWFCVVMPALILTYLGQ GALVINQPEAVRNPMFYLAPEGLRIPLVI  
 LATIATVIASQAVISGAYSLTKQAVNLKLLPRMVIRHTSRKEEGQIYMPLVNGLLFVSVM  
 VVVLVFRSSESLASAYGLAVTGTLVLVSVLYLIYVHTTWWKTALFIVLIGIPEVLLFASN  
 TTKIHDGGWLPLLIAAVLIVVMRTWEWGS DRVNQERAELELPMDKFLEKLDQPHNIGLRK  
 VAEVAVFPHGTSDTVPLSLVRCVKDLKLLYREIVIVRIVQEHVPHVPPEERAEMEVLHHA  
 PIRVVRVDLHLGYFDEQNLPEHLHAIDPTWDNATYFLSALT LRSRLPGKIAGWRDRLYLS  
 MERNQASRTESFKLQPSKITITVGT EHL

>RXN02372 TRANSLATE of: rxn02372.seq check: 3258 from: 1 to: 1887



VPPAPKLAALGLQHVLAIFYAGAVIVPLLIAQSLNLDATTIHLINADLLTCGIATLIQSV  
GIGRHIGVRLPIVQGVTTTAVAPIIAIGLVTDGQGGVASLPAIYGAVIVSGIFTFFAAP  
VFARFLKFFPPVVTGTVLLVMGASLLSVSANDFVNYADGVPAARDLAYGFGTLAVIILAQ  
RFFRGFMGTLAVLIGLVGGTAVAILGDANLDEVGNAEAFDITTPFYFGVPEFNAVAIFS  
MIIVMIITMVETTGDVFATGEIVGKRTRRSVDVTRALRADGLSTLMGGVMNSFPYTCFAQN  
VGLVRITGVKSRWVAAAAAGFMIIILGVLPKAGAIVASIPSPVLGGASLALFANVAWVGIO  
TIAKSDLADSRNSVIVTSALGLAMLVSFRPDVAQAFPEWARI FVSSGMSVGAITAILLNL  
LFFHVGRQSGGQVATSKSGERINLDAVNKMDRTDFVETFAPLFNSKTWPLETAWESQPFA  
NVTELREAIQVAVLTAPLS DREELIHDYPDMAQLILATEEEAATISQDRGSIGLDDDDV  
DQEKLITVTEQYRERFNMPYVAYFDTMDSVDTVVAAGLRRLDNSDEQHRQALSEIIEIA  
NDRFDILLADANPARSAFDRKFTETDFLG

>RXN02395 TRANSLATE of: rxn02395.seq check: 9305 from: 1 to: 1890  
MSTNSGNNLPESQESPEEPHYPHDTHPGLVPGISVDAQRNKFGLDKTVFGVTAALILAFI  
AWGISSPDSVSSVSTMFWSAMTNTGWLLNFVMLIGIGTMLYIAFSRYGRIKLGTDEDEP  
EFSRFSWIAMMFGAGIGVGIFFFGPSEPLWHYLSPPPHTVEGSTPESLHQALAQSHFWG  
LSAWGLYALVGGALAYSSYRRGRVTLISSTFRSLFGEKTEGIAGRLIDMMAIATLFGTA  
ATLGLSAIQVGQGVQIISGASEITNNILIAIIAILTIGFIISVSGVSKGIRYLSNLNIS  
LTLGLVLFVFITGPTLFLNLIPSSVLEYGSEFLSMAGKSLSWGEETIEFQAGWTAIFYWA  
WWIAWTPFVGMFIARISRGRTLREFALITMAIPSFILILAFITFGGTAITMNRENVDFD  
GSSSKEQVLFDMFSNLPLYISITPFILIFVLAVFFVTSADSASVVMGMTMSSQGNPAPNKLI  
VFWGLCMMGIAVVMLLTGGESALTGLQNLTLIAIPFALVLIVMAIAFIKDLSTDPAAI  
RQRYAKAAISNAVVRGLEEHGDDFELSIEPAEEGRGAGATFDSTADHITDWYQRTDEEGN  
DVDYDFTTGKWADGWTPESTEERGEVDAKKD

>RXN02424 TRANSLATE of: rxn02424.seq check: 9493 from: 1 to: 600  
MTNELTLHHISVSQMDNNCYLLAANGNGLLIDAADDAALLKLAEDAGVTITKVLTTTHRH  
ADHVRALPEVLQKTGATHYAPFLEVPALPSAVDVELHHGDSIEFEGHVFPISILRGHTPG  
GAVLTAEIDGKTHLFVGDSLFPGLGKTSSEGDFVRLFNDVKERIFDTYDDDSIVWPGHG  
KETTLGAERPQLEIWWERRW

>RXN02442 TRANSLATE of: rxn02442.seq check: 5164 from: 1 to: 849  
MKFFTDALIVPFDVSFISRALVAGCLAAILCSLIGTWVILRRLTFFGDAMSHGLLPGVAT  
ASLLGGNLMFGAAISALIMSAGVWTSRKSSLSQDVSIGLQFITMLSLGVVIVSHSDSHA  
VDLTSFLFGDILGVRPSDIFIATVGLGLTIFLFHRQFTALAFDERKAHTLGLNPRFA  
HLLMLALIALATVVSFQVVGTLVLFGLLIGPPATAALLVQDKASISLIMIVASLLGCAEI  
YLGLLISWHASTAAGATITLLSAAIFFATLLTKSAISRLNFTA

>RXN02443 TRANSLATE of: rxn02443.seq check: 7945 from: 1 to: 954  
VILKDI FNNGELFGASSAKNFRKLLAVPAVAASLAFGITACSAVDDTPDIVVTNIGDV  
VSHIVGDSADVQVLMKPNADPHSFGVSAQDAAAMEHADLIVANGLGLEEGLQSNVDNAKS  
QGVVPLEVGEHIDVIDYSPGVDPHFWDTPARMIAATEVIEAELIKELDPSLTESITQSA  
QHYREELVALDEEVTELLSGVAPENRKLVTNHNVFGYLASRFNYTVIDTIIIPGGSTLAAP  
SASDLNDISTAIEDNNVPAIFTDTSSPQRLAEVLASNAGIDVQVVSIFTESLTDADGEAP  
TYISMQKINAERIASTLS

>RXN02447 TRANSLATE of: rxn02447.seq check: 8454 from: 1 to: 1095  
TVVPVYLAELAPLEIRGSLTGRNELAIVTGQLLAFVINALIAVTLHGVIDGIWRIMFAVC  
ALPAVALFLGMLRMPESPRLVNQGRYDDARRVMETVTRPERAKAEMDEIIAVHSENNAA  
LPGVKQSSGQASGQVSSKHTHMSIGEVLSNKWLVRLLIAGIGVAVAQQLTGINAIMYYGT  
RVLEESGMSAEMAVVANIAFGAVAVIGGLIALRNMDRLDRRTTFIIGLSLTTFHLLIAA  
AGTLLPEGNSIRPFAMILVVGFLSMQTFNLVAVVWVLAEIFPVRMKGIGTGISVFCGW  
GINGVLALFFPALVSGVGITFSFLIFAVVGVIALLAFVTKFVPETRGRSLEELDHAFTGQ  
IFKKA

>RXN02487 TRANSLATE of: rxn02487.seq check: 2200 from: 1 to: 1704  
MSAYETKEWLQHYPEWTPHSLEYGDTLLDVYDNNLAINADKPATYFFGRSQTYGELDKE  
VRKTAAGLRALGVRPGDHVAIILPNCPOHIAAFYAVLKLGAUVIEHNPLYTAHELLEPFK  
DHGARVAIVWDKASPTVEQLRGQTQLETIVSVNMINAMPPLQRLALRLPIPALRKSRESL  
SGAAPNTVPFETLTSAAMGGDGDVSEPTVTKESVALILYTS GTTGRPKGAQLTHGNLF

FNLLQGKHWVPGLGDKPERMLAALPMFHAYGLTMVGTLSVFIGGEMVLLPTPRIDLIMNV  
 MKKHTPTWLPQVPTLYEKIVDASEKEGIPKGVNFAFSGASTLSQRTVERWEKHTGGRLV  
 EGYGLTETSPIIVGNPMSDHRHQGYVGIPFDTIVRIANPENLDETMFDGSEGEVLVKGP  
 QVFKGYLNQEEATKNSFHGEWYRTGDVGVMEEEDGFIRLVARIKEVITGGFNVYPAEVEE  
 VLAHPDIEDSAVVGIPREDGSENVVAAITLVEGAALDPDGLKEFARKNLTRYKVPRTFY  
 HFEEMPRDQMGKIRREVQAELLKKLGK

>RXN02512 TRANSLATE of: rxn02512.seq check: 4913 from: 1 to: 963  
 MKPKDFCTAENWAENLSALGYLAGWRFVRMLPLPIARRVFDLGADLASKSGKMGQLRAN  
 LARVGAENVTOALVKQATRSYARYWLEAFRLPAIARDPELLARLRKGTVGLDLLDES  
 AGKGVVLTLPHSGNWDMAFLISHHGQFTTVAERVKPERLFEAFVEFRESLGFEVLPLT  
 GGERPPFEKLKERLTSGGIVCLLGERDLRHSVETTTFFGEKTSMPAGPAQLAIETGAALH  
 VVHPWFDDDGWGLSVSDAVTVDNLSDTVQRIAHLFMANITAH PADWHMLQPLWFGDLDP  
 RLKRSREQTNVHKPVALQEDN

>RXN02515 TRANSLATE of: rxn02515.seq check: 4857 from: 1 to: 756  
 MSTLEIRNLHAQVLPSESAEPKEILKGVNLTINSGEIHAIMGPNNGSGKSTLAYTLGGHP  
 RYEVTAAGEVLLDGENILEMEVDERARAGLFLAMQYPTIIPGVSVANFLRSAATAIRGEAP  
 KLREWVKEVRTAQEALAIIDPEFSNRSVNEGFSGGEKKRHEVLQDLLKPKFAIMDETDSG  
 LDVDALRIVSEGINSYKQETEGGILMITHYKRILNYVKPDFIHVFANGQIVTTGGAELAD  
 KLEADGYDQFIK

>RXN02547 TRANSLATE of: rxn02547.seq check: 8918 from: 1 to: 2139  
 LELNNAARLTVDEYPAAREALESAGQRNVEDRTRAVDEFKAADQELSSLSKGSSNIEYRL  
 LQVRENLCQDLGVSPRDMPFAGELIDPNNAEWEPVVQRILGGFAAEMLVPHGLLPRVRDW  
 VNAKHLAALLKFNGVVTTGEYKTSRFPADSLIRKVDVVESPFRDWVNQELGKRFNIRCVR  
 TPEELSALGPRDQGVITILGVRKFAQQTGDPTRWEKDDRRKLGDRSTYRLGSTNDKAVET  
 LRET VKAGKAVVQAADNRIAANRAELRELERQYQASQEILKVSQAQIDVESADAAIAELD  
 RLLEELNNTPEATELSARHEAAKQTLARVSDLLVAAQSEETVASMNLKRAETELKRLESL  
 PVAEVSEEIAREVEKLF LANTRRVHAANVDEQTIALREDLDKQIDANEELRCENQIVG  
 ILRSYIETWPANRADLQAEPEFVGEAINRLGELRSDRLAEFTAKFLGLMNEMSTRNLGQI  
 SRRLRDARREIEERIEPINASLAQSEFNEGRFLHIDIRDQSGPIVREFQOKLDAATSGDL  
 GTSTEKQAFARYALIAEII SKLASHDSADARWRNTVLDTRRHVRFIGLERDSGDATVNTY  
 VDSASLSGGQAQKL VFFCLAAALRYQLAEPGAHYPTYATVILDEAFDRADPAFTRQTMNV  
 FHSFGFHMVLATPLKLIQTLGDYVGSTIVVSYTEKPNQAQGAIQGNSSFSRIEK

>RXN02566 TRANSLATE of: rxn02566.seq check: 3653 from: 1 to: 1209  
 MHASSPQPHQRTRVLSGLIFAQIMVGASNGVTLSMGSLLAHLAAGASWGGSAATLTIG  
 AAIFSIPLARMVSTYDRRTSLSTGMLLGCVGALLAILGAQFGLFPVLLAFLFLGSMASV  
 NLQARFAATDVASEETRGRDLSIVVWSTTIGAIAGPNLFEP SARFSETLGLEQHAGAYLL  
 CLFGQLIAIAVWRFTLPKGLKPEATPNAPTEKKRLTPKALQAITSVATAHFSMVGLMSMA  
 AIHMQHGASLTIIGFTISLHVAGMYALSPVFGLLTDKLG RNVTIYSGFAMLATSAAFLI  
 IWPEPQWAMITSMILLGLGWNLSALVGSSTLLVDATPIHRTYAQGRSDLT MNLAGASGGL  
 IAGPLIAMGGMPLLAGVVLAVALQTVLSFRTRSIEKTPASCF

>RXN02571 TRANSLATE of: rxn02571.seq check: 6786 from: 1 to: 1029  
 VVALTQIVGPSGSLTRELEKRYRETPGAVMLTADPRAHITYLRATVAEELAFGLEQIRGI  
 VPAQMWERVRNIGLLENLLDRAPAQLSGGQTRRLAIGTVAILAAPTMLLDDPLSGLDTS  
 SRAQLITMLESYEGDVIVA AHKRWLDAPTVYLGDELSL PARVEFSGPSRTFSAITGTR  
 GQORRRWWQFNESQPQFQIGPLDITVSAGQVLWLQGPNGSGKSTLLRGLANEPGTEMLQ  
 NPSDQVIDSTVANWVPGSNSEEHPLDLSQRELRLAQCDAA LGNNPEVLLADEPDVGLDVG  
 GRNAIHQRFADFLNGGALILTCHDET FVAEVAEYAI VKEMGL

>RXN02581 TRANSLATE of: rxn02581.seq check: 7801 from: 1 to: 1860  
 MDLDKAIGSFFDENGELNLPFLTLAAMGEFMYQADIAEGGGDKPRMHFWDFSED RDGKL  
 IQYTRNEIDTRIKAVAGRLQQVATLGDR AAILANNSPEYIFSFLGAIYAGMVPVPLYDPN  
 EPGHADHLNAV FADSEPVVLTNSKSAGAVRKHFSSLPAAERPRI LSVDSL PDSLADSYE  
 NPMLTEAGRRLAALRQSAPIDLT AFLQYTS GSTRT PAGVVLTNRSILT NVLQIFSA AQLK  
 TPLRLVSWLPLHDMGII LAAFVTMLGLDNEFMNPRDFVQQPSRWIKQLNRRES DVDVNV  
 YTVVPNFAL ELAARYAKPAEGETL DLSALDAI IIGSEPV TENALTTFREAFEPYGLPVQT

LRPSYGLAEASLLVTTTPQTENRPLISYFDREALAENRVELVEKGNNKAVAFVSNQVAAAP  
 QQLVIVDSETGTELADGQIGEIWTHGENTAAGYLDREEDTAETFRNRLTTRLEENSRAEG  
 AADDNYWMATGDLGVIVDNELYITGRLKDLIVVAGRNHYPQDIEYTVQAASAHIRADSV  
 AFAVPGDDIEKLIILAERD TTANEADDAAAEEAIRSAVGTAGVVP EIRILAPDEIARS  
 SSGKIARRVNQRNYIQEQAN

>RXN02595 TRANSLATE of: rxn02595.seq check: 5016 from: 1 to: 1164  
 VIVVAMASIMACLKAAARLNNPMKILLLCWRDTTHPQGGGSERYLERVGEFLADQGHEVVF  
 RTAGHTDAPRRSFRDGVRYSRSGGKFSVYPKAWVAMMLGRVGIGTF SKVDVVVD TQNGIP  
 FFGKFFSGKPTVLLTHHCHKEQWPVVGRLAKVWGLIESQIAPRAYKTAPYVTVSEPSAE  
 ELIALGVDQQRHIVRNGVDPVPLHTPKLDRDGQHAVTL SRLVPHKQIEHAMDVVAALDG  
 VVLDVVESGWVQKELVDYARTLGVS DRVVFHGQVAEDHKHALLERATIHLMP SRKEGWGL  
 AVTEAAQHGVPTIGYRSSGGLRDSVVDGETGLLVDSKAELISATKTLLIDASLR SKLGAS  
 AKQRAENYKWD TAGAQFEELLGLASKK

>RXN02613 TRANSLATE of: rxn02613.seq check: 5283 from: 1 to: 957  
 MKFKKIALVLAFLGLASCSSASGDPATNADGSIDLSKVTLNIGDQIAGTEQVLQASGEL  
 DDVPYKIEWSSFTSGPPQIEALNAGQIDFAITGNT PPIIGGPTNTKVVSAYNN DALGDVI  
 LVAPDSSITSVADLAGKKVAVARGSSAHGH LIQQLEKAGVSVD DVEINLLQPSDAKAAFQ  
 NGQVD AWAVWDPYSSQAELEGAQVLVRGAGLVSGHGFVASDEALDDPAKEAALADFLDR  
 VADSYEWAEDNTDEWATIFSQESGFDPEASQLNTRSLRHQVPLDESVNTYQNALIDAFVS  
 AGLVEDFN FEDTV DTRFEG

>RXN02614 TRANSLATE of: rxn02614.seq check: 5216 from: 1 to: 729  
 MTATLSLKPAATVRGLRKS YGTKEVLQIDLTINCGEVTALIGRSGSGKSTILRVLAGLS  
 KEHSGSVEISGNPAVAFQEPRLLPWKT VLDNVTFGLNRTDISWSEAQERASALLAEVKLP  
 DSDAAWPLT LSGGQAQRVSLARALISEPELLLLDEPFGALDALTRLTAQD LLLKTVNTRN  
 LGVLLVTHDVSEAIALADHVLLDDGAITHSLTVDIPGDRRTHPSFASYTAQLLEWLEIT  
 TPA

>RXN02638 TRANSLATE of: rxn02638.seq check: 9546 from: 1 to: 876  
 MVKRFGFFVEDSLPKVPLHPEESRET FYGRIIISAVRTVMKAQDVQISIFGAENIPTTGG  
 ALFASTTLVIMTSFWVVS PAFVRGKRLVRFM AKKEIFDTPVVG TLMRWMKHVSVD RSAGA  
 GSMEDARKRLDAGSLVGIFPEATVSR SFEIKELKTGAVRIADSANVPLLPLIIWGGQRII  
 TKDIERDFGRSHIPVFISVGE PVDASGDPDEATERLYEAMKKLLDETRTAYEQKYGP FEG  
 GELWRPKSLGGGAPTLEQAKMLEIAERERRQAKRAAKVAKKRTTFIRKIFKK

>RXN02662 TRANSLATE of: rxn02662.seq check: 3 from: 1 to: 264  
 MRRKLT TTTLENKPGARLGGFRALAPTSKIALV FLLLI FLLAIFAPLIAKYDPLASGTPVQ  
 PPSGEHWFGTDAIGRDIFSRVATAPEPP

>RXN02794 TRANSLATE of: rxn02794.seq check: 5710 from: 1 to: 1074  
 MLLSARTHTSFQELGLNASRRKAINWTLALT VVLIASMFVGV LIGASGTSVFSTWTVISH  
 HLFGTELGGSDTADAI IWYIRTPRVLLAAIVGAGLALAGAIMQVLVRNMLADPYILGVNS  
 GASCGAAAALLFGVGAGFGDYALQGS AFLGAMAASGLIFFVARAAGRISSTRLLMSGVAI  
 GYMLSAATSFLIFSSDSAEGSRSVLFWLLGSLGLAAWNGPMAIIFLIVGIALALLMVLGP  
 QLDALNSGDETALT LGVSPDRLRILLVITCLLVGSMVAMAGSIGFIGLVIPHLARRFVS  
 GKHRLMLPVSALMGAILLIWADIAARTLLAPQEIPIGIIT ALIGAPFLLILVRRMHTY

>RXN02809 TRANSLATE of: rxn02809.seq check: 5264 from: 1 to: 375  
 NLSVPAALTNALS YLSAEWNNKAAGIVSYGSAMGVRAAEHLRGILSELQIAHVQKTGLLS  
 IFTDFEYPNFKPSEQGISSVDAMLEQLV VVWTKAMSTIRESANVYHLRTPHKS GELPDWDS  
 PLFVF

>RXN02836 TRANSLATE of: rxn02836.seq check: 9870 from: 1 to: 555  
 MTIDEGRRQFEVNVFGAMALTRLVLPHMQKQKWTIVNITSMGGKIYTPLGGWYHGTFKA  
 LEALSDALRLEVAPFGIDVVVIEPGGIATEWGGIAADNLD AVSKDSAYKRQADAVSKSLR  
 SEANSNRNSPPSVVADAIGKAVTARHPKTRYAIGFGAKPLIASRNILTDRQFDPVITRAT  
 GVPRD

>RXN02922 TRANSLATE of: rxn02922.seq check: 7833 from: 1 to: 1080



MISPQTIIDNLAPVLAIEAATAAQREQDREFSRDLAKQLSAGGFTKLRI PVEFGGLGFSL  
PEAFEVLVAAAAADSNI AQGLRPHFLAVESLLIAPYSEHRTKWLRKIAEKGVVIGNALTE  
VGNKPGELKTKIRKEGESYVLSDTKFYSTGSLYADWIQVHAKDEEDQDVFAFVDRDASGV  
VLVDYWDEFQQLFASGTSFFEKVVVDPLDIVTRDYTAPSAFQALAQSHHLSTLTGISQA  
ITRDIVTYVQNRTRIFSHGSGDLPRFDPQVQVVEVKAKSYAVEKIFQGFQELDLVVD  
KAKAGTATEVDLAAVDLSAYQAQLAVAPLVLSQATQAFEVGADALNGGHVAAQYTIGSLS

>RXN02923 TRANSLATE of: rxn02923.seq check: 3360 from: 1 to: 738  
LSILLGGTSDIAGEIATLTCHGEDVVLAAARRPEAAQGLAEDLRQRGATSVHVLSEFDAQV  
LDTHRELVKKTQELAGEISLAVVAFGILGDQERAETDETHAVEIATVDYTAQVSMMLTVLA  
DELRAQTTPAAIIVAFSSIAGWRARRPNYVYGSTKAGLDAFCQGLADSLHGTHVRLIARP  
GFVIGSMTTGMKPAPMSVYPRDVAAAVVSAYTSKKRSTTLWIPGRLRVLAWIMRMVPRPV  
WRKMPR

>RXN02929 TRANSLATE of: rxn02929.seq check: 8015 from: 1 to: 1038  
VLKRIFLNPWVATLSVVILGFVVLFSFGSGVIDLSPTAVIRHLSGQDTLTPRDQAIFFD  
IRLPRIIAGVIVGATLAISGASYQAVFRNPLADPYLLGVSAGSGLGVTAVIVGGTVLGF  
APSIGVIGAAAFVGGVAAVLATLMVSRGVGQGSSTTVVILAGVAVAAFASSIQTYYIQRHI  
DTVARVYVWMLGNLNVNWMISIFIVAVVAGLCAAVIMSCARLLDVMAGDVEARTLGVD  
GLVRIGIVIVATLGTAAVVSISGLIGFVGIIIVPHALRLIVGPGHRILLPLSFVWGAIPLV  
LADTAGRTLMAQELPVGVVTAALGAPFFLFILRRTSRQRPKRS

>RXN02933 TRANSLATE of: rxn02933.seq check: 4913 from: 1 to: 810  
MPLSGKIGGFIVAVVFVLAALSFIWTFDPVQAFQERLEGSSLRHLLGTDRYGRDVL  
IMVGSRVTLVGGIIAIAAALIGTPLGIAAGMRRGMVETFMVRGADLMLAFPALLAIIS  
GAVFGASTWSAMVAIGIAGIPSFARVARAGTLQVTSQDFIAAARLSKVSSARIALRHILP  
NITSMILIVQASVAFALAILAEALSFLGLGTTPPDPSWGRMLQTAQASIGVTPMLAVWPG  
AAIALTVLGFNLFGDGLRDAIDPKREVGRA

>RXN02947 TRANSLATE of: rxn02947.seq check: 6735 from: 1 to: 1314  
MTAAQTKPDLTTTAGKLSDLRSRLAEQAAPMGEATVEKVHAAGRKTARERIEYLLDEGSF  
VEIDALARHRSKNFGLDAKRPVTDGVVTGYGTIDGRKVCVFSQDGAFFGGALGEVYGEKI  
VKVMDLAIKTGVPLIGINEGAGARIQEGVVSLLGLYSQIFYRNTQASGVIPQISLIMGACA  
GGHVYSPALTDIFVMVDQTSKMFITGPDVIKTVTGEDVTQEELGGAHMHMATSGTSHYSA  
SDDSDALDWVRELTSYLPNNRAETPRQEAIDIMIGSIQENINDVDLELDTIIPDSPNQPY  
DMKEVISRIVDDAEFFEIQEDYAENILCGFARVEVRSVGIVANQPTQFAGCLDIKASEKA  
ARFIRTCDAFNIPILEFVDVPGFLPGTNQEFDGIIRRGAKLLYAYAEATVGKITVITRKS  
YGGAYCVMGSKDMGAGLV

>RXN02955 TRANSLATE of: rxn02955.seq check: 3206 from: 1 to: 522  
MMNFKSIVCVTAWQVFSRQVLHSPSTWSEELSKLLFVWLSFAGSAFLFGERGHIADVDFIA  
RKLPVSAQRVLQVIVQLLIVVFAILGMIWGGYLAASIAWNQQLTALPLTLGWVYVVIPIA  
GVFIALFAIIDLIEVATGKEEYPLVDESEEPRLDLELEAQSAIDSASSAEGRN

>RXN02966 TRANSLATE of: rxn02966.seq check: 4215 from: 1 to: 1407  
MLFERIYEEGLAQASYFIGCQREGKAIIVDARRDIQTYLDLAAKNNMVISAVTETHIHAD  
YLSGTRELAAATGAEIFLSGEGGADWQYGTGTTLMHNSTIKLGNITITAKHTPGHTPEH  
LSFLITDGAVSKDPGFMLSGDFVFGVDVGRPDLLDEAAGGVDTRFAGAQQFLFHSLEKEQFL  
ALPDHIQVYPGHGAGSPCGKALGAI PSTTVGYEKANAWWAPYLRSDDEAGFVEELLDGQP  
DAHAYFARMKKQNKQGPVAVLSTLSPLVKLEAEVVEKLGSEAVFVDTREQNQVHLGTVVG  
ALNIPRGAKASNFAAWVIDPQKDAQDLIVLAPDANTAADFRDALLRVGIDTVRYFTNSID  
GLPTFVPELISPAELAETNYDALIDIRAKSEFAAGSIPGAQQLSGGSAMWRLNELPAGGT  
LVTFQCQSGARNTVVANALRRAGFTVIELEGSYAAWEKSAANPKNLQTAV

>RXN02979 TRANSLATE of: rxn02979.seq check: 3131 from: 1 to: 234  
MTAPNTLKQTTLSRDEFSCPCSVSKIENKLNGLDGVDAEVKFSSGRILVDHDPKVS  
DLVAVAEVEGYTAKPSAI

>RXN02987 TRANSLATE of: rxn02987.seq check: 9782 from: 1 to: 234  
MTAPATLKNTTLSRDEFTCPSCVAKIENKLNGLDGVDAEVKFSSGRILITHDPQKVS  
DLVTAVAEVEGYTAKPSAI



>RXN02991 TRANSLATE of: rxn02991.seq check: 416 from: 1 to: 615  
MANTVRATVLYDAPGPKGRRFNLIITILTVVLGLALLFWIGSMLSGNGQLDANKWTPFIN  
SQTWTTYILPGLWGTLSAVFSVILALVMGTALGLGRISEIRILRWFCAVIETFRAIPV  
LILMIFAYQMFAQYNIVPSSQLAFAAVVFGLTMYNGSVIAEILRSGIASLPKGQKEAAIA  
LGMSSRQTTWSILLPQAVAAMLPAL

>RXN02992 TRANSLATE of: rxn02992.seq check: 8686 from: 1 to: 222  
IVPLGNTLIALTKNTTIASVIGVGEASLLMKATIENHANMLFVVFAIFAVGFMILTLPNG  
LGLGKLSERLAVKK

>RXN02993 TRANSLATE of: rxn02993.seq check: 5702 from: 1 to: 672  
VAEYVNSIADDDKGWDHPTIEWRESPSAQRETLIQNGEVDMAATYSINAGRSESVNFGG  
PYLLTHQALLVRQDDRIETLEDLDNGLILCSVSGSTPAQKVVDVLPVQLQEYDITYSSC  
VEALSQGNVDALTTDATILFGYSQQYEGDFRVVEMEKDGEFPTDEYYGIGLKKDDQEGTD  
AINAALERMYADGTFQRLLENLGEDSVVVEEGTPGDLSFLDAS

>RXN02996 TRANSLATE of: rxn02996.seq check: 4074 from: 1 to: 669  
MNNNVSDQKLSGKELAALEKQAAKTLELGDKKWLIAAGVVLFAIALVLPHIRGVMGWQVL  
TLNVAEDAGITLGEYGFYWLGTIGVFLSLGTVVFKRTWMAWISWIFSCVTLVFAVFAI  
WMRQTTTSTQVNFVNIGMMLAVIAAILAVWGLSSVILARSQRQMEIAEMRAENPDLDGVA  
ATQRALLEQQQSNPEDNPLLVDRRARIARRREREQDAQGEQA

>RXN03060 TRANSLATE of: rxn03060.seq check: 6265 from: 1 to: 852  
MSNPAASTPANNSDDVAKENWDSSFTPKTDIDSSQPVNNSTGEAAARAVNLYKAYGQGD  
TVTALDHVNVEFEKNKFTAIMGPSGSGKSTLMHCMAGLDAATGGSFIGDSDLRLKDK  
MTSLRRDRLGFIFQSFNLVPTLTASENITLPTDIAGRKIDQSWFDEITSRLGLTERLKH  
PAELSGGQQQRVACARALVSRPEIIFGDEPTGNLDSNSSREVLDIRTAVDQDDQTVVIV  
THDAKAASYADRVIFLADGRIVNQLFDPTIEEILATMNGIEDIA

>RXN03065 TRANSLATE of: rxn03065.seq check: 80 from: 1 to: 393  
MISIGTDLVHISAFAEQLAQPGSSFMVFSAGERRKANERQASRYAEHLAGRWAAKESFI  
KAWSQAIYGQPPVIAEEAVVWRDIEVRADAWGRVAIELAPELAADVRESIGEFSSSLIS  
HDGDYAVERAC

>RXN03079 TRANSLATE of: rxn03079.seq check: 7356 from: 1 to: 1017  
LSRTGVSKPKLTAPVVIIGTLVLLIIAFTASLMLGPVTVPLNELATNPVVTDIRAPRII  
IAALVGAALAVSGAIMQTVFHNPLADPGIVGVSSGAAVAVALVITGASFFGQWTVPFAA  
FVGALVTVAVVYLIASSRAMDGRGADPATLVLVGMAITAFGLAVISSATANAPQDSELRS  
VTFWLNGDLVSRTWEHVGVAIPIIIVGLILAIGGSRDNLNLLLDGSTAQTSGLNVNRARI  
ILLALAALLTATAVAVSGTITFVGLVPHLVRIVLGADHRALLPAAAILGATFVIVSDTV  
ARMIFSPIVLQTVGVVAFVIGSPIFLYLLLSMRKRRGLGL

>RXN03080 TRANSLATE of: rxn03080.seq check: 3725 from: 1 to: 780  
MPQLVEIRDNLNVEFPSRHAVKNVSFSAPAGKVTALIGPNGAGKSTALSIAIGLVESTGEV  
MVGSGSVASKSAKARARLLSLVPQNTRELIGFSARDVVAMGRYPHRRGFAVETDADRRAT  
DDALRAINALDIAEQPVNELSGGQQQLIHIGRALAQDTAVVLLDEPVSAIDLRHQVEVLQ  
LLRARANSGETTVIVVLHDLNHVARWCDHAVLMADGEVVSQGDIREVLEPATLSTVYGLPI  
AVRDDPETSSLRVIPHPNPF

>RXN03081 TRANSLATE of: rxn03081.seq check: 3848 from: 1 to: 459  
MKKSLIAIVASALVLSGCTSDSSDSSGTSGTVETTSITTSVAAADGAFPRVTLDSSIT  
LESKPERIAVLTPEAASLVLPITGADRVVMTAEMDTADEETAALASQVEYQVKNNGRLDP  
EQVVAGDPDLVIVSARFDTEQGTIDILEGLNVP

>RXN03082 TRANSLATE of: rxn03082.seq check: 9827 from: 1 to: 321  
MVMPESAMLTGLIREAGGTPVVDLSLGAAGTITADPEQVVAMAPEIIIIQDFQKGRENFA  
NFLSNPALANVPAIENDKIFYADTVTTGVTAGTDITTGLQQAEMLS

>RXN03084 TRANSLATE of: rxn03084.seq check: 3960 from: 1 to: 918  
MSSRRKLSSALIVLLAAALPLTACSSSSSEEEASTSSATREFTDAHGTTTEVPENPQRVVVL

EPLELDTAIALGITPVGA AVANNVTGIPAYLGVDGIEPVGTVSEPNIEAIAALEPDLILG  
TDSRHAIEIYDRLESIAPTVMFMTTHVDPWKDNVVFIFGDALGKKQESEDLIQGFNDKCEEIK  
SEHDVEGKTVNMIRPRDEQTMSTLYGPTSFAGSSLECAGLTIPDQEWKDDLQADIAPENFM  
LATADYVFTATDVTDENELPEVIRENREQFPSLTLVDTSYWVSGVGPLGGSKVLEDIDA  
FLDAQQ

>RXN03095 TRANSLATE of: rxn03095.seq check: 5530 from: 1 to: 369  
MNADKKMCGMNPDSQYVELAVEVFGLLADATRVRIILALRNSGELSVNHLADIVDKSPAA  
VSQHLARLMARIVSTRQEGQRFYKLTNEHASQLVSDAIFQAEHTIADGQTPPHHRER  
EQS

>RXN03097 TRANSLATE of: rxn03097.seq check: 8524 from: 1 to: 555  
ISASAGAIGWLILEYIFKKTTSLLGALLGALAGLVVITPAAGYVTYLSATIMALIGGICC  
YIVINYIKVKLKYHDALDAFGIHGVGGIIGAVLTAVFQSKKANPDIENGFIYTGDIHIIL  
VQILCVTAVVIFSIVMTFIIAKVIKLITPLSVTEQETNIGLDKIVHGEHAYFEGELNRFN  
KHIRY

>RXN03103 TRANSLATE of: rxn03103.seq check: 5397 from: 1 to: 243  
MSAKRTFTRIGAILGATALAGVTLTACGDSSGGDGFLAAIENGSVNVGTYDQPGGLGRN  
PDNSMSGLDVDVAEYVIQLHR

>RXN03109 TRANSLATE of: rxn03109.seq check: 7721 from: 1 to: 654  
MNVKEVDVEKQKAGRVPGAIARRTVRIVLFVALGAIVIAASLWSILVGQYTIPIRDLPA  
ILASGPTGAQTMAEQVWQIRMPRIVLGLLVGAALGVAGALLQAVFSNPLAEPSIIGVTS  
GAGVGAAVIVFNLTLFGTSTVAVGAFITAVITTILVYQLARSRGRVQVINLILTGIIN  
AVSGALTSVLDLHRADELPRRNIFCRWVPHGSHGARQR

>RXN03110 TRANSLATE of: rxn03110.seq check: 3354 from: 1 to: 1362  
VLIERIYDEDLAQASYFIGCAHNTAVVVDPRRDIAVYLDMAKKNGMEIVGVTEETHIAD  
YLSGTRELAAATNATMYVSGEGGADWQYEFDAERICDGSEIRLGNLVLTAHVTPGHTPEH  
LSFLLKDGAFADPEGFMLTGDFVFAGDLGRPDLDEAAGGVDTRFEGARQMFKSLKEKFL  
TLPDHIQIFPGHSGSACGKALGSVPSTTLGYERQFAWWGKYLEADDEQGFIDELLEGP  
DAPAYFGRMKRQNRQGPAIMGARELLPQLEASDLHDVIVVDTRSADEVHQGTAVAGVNIP  
AGNSMAKFGSWTVDEPKDSRALVLLAASQIGAMEMWDMVRVGDNDVAGFITNFDGVDLV  
APQTVSPDQLDELEYDLLLDVRNRSEVEEGYIPGALHINGASVLWNLEKLPRDGKIVSYC  
KSGTRSSIAASTLRNAGFDVVELQGSYDNWVRHN

>RXN03111 TRANSLATE of: rxn03111.seq check: 3457 from: 1 to: 6036  
LKTLLRAAVAAGAGTNVSDIVERANALLALVADDLIGTLPGFDPVAVANNSEDPAFDTAQ  
SAVSVPGIFVSQIATLDSLEAQRDLVDQAVSSIGHSSQGVLGVLHLLNDATRADELVAIAQL  
IGAAITRTARMTGLIAQGDNPMLSIAGISREQLQQAIDAACAEVPAEIRPVIGLRNSRD  
SYVLVGRPDNDARVVKVIEAMAAKDKKAIEDKLRGGSFAFSRITPLKVQAAFHHPAMNMA  
VEQTVAWATTAGLDVELTREIAADVLVNPVDWVARVNEAYEAGARWFLDVGPDGGIVKLT  
ANILEGRGADSFYVGDAAGQAKIFDAGMAPELPVDYQEFAPRVEHVDGTPRLVTKFTELT  
GRTPMMLAGMTPTTVDPVIAVAAAANGGHWAELAGGGQVTPELLETHIAQLTDMLEPGINA  
QFNSMFLDPYLWKMQIGGKRLVPKARANGASIDGIVITAGIPEKDEAVALVKELMRDGF  
WIAFKPGAIAKQVNSVLAIKEVPELPIIIQIEGGVAGGHHSWEDLDELLIATYGVKVRALD  
NVVLCVGGGIGSPERAADYVTGSWSTSYGLPAMPVDGILVGTAAMATKEATTSQAVKELL  
VSTQGSDEWVPAGGAKNGMASGRSQLGADIHEIDNSFAKAGRLLDEVAGDETAVQARRDE  
IIEAIGKTAKVYFGDIGSMTYEQWLNRYLELSGPVDGQWIDASWAARFAQMLERAEARLI  
EQDHGQFEPSLTVEDGVDKLVAAYPHAATDLLTPADVAVFLGLCRTPGKPVNFVPVIDKD  
VRRWWRSDSLWQSHDDRYTADQVAII PGVVAVAGITKANEPVADLLDRFVDATIERIDEH  
DSRSRDIMGKVLSSPGTFWAGRNIPSVIHSLGHADKWSRSEFEAFHSPTGANLVYEDAHE  
AMLTVPPLAGSTAFGTAEKIRFTSPIDALPSAVPLVTQEDAEAMGELTRIAAGGTLAT  
VNNGTATWETSVDAGVIADYNNVTAGYLPASVVPAPHTAPDVLVGRAPVAFVAVKSAVIP  
GTDSASVVEGMLSLVHLEHHIVLKSVDVPTDGALKVSATADEVVDTDLGRLVIVRAEIDA  
EGNLIATLAERFAIRGRKGNVARTNTSALPTTVDTPRSARAVATVVAPESMRPFAVISG  
DRNPIHVSDVAASLAGLPGVIVHGMWTSAGELIAGAAFNDEQIQTPAAKVVEYTATMLA  
PVLPGEEIEFSVERSAVDNRPGMGEVRTVTATVNGNLVLTATAVVAAPSTFYAFPGQGIQ  
SQGMGMEARRNSQAARAIWDRADAHTRNKLGFSEIVEIVENNPREVTVAGEKFFHPDGVLY  
LTQFTQVGMATLGVAQIAEMREAHALNQRAYFAGHSVGEYNALAAAYAGVLSLESVLEIVY

RRGLTMHRLVDRDENGLSNYALALRPNKMGLTADNVFDYVASVSEASGEFLEIVNYNLA  
 GLQYAVAGTQAGLAALRADVENRAPGQRAFILIPGIDVPFHSSKLRDGVGAFREHLDSL  
 PAELDLVDLVGRYIPNLVARPPFELTEEFVASMAEVVESTYVNEILADFKAAASADKQKLAR  
 TLLIELLAWQFASPVRWIETQDLLIKGLQAERFVEVGVGSAPTLANMMGQTLRLPQYADA  
 TIEVLNIERDRPVVFATDEVVREVAVEETPAAPAETTETPATPATPAPVAAAAPATGGPR  
 PDDISFTPSDATEMLIAIWTKVRPDQMGATDSIETLVEGVSSRRNQLLLDLGVEFGLGAI  
 DGAADAELGDLKVTVSKMAKGYKAFGPVLSDAAADALRRLTGPTGKRPGYIAERVGTWE  
 LGQGWADHVVAEUVVIGAREGASLRGGDLASLSPASASDLDLDAVQAVASRRGVA  
 VSLPSAGGAAGGVVDSAAALGEFAEQVTGHDGVLAQAARTILTQLGLDKPATVSVEDTAE  
 DLYELVSKELGSDWPRQVAPSFDEEKVVLLDDRWDASAREDLALLANSQQLISMSQAQA  
 KLLQHKLNSLDLMISQLGSRTKLLGLRRQCCG

>RXN03126 TRANSLATE of: rxn03126.seq check: 1681 from: 1 to: 894  
 VQEQSKQKDLQADIARITAVKSDTVPNSSQSMFTGAAWNNDIVRGFKQHELWLQLGWQDIKQ  
 RYRRSVLGPLWITITATGVMALALGLLYSVLFKIPAEFLPHVTVGLIWNFISGCIKEGS  
 DIFIDNEGLIKQLPSALSVHVYRLVWKQALFLAHLNVIWVILMMIFPRPLGWDVLLIIPA  
 MFLLVINGVWVVMFFGIIATRYRDVSPLEAGTQLLFYVTPIVWMTSTLQSQSAEIGNRA  
 RLAEINPLYHYLEIVRAPMVGADLPAYHWWIVLAFTFVGLGLALLAMKQWRFRVSYWV

>RXN03132 TRANSLATE of: rxn03132.seq check: 1885 from: 1 to: 420  
 MNVNQQLGARTAMNHPETATVLRISDMVSTETNPRRKSRLQELIYATASAWPHYPIAHA  
 AQAQVQLARPMRVFELQSFEGVKHALHHIDLRPALEWDIMGFPEPDTLPILLSDLRDP  
 YATTAVPPQSTPRSAHRSTH

>RXN03157 TRANSLATE of: rxn03157.seq check: 7995 from: 1 to: 438  
 GHLDIVTRAAAQFSEVTILVTANPNKNSGLFTVAERMDLIRESTAHLDNVKVDTWASLLV  
 DYTTEHGIGALVKGLRSSLDYEYELPMAQMNRRLTGVDTFLLTDEKYGYSSTLCKEVA  
 RFGGDVSGLLPEVVAKAVTEKYSNQH

>RXN03160 TRANSLATE of: rxn03160.seq check: 3585 from: 1 to: 468  
 VNRIAEIARISFGVLGFSAFGGPTAHLGYFRTEFVERRRWLDDRQYSEIVALSQLLPGPS  
 SQVGMMLGYHRAGFSGMAIAWLMFTWPSLALMAAFALLFDATSASWTGLLAAVAVVFK  
 RSHRAWRGSMASSTPGRRPPSGVGLGASRVLGPPQRG

>RXN03164 TRANSLATE of: rxn03164.seq check: 9986 from: 1 to: 870  
 MIYRRVGNISGLKLPALISLGLWHNFGDDKPLSTQRSIIHRAFDRGVTHFDLANNYGPAGS  
 AETNFRILREDLKSHRDELISSKAGWDMWPGPYGFSGSRKYLVSLLDQSLTRLGLDYV  
 DIFYHHRPDPDTPLEETMYALRDIVASGKALYVGISSYGPETAEEAEFMAEEGCPLLIH  
 QPSYSIINRWVEEPGDDGENLLQSAANGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG  
 KSLSEGMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQREYAGALP

>RXN03183 TRANSLATE of: rxn03183.seq check: 124 from: 1 to: 417  
 EAEATAGKFEVQPLVGKDGVGSTLGGYNNGINVNSENKATARDFIEFIINEENQTFAD  
 NSFPPVLASIYDDESLVEQYPYLPALKESLENAAPRPVSPFYPASKAIQDNAYAALNGN  
 VDQATTDMAAIENASS

>RXC00354 translate of: RXC00354.seq check: 80 from: 1 to: 813  
 MGKLLFVDIGGTLLDYSNEVPRSAVDAIRKARAKGHRVYLSSGRSSAEVTSQWLDIGVDGLIG  
 ANGGYVESAQESVFHRRLSGEETHRIVEWLYNRGLEFYLESNNGLYASRGFREASKPVLSRLS  
 EKTDVTVDSDMYPDMFWGASLDRDDVNKISYIFNSQEDLDAAREAFPNEHTTWGGQTGALF  
 GTIGVSVNKKIGVDRLLKYLNADRANTIAFGDSDEDLSLFEASAYGVAMGEATESLKAAADL  
 VTDVAVGQDGLRNAFLKLELIDA

>RXC01748 translate of: RXC01748.seq check: 8341 from: 1 to: 780  
 MADAKKQADKAAKKQVRAAKKAQRKETRSQMWQVFNMQRKQDKALIPLLLAILGIPLVFLIGLIWGG  
 QWWMLPIGIAAGVVAAMFIFTRRVERDVYKRAEGQQGAAGWAVENLRSGVGMTWRTKTAVAVTTQMDAV  
 HRVIGLCGVVLVGEPSHRLKPMQAQKKRLNRVAPGVPVYEIITGNNEGQTPIAKLQRELKLPVPRNYK  
 KNDVAALAAARIEAMDNVGNAPGGSLPKGPLPKGASMSGMNRARRQAERKGEA

>RXC01749 translate of: RXC01749 .seq check: 7382 from: 1 to: 1617



VSFLVENQLLALVVIMTVGLLLGRIKIFGFRLGVAAVLFVGLALSTIEPDISVPSLIYVVGLSLFVYTI  
GLEAGPGFFTSMTKTGLRNNALTLGAI IATTALAWALITVLNIDAASGAGMLTGALTNTPMAAAVVDAL  
PSLIDDTGQLHLIAELPVVAYSLAYPLGVLIVILSIAIFSSVFKVDHNKEAEEAGVAVQELKGRRI RVT  
VADLPALENIPELLNLHVIVSRVERDGEQFIPLYGEHARIGDVLTVVGADDEELNRAEKAIGELIDGDPY  
SNVELDYRRIFVSNTAVVGTPLSKLQPLFKDMLITRIRRGDTDLVASSDMTLQLGDRVRVVAPEKLR  
ATQLLGDSYKKLSDFNLLPLAAGLMIGVLVGMVEFPLPGGSSLKLG NAGGPLVVALLLGMINRTGKFVW  
QIPYGANLALRQLGITLFLAAIGTSAGAGFRSAISDPQSLTIIGFGALLTLFISITVLFVGHKLMKIPF  
GETAGILAGTQTHPAVLSYVSDASRNELPAMGYTSVYPLAMIAKILAAQTLLFLLI

>RXC01971 translate of: RXC01971.seq check: 8803 from: 1 to: 831  
MSKKKPRPIPVPAQFIPGLIDAHTHLASCGLAGLVERAKEAGVEKLCTVGDGLAEAELEAAQQFG  
NVFAACAIHPTKADQLDGAARARLTQMAADPNCVAIGETGLDSYWIKHDPEDTAALDVQEEALRWHIDL  
AISADKPLMIHNREADADLMRVLADAPPPKDTILHCFSSPLDVAKEALDRGYVLSFAGNVTFKRNEELR  
EAARIAPISQILIETDAPYMTPEPFRGSRNEPSLIGHTALCIAEVRGMAVEDVAAALNENFDRVYGVTN  
L

>RXC02697 translate of: RXC02697.seq check: 1664 from: 1 to: 1527  
MTLFQRLTNPVVLGGLAGVLLLLGSFGGGAIRYRGGVLDALGLNFLAFGHAQGISNTVLWVGQLLLIGA  
WVHLGRRLFKKKVADDTADAADLGLVKRTLYAMVVPLIFAAPMMSRDVYSYLMQGAMLRDGFDPYTEGA  
AVNPGPMLLEVSHDWRNTTTPYGPLHLWIGDMITTVVGDNVTLGVVAYKILSIIGLAVTGWSIVRIAQH  
FGANPAIALWIGVANPVMIIHMIGGMHNESELMVGLVSVGLLLALKKRFBVAGVALIAVAVSLKATAAIAL  
PFVWVWIGMHFFAGFLATKKGKDSPTLKQQVPAFFATGAAGVAVTG VVVSAITWASGASWGWISEISGNS  
KVINPLAFPSLVASVITMVAEVFVDDFDYNAVNVVRSISMLIMLGGVVCWWLFRQNERRAVTGTAAA  
YAVAFVFNSTLPWYYASLISLLGTFKPPMWLIRFAAGASVFIALMFTGSGNHQLYNIIVTVIIAAIIAW  
LATVVI FDDTDPATTATEKPSPTVS

>RXS00148 translate of: RXS00148.seq check: 5482 from: 1 to: 2211  
MTSIPNFSDIPLTAETRASESHNVDAKGVWNTPEGIDVKRVFTQADRDEAQAAGHPVDSLPGQKPFMRG  
PYPTMYTNQPWTIRQYAGFSTAAESNAFYRRNLAAGQKGLSVAFDLATHRGYDSDNERVVGDMAGVA  
IDSILDMRQLFDGIDLSSVSVSMTMNGAVLPILAFYIVAAEEQGVGPEQLAGTIQNDILKEFMVRNTYI  
YPPKPSMRIISNIFEYTSKMPRFNSISISGYHIQEAGATADLELAYTLADGIEYIRAGKEVGLDVKF  
APRLSFFWGISMYTFMEIAKL RAGRLWSELVAKFDPKNAKSQSLRTHSQTSGWSLTAQDVYNNVART  
IEAMAATQGHQTQSLHTNALDEALALPTDFSARIARNTQLLLQQESGTVRPVDPWAGSYVVEWLTNELAN  
RARKHIDEVEEAGGMAQATAQGI PKLRIEESAARTQARIDSGRQALIGVNRYVAEEDDEIEVLKVDNTK  
VRAEQLAKLAQLKAERNDAEVKAALDALTAARNEHKEPGDLDQNLKLAVDAARAKATIGEISDALEV  
VFGREAEIIRTL SGVYKDEVGKEGTVSNVERAIALADAFEAEGRRPRI FIAKMGQDGHDRGQKVVASA  
YADLGMDVDVGPLFQTPAEAAARAADVDVHVGMSSLAAGHLTLLPELKKELAAALGRDDILVTVGGVIP  
PGDFQDLYDMGAAAIYPSGT VIAESAIDLITRLAAHLGFDLDVDVNE

>RXS00149 translate of: RXS00149.seq check: 63 from: 1 to: 1848  
LTDLTKTAVPEELSENLETWYKAVAGVFARTQKKDIGDIAVDVWKKLIVTTPDGVDINPLYTRADESQR  
KFTEVPGEFPFTRGTTVDGERVGVGTETFGHDS PKNINA AVLNALNSGTTTLGFEFSEEF TAADLKVA  
LEGVYLNMAPLLIHAGGSTSEVAAALYTLAEEAGTFFAALT LGSRLTAQVDGSHSDTIEEAVQLAVNA  
SKRANVRAILVDGSSFSNQGASDAQEIGLSIAAGVDYVRRLLVDAGLSTEAAALKQVAFRFAVTDEQFAQI  
SKLRVARRLWARVCEVLGFPELAVAPQHAVTARAMFSQRDPWVNMLRSTVA AFAAGVGGATDVEVRTFD  
DAIPDGVPVSRNF AHRIARNTNLLLLLEESH LGHVDPAGGSYFVESFTDDLAEKAWAVFSGIEAEGGY  
SAACASGTVTAMLDQTWEQTRADVASRKKKLTGINEFPNLAESPLPADRRVEPAGVRRWAADFEALNR  
SDAFLEKNGARPQITMIPLGPLSKHNIRTGFTSNLLASGGIEAINPGQLVPGTDAFAEAAQAAGIVVVC  
GTDQEYAETGEGAVEKLREAGVERILLAGAPKSFEGSAHAPDGYLNMTIDAAATLADLLDALGA

>RXS00948 translate of: RXS00948.seq check: 5347 from: 1 to: 1119  
MANVVLVDRMEPLVSKLFTPIQIRDITIPNRVWMSPMCTYSAATGSGLP TDFHQAHYAARAAGGVGLVM  
VEATGVNPVAPISPVDLGLWSDQIEPFSRVTAAIRAGGAVPAVQLAHAGRKASTDAPWNGGGYVGPET  
NGWETVGPSPPLAFPLPAPRELTVSEIQEVVQQFAGAAVRADQAGFDVVEIHA AHGYLLHNFLSPISNK  
RTDSYGGSLNRRARIVLEVIDAIRAVWP EEPVFMRISTTDWVEENPQDDRESWTLSQSRQLALWASEH  
GVDLIDASSGGLDIVPIPHDRDYQTAKAADLHASTGVTVA AVGRIDDAQTAHNLVDSGDVNAVFLGRPL  
LKDP SWANQAALALGAEPYVHQYDYVL

>RXS01166 translate of: RXS01166.seq check: 5407 from: 1 to: 1305  
MGYTNLNDTRVLRAGSCDAWRTMSPLVQQGSEAVFRRIMGLSRPDRKPGFDDVPHFGAAVRVPGLKH  
GTLVNAAPLKVLGARGEPNPASSYRFEYITGDSAGRAITATGAVLFSTRPWT TGPRPAIAMAPSTQGVA



QHCDPSHTCAIGLNAFYDKPFDAL IAYELPVILWFLAHGLDVVFIDYPRDPATGVQYYCDSIAAAKSL  
DAVLASRQLGLSPEAPLGLWGFSQGGGATGWAAQLQDYAPDVRPKAAVVGAPPVDLFRVLDTVDGGLLT  
GVIAYAIAGLAVNSSEMFEIIMSVLNERGVSDVLKNITSCAGGSLLASGYSSSRGWTHQGTPLADILDD  
LPLVVAEFGKQKLGRVAPEIPVLLWGSKNDDVIPIDPIRELRDSWADKGTPLTWHESQAPRVPGRTGLN  
HFGPYFRNLEKYSGWLIDHLV

>RXS01746 translate of: RXS01746.seq check: 830 from: 1 to: 753  
MTAPRDPFFPADLSIRASAEPIEIQRGLIDYQEAWDYQAELATRRANDEIPDQLLILEHPSVYTAGKR  
TQPEDLPTNGLPVINADRGGRTWHGPGQLVIYPIIKLADPIDVDYVRRLEEALIQVVGDMGVAGAGR  
IDGRSGVWVPAHDGWVDSKVAAGIRITRGVAMHGVAINCNNTLDFYEHIIPCGIADAGLSTLSRELKR  
DVSVEELVEPSIRALDDALAGRLVVSDFSGSAPDPTKNLPKRG

>RXS01747 translate of: RXS01747.seq check: 6480 from: 1 to: 1044  
VTIAPEGRLLRVEARNSETPIETKPRWIRNQVKNQPEYQDMKERVAGASLHTVCQEAGCPNIHECWES  
REATFLIGGANCSRRCDFCMINSARPEPLDRGEPLRVAESVREMQLNYSTITGVTRDDLDDEGAWLYSE  
VVRKIHENLPHGTGVENLVPDFSGKKDLLQEVFESRPEVFAHNVEVPRIFKRIRPAFRYERSLDVIRQA  
RDFGLVTKSNLILGMGETKEEITEALQDLHDAGCDIITITQYLRPGPLFHPIERWVKPEEFLEHADA  
EMGFAAVMSGPLVRSSYRAGRLYAQAMEFRGEEIPAHLAHLKDTSGGSTAQEASTLLERYGASEDTPVV  
SFN

>RXS01879 translate of: RXS01879.seq check: 6847 from: 1 to: 933  
VKITAKAWAKTNLHLGVGPAHDDGFHELMTVFQTDIDFDTVTLTTLDEELVEEGSVVKQLSVTGARGVP  
EDASNLAWRAVDALVKRRAEKTPLSAVSLHISKIPVAGGMAGGSADAAATLRAVDWIGPFGEDTLLE  
VAAELGSDVPFCLLGGTMRGTGRGEQLVDMLTRGKLHWVVAAMAHGLSTPEVFKKHDELNPESHMDISD  
LSAALLTGNTAEVQWLHNDLTSAAALSLRPELRSVLQEGIRSGAHAGIVSGSGPTTVFLCESEHKAQDV  
KEALIDAGQVYAAATATGPAASTADQRGHILTVS

>RXS02023 translate of: RXS02023.seq check: 8728 from: 1 to: 768  
MAPKQTPSPEKNRNLVGPVLQRRQTEGTFDQRLLEMRADHNWKHADPWRVLRISQSEFVAGFDALHEMPK  
AVTVFGSARIKEDHPYKAGVELGEKLVAADYAVVTGGGPGLMEAPNKGASEANGLSVGLGIELPHEQH  
LNPYVDLGLNFRYFFARKTMFLKYSQAFVCLPGGFGTLDELFEVLCMVQTKVNPFPVILIGTEFWAGL  
VDWIRHRLVEEGMIDEKDVDRLMTDLDLQAVKFIVDAHAGLDVARLHN

>RXS02106 translate of: RXS02106.seq check: 9598 from: 1 to: 1056  
MNNHFELKVPGGKLVVDVTTDLDSIADVKGISGDFLEPDEAFFALGRALQGASVGDNTDRLQAKLDAA  
LAEYDDVELHGFSTADIALAVRRRAVTGAQDFTDYEWELHHPGVLPPLNVALDELLEDQVQASGQRGPTM  
RIWDWDDRATVIGSFQSYVNEINQEGVNEHGVTVVRRMSGGAMFMEGGNCITYSLYAPESLVAGLSYE  
QSYEYLDWRVIAALKTHDWDVAVYVPINDITSTGGKIGGAAQKRRSGAVLHHVTMSYDIDADMMTQVLRI  
GKVKISDKGLRSKRVDPRLRRQTGASREQIIDTLKSTFSARYGAQEVELSDEDEFAAGHDLVKTKYATE  
EWTKRVQ

>RXS02228 translate of: RXS02228.seq check: 9755 from: 1 to: 903  
VVTPIAVVGPTASGKSALGIALAHKLDGEVVNVDSMQLYKGM DIGTAKLTVEEREGIAHHQLDWDVTE  
TASVARFQSDAVADVEDIMSRGKTPILVGGSMLYVQSLVDDWQFPPTDSAVRARFEARLADIGVEALHA  
ELTQLDPEAAAVIESNDPRRTVRALEVIELTGQPFQASQPPKDAPPRWGTRIIGLKTTPPEWLNPRIEQR  
TARMFEQGFVAEVEHLVQQGLIADSTAGRAIGYSQVLAAMAGEMTWEDAFERTVTGTRRYVRRQRSWFN  
RDHRVSWVDASGDPTAQALEILGLQ

>RXS03212 translate of: RXS03212.seq check: 3878 from: 1 to: 1452  
ASLNWSVIVPALVIVLATVWVGIGFKDSFTNFASSALSAVVDNLGWAFILFGTVFVFFIVVIAASKFGT  
IRLGRIDEAPEFRTVSWISMMAAGMGIGLMFYGTTEPLTFYRNGVPGHDEHNVGVMSTTMFHWTLHP  
WAIYAIVGLAIAYSTFRVGRKQLLSSAFVPLIGEKGAEGLGKLIDILAIATVFGTACSLGLGALQIG  
AGLSAANIIEDPSDWTIVGIVSVLTLAFIFSAISGVGKGIQYLSNANMVLAALLAIFVFFVVGPTVSILN  
LLPGSIGNYLSNFFQ MAGRTAMSADGTAGEWLGSWTIFYWAWWISWSPFVGMFLARISGRSIREFILG  
VLLVPAGVSTVWFSIFGGTAIVFEQNGESIWDGAAEEQLFGLLHALPGGQIMGIIAMILLGTTFFITSA  
DSASTVMGTMSQHGLEANKWVTAAGVATAAIGLTLTLLSGGDNALSNLQNVITIVAATPFLFVVIGLMF

>RXS03220 translate of: RXS03220.seq check: 3878 from: 1 to: 960  
MGLREILSSKWLVRILLVGIGLGAQQLTGINSIMYYGQVVLIEAGFSENAALIANVAPGVIAVVGAFI  
ALWMDGINRRRTTLITGYSLTTISHVLIGIASVAFPVGDPLRPYVILTLLVVVFGSMQTFNLVATWVML

SELFPLAMRGFAIGISVFFLWIANAFGLFFPTIMEAVGLTGTFMFAGIGVVALIFIYTQVPETRGRRT  
LEEIDEDVTSGVIFNKDIRKGKVH